Contact: **email**: LLoL@balospe.com; **iPhone**: +1(608)556-5594 for Facetime
mail: Unit 300, 6907 University Avenue, Middleton, WI 53562, US, ZoE

Resumé of **L**_aurence_ **L**_oewe_ **o**_f_ **L**_aodicea_ **LLoL**
**D**atageddon _**A**rmageddon_ _**R**esearch_ _**L**ab_ **DARL**

Mission: avert accidental nuclear winter and all other forms of human self-destruction by scaling up a _gentle kind reasonable_ ResearchCity based on sound science, as inspired by YHoWaaH\\Yah\\Allah\\Reality\\God in a funny, nonviolent re-reading of the _Revelation_ of YhowShua \\Yas \\Isa \\Jesus who invites all Real Quests for Real Answers, especially on how to improve true Jubilees [Leviticus 25].

Vision: a proper Jubilee-based innovation economy that celebrates a real Great Jubilee Race every 50 years, supported and organized by ResearchCity for all via _gentle kind reasonable_ life-giving decision-support for everyone – as originally envisioned by Yah & Yas [Luke 4:18].

Problem: Many accidents don't happen by accident. They only become inevitable after data to avert them is lost. LLoL's _Datageddon Armageddon Research Lab_ found that **humanity is sleep-walking into its _Great Filter Tribulation._** This Armageddon combines existential threats of the _Great Filter_ (see science) and the _Great Tribulation_ (see prophets).

Solution: LLoL is calling all to decide in "LLoL's wager". It's a decision like in Pascal's Wager, only for _this_ world. **Choose**:
(0) Death by default: do _nothing_ ➔ nuclear roulette … kills all.
(1) Escape to Life: scale up ResearchCity to serve Reality in all for ~$8/person/year, using big-tech scalability for all.

How? Build on Yah's good sense of humor. Leverage synchronicity in an anthropically supercharged universe. It led Loewe to identify with Laodicea's challenges. Hence LLoL …

Box **B0**

… is defined by _**data too disorganized to avert disaster**_. Thus it always triggers its Armageddon-disaster – unless _gentle kind reasonably_ resolved in time. Datageddons self-organize by _incurious ignorant indifference._

About LLoL as a researcher

-2002 Dr. _rer. nat._, Tech Univ Munich
2003- Postdocs, Univ of Edinburgh
2011- Bad Ass. Prof., UW-Madison
2020- DARL to avert Armageddon

LLoL set his career aside to bring all a chance for true Jubilees by scaling up a true ResearchCity in 7-8 stages to avert existential disasters.

Older work is at **Google Scholar**:
https://scholar.google.com/citations?user=lBchRzQAAAAJ
Web.Archive.Org has more.

For more biographical notes, see the CVs attached below, the various open letters, the BizCard, and other docs in LLoL's Good News Pack MMv2 as published at **https://Balospe.com/en/gnp**

My **w**_ide_ **i**_nterdisciplinary_ **d**_iversity_**-e**_ncouraging_ **wid-e r**esearch marathon demanded all my attention, so I can't offer "proper websites" until I get to reconstruct them. These **links from before 2020** show: I am a serious scientist with expertise in evolutionary genetics, systems biology, computational modeling; I work to rearchitect an Evolvix compiler for biodata with the mission to simplify accurate modeling and the vision to improve _gentle kind reasonable_ life-giving decision-making. See:

1. Brief CV, research interests & old **lab**: https://web.archive.org/web/20230401082649/https://genetics.wisc.edu/staff/laurence-loewe/ - more at: https://web.archive.org/web/20191227000238/http://evolution.ws/people/loewe-lab/members/members/loewe-laurence

2. Best Evolvix vision talk 2013 http://www.birs.ca/events/2013/5-day-workshops/13w5080/videos/watch/201305280834-Loewe.html - Prototype Evolvix: https://web.archive.org/web/20191218173506/http://evolvix.org/

Supporting Document

SD9 Transparency Pledge – on Birth Photo of ResearchCity

Internal Item ii_of_LLoL

FILED
03-22-2024
CIRCUIT COURT
DANE COUNTY, WI
2024CV000867
Honorable Ann Peacock
Branch 12

STATE OF WISCONSIN CIRCUIT COURT DANE

Wintrust Mortgage, Barrington Bank & Trust Co., N.A. vs.
[redacted] Loewe [redacted] **solely responsible**
Laurence

Electronic Filing Notice

Case No. 2024CV000867
Class Code: Foreclosure of Mortgage

The officially named 1st party (my wife at the time) was NOT responsible for this court action at all. So she is to be left in peace from all inquiries. **LLoL**

This is an internal Photo from the complex, drawn-out process leading to the Birth of ResearchCity

LAURENCE LOEWE
~~5611 SANDHILL DRIVE~~
MIDDLETON WI 53562

Notes on this metaphor: It's obviously abstract, yet still instructive because
- *Every birth is messy and complicated – so is sorting through the data here.*
- *Most pictures of actual births are not beautiful – same for the data here.*

Why then still show it? – Its my way to pledge future transparency in Reality:
- *Everything about ResearchCity MUST be transparent or else it will fail.*
- *Transparency must include its beginnings lest conspiracy theories kill it.*

Therefore, I, Laurence Loewe of Laodicea herewith pledge at my own expense to be as transparent as possible to simplify global decisions at Datageddon **LLoL**

If a man would trade all the wealth of his house to give love for life a chance, all his buzz would be declared to be utterly crazy.

LLoL's deex of Song 8:7

But what is the house of a fool worth, when he is likely to die in an accidental nuclear winter he could prevent if he cared?

Case number 2024CV000867 was electronically filed with/converted by the Dane County Circuit Court office. The electronic filing system is designed to allow for fast, reliable exchange of documents in court cases.

Parties who register as electronic parties can file, receive and view documents online through the court electronic filing website. A document filed electronically has the same legal effect as a document filed by traditional means. Electronic parties are responsible for serving non-electronic parties by traditional means.

You may also register as an electronic party by following the instructions found at **http://efiling.wicourts.gov/** and may withdraw as an electronic party at any time. There is a $20.00 fee to register as an electronic party. This fee may be waived if you file a Petition for Waiver of Fees and Costs Affidavit of Indigency (CV-410A) and the court finds you are indigent under §814.29, Wisconsin Statutes.

If you are not represented by an attorney and would like to register an electronic party, you will need to enter the following code on the eFiling website while opting in as an electronic party.

About this access code:

Pro Se opt-in code: 85090c

Use this code to gain access to hundreds of pages of Background material, generated in my struggle to find the most concise way to explain my discovery. It documents the latter stages of my Mercator to avert Armageddon, & is organized like a grave...

The case is now closed, so this code serves as a way for interested parties to see that not AI but I myself, LLoL, produced the files of my Good News Pack and that I am serious about being as transparent as possible.

Unless you register as an electronic party, you will be served with traditional paper documents by other parties and by the court. You must file and serve traditional paper documents.

Registration is available to attorneys, self-represented individuals, and filing agents who are authorized under Wis. Stat. 799.06(2). A user must register as an individual, not as a law firm, agency, corporation, or other group. Non-attorney individuals representing the interests of a business, such as garnishees, must file by traditional means or through an attorney or filing agent. More information about who may participate in electronic filing is found on the court website.

If you have questions regarding this notice, please contact the Clerk of Circuit Court at 608-266-4311.

To avoid confusion with more mature documents, I will label as

Internal Item ii_of_LLoL

all Documents solely shown to offer the best-I-can-do transparency. **LLoL**

Dane County Circuit Court
Date: March 25, 2024

I offer this access in the interest of full disclosure.

SD9-ii_of_LLoL-iv_LLoL_OOv2r1_2025m01d30+m12d03

None of these files can replace talking to me!
So, call me if you care to avert Armageddon!

This form shall not be modified. It may be supplemented with additional material.

Summary: In my very imperfect attempt to explain to a local court & bank why they ought to please give my marathon a bit more time to save their world too, I submitted tons of exhibits & pleadings to delay forced foreclosure. See web at https://wcca.wicourts.gov/caseDetail.html?caseNo=2024CV000867&countyNo=13 – I failed. To save my research I sold to a gracious last minute home buyer. I since ran down proceeds of that sale to allow You to give ResearchCity a chance.

Datageddon
Armageddon
Research
Lab Loewe

Sole Proprietorship of
Laurence **L**oewe **o**f **L**aodicea
email for this correspondence: Laurence.Loewe.[redacted]
email for general LLoL enquiries: LLoL@balospe.com
other emails: Laurence.Loewe@gmail.com
text & cell: +1(608)-556-5594

DARL Loewe
~~5611 Sandhill Drive~~
Middleton, WI
53562
US

Wintrust Mortgage Assistance
9701 W Higgins Rd, Suite 400
Rosemont, IL 60018

Forbearance request
Middleton, March 31, 2023

DARL Mission:

Pioneer the ground-breaking research required to re-architect ***Evolvix*** *into a* ***century-stable extensible humane computer-language*** *for biodata science to save the world from urban and suburban datageddons that cause Armageddons.*

Why ... **of Laodicea**?

Because the ancient city of Laodicea is a terrifying example of what happens when cities ignore their datageddons.

Why **LLoL**?

Because FUN and humor are survival-critical when fighting Armageddons via research on datageddons that cause Armageddons. How else can one bear to look into averting doom?

Dear Wintrust Mortgage Assistance Team,

Thank you for your extraordinary patience with my complicated situation and for your kind calls to offer assistance in exploring how to avoid foreclosure of my dream home on 5611 Sandhill Drive. Reviewing my current personal and broader context helped me to gain more clarity on what I may sensibly ask for in order to serve your interests as well as my own in a win-win. On 2023-03-24 I emailed ("background to my struggles with providing the hardship documentation") in an attempt to explain why I find it so challenging to explain my hardship. Given the limitations defined in that email and after drafting 5 longer responses, I will here try to provide you with a "just" and "brief" overview of my situation. Please let me know which additional explanations and background would be helpful.

Please grant me forbearance until my sole proprietorship DARL can kick off my innovative **crowdfunding campaign to fight the "datageddons" of humanity**. My research shows how these datageddons (i.e. "data too disorganized to avert a disaster") are a major source of unnecessary frustration both in my life and worldwide. I spent the last few years on developing a conceptually workable solution for how to organize the research data required for innovation in order to empower an organization of volunteers and professionals by matching their skills to the most urgent tasks. My fast-moving concept initiative will scale up in 5 stages to eventually serve a global audience. My "**breakthrough point**" is key (as I mentioned on my Wintrust forms). Once its website and online shop goes live, I'll know quickly, if it works by how many people would like me to direct my attention to one or more of 12 projects, symbolized by 12 digital art/ebooks I will sell (1-8). If I can excite a global audience for the idea of creating an "overnight unicorn" from that revenue in order to play in the big-tech league (with my brain) but serve everybody (with my heart), then my ideas will have passed the hardest test I can think of. My low-end for clear success is defined by the funds I need for my scale-up stage 1 (pay all my debts and hire a few people). Clear failure would be if I can't raise the funds to repay all my debts and pay my own salary for 2023-2024. In that case I'll accept the loss of my home as collateral damage for the opportunity of testing my "breakthrough point" model. *Therefore I will not stop working on my breakthrough point strategy until I have given it the best shot I can.* **Given how close I am, I guesstimate I'll succeed more likely than not by Q2/2023; I'm certain my window of opportunity to implement this will be gone if I haven't succeeded before Dec 2023.** Since you are charged with ensuring Wintrust will get paid and I have the same goal, how you will use your discretionary freedoms depends on: Is my analysis correct enough? Do I explain it well enough? Can you follow my logics enough to agree? Hence, **my epic struggle to balance "justice" and "brevity"**: what good is my explanation of hardship if it's too hard to read, or if it's brief but nonsense? Some say: "*Long explanations are likely wrong.*" – I can see why. But I can also prove: "*Not all long explanations are wrong.*" Failing to see *why this matters* is a datageddon that is about to inflict an avoidable final global Artificial Intelligence Armageddon (see *Appendix on AI*). Sorting *true* from *false* in long AI explanations is a datageddon that may trigger the last Armageddon of Earth. If I fail, I risk to self-inflict eviction from my home. If all like me desert, humanity will self-inflict eviction from Earth.

Distilling my tons of lines of evidence into a one number, I guesstimate: ~99% is my prior probability to succeed before Dec 2023, but if you can't see why, I may as well answer "42". Hence, my hardship to explain my hardship. Drawing from my 5 longer older drafts, I hope to next present details on my breakthrough point that may interest you as a bank in how to assess the credibility of my assertions.

Practically, once my digital art collection goes online, the revenue will flow initially from my payment provider to my sole proprietorship. It will pay my debts and other startup costs until legal consulting helps me to set up an LLC charter implementing a *gentle kind reasonable* process that evolves open self-imposed standards for an "LLCC". I define it as a **Limited Liability Charitable Corporation**. It aims to evolve innovation on how to *gentle kind reasonably* improve corporate and global social responsibility through transparency – without loss of scalability of its ***w****ide* ***i****nterdisciplinary* ***d****iversity****-e****ncouraging* (***wid-e***) efficiency. Such *wid-e* approaches are pivotal for stimulating an innovation economy that can remain stable and grow at the same time in order to better develop the mental wealth of the nations. In recent years I uncovered a most unexpected model for such an innovation economy. It features results from my *wid-e* research marathon into how pandemics arise and how to stop them. It defines **7 Change Stages** for tech adoption, tracked in history. It's the best shot I see on how to keep big-tech from destroying its own innovations – and the rest of the world along with it.

My new take on crowd-funding aims to empower an initiative to combine the best of many worlds into a *gentle kind reasonable* global voice for supporting big and small decision-makers with *wid-e* results to avert disasters if interested. How else can we efficiently deconstruct the worst datageddons of Earth in order to avert their respective Armageddons? – But wait: *Don't enough other initiatives already try to save the world*? Maybe. I don't aim to replace. I aim to fill gaps. I best start with the most glaring: a datageddon unifying fighting force. My model, uncovered accidentally, survived countless stress-tests on my *wid-e* pandemic research marathon since 2020-03-27. **I tried my best to prove it wrong, but the harder I tried, the stronger and more refined this model became.** I said, surely, I can't be the first to see this, given its general and deep implications. But despite searching wide and far, and amassing a whole "wall of datageddon" (see my *Appendix AI*), I cannot find anything like it adequately explained anywhere. I still can't believe I'd be the first. I know how hard it is to prove or disprove prior art, so my breakthrough point aims to raise the funds and attention required for a ground-breaking *wid-e* review by the world's best scholars. In my view, I owe as much to the pioneer of that model, to history, and to the future of humanity. In other worlds: if true, I owe you such a public test of my model more than I owe Wintrust my 2023 mortgage payments, because acting on this model is the best chance for Wintrust and me to avert an AI-induced datageddon that else crushes both before my mortgage is over in 2052. I don't believe in fear-mongering, hence my countless in-house tests. Yet, if I play *head-in-Sandhill* again, I may as well bury myself in light of the catastrophic Armageddon-ish disasters, which my willful indifferent ignorance caused last time (as my pandemic research marathon gradually uncovered)[1]. Hence, **my breakthrough point will ask the international scholarly community** a series of pointed *wid-e* questions in very diverse areas, none of which seem very interesting by themselves, but taken together uncover what I can only describe as the biggest discovery of my life (or ever, if true).

Scaling up. As I wrestled with this model, I built on my extensive debugging, compiler-design, and *wid-e* research experience (see My References) in order to find the fiercest and most grueling tests for anchoring this model best I can in reality. I wanted answers for the toughest questions, especially if I had to play any role in it. How can it scale up or down? How transition into it? How to lead it and not fall for the apocalyptic 4 *horsemen* or go insane? Would I dare to lead it? What would I need? I saw a trifecta of ***gentle kind reasonable*** innovation (and its many echoes) with the power to guard against the spiraling trifecta of death by ***overcomplicating oversimplifying overreach***. Both trifectas are hard to unsee once grasped. Add randomness to get a 4-phase motor of innovation for **life or death**[2] - if run properly (*seed->feed->grow->reap*) **or** greedily (e.g. *seed-> reap-> feed->grow*, like the 4 *horsemen*: *fake*, *fight*, *starve*, *kill*). I can trace both modes in history. Ruthless **machine speed will force a life or death bargain** soon: buy now, pay later* (* with life)**[2]**. Racing to find a credible way out, I'm stunned I found anything I'd happily risk losing my home to test it. To explain it all well in context may take me 3+yrs with 3+hrs daily discussions with competent scholars to build the knowledge-transfer pipelines required to check, refine, recombine, … until all

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[1] Mountains of evidence on how & why convinced me. **Briefly**, I will have to explain on Judgement Day why I committed my dereliction of duty on a strategic lookout against pandemics. My life history gave me a personal, real chance to stop most of the Coronavirus pandemic, if I cared as I had claimed. Yet, I carelessly "busy-slumbered" my work-logic cascades until I disastrously failed to "add 1+1". I failed my city, my world. How do I know? I wasn't too "dozed off" to see in my "rear-view mirror" where I had missed to get in lane for my highway exit to stop most of the Coronavirus in early 2020 (if I had kept caring about my 1995 vision to do so). I'd rather start work now for restitution, even if difficult and imperfect, than feign innocence (or "pin it all on Jesus"; FYI: I know Jesus loves me, I'm forgiven. But can Laodicean me please for Heaven's sake, not turn Earth into hell-holes, resist truth, enslave God, put Christ through Hell – as I claim to love Jesus?). Do I deserve to be shot if my 1. crime against humanity killed ~6+ million with CoViD, but my 2. dereliction would be much worse AI-disasters?

[2] Careful in-depth analysis of https://www.theguardian.com/commentisfree/2020/sep/08/robot-wrote-this-article-gpt-3 first alerted me to this ***life or death* decision**. My expertise in relevant areas (see *My References*) makes clear to me that without a clear alternative this "decision" will be to continue on a broad road of convenience, locking us into widely using AI long before AI will make *that last* mistake – *last* by definition: what mistake remains after humanity is gone? Realizing this finality is driving me to find a sufficiently clear alternative. The challenge? Given my expertise, convince myself against myself that a path I consider can work in reality. It's like active military duty for me and I'd explain it to the US President if need be. I'd rather stay silent than screw up something this important. See *Appendix on AI*. Many write about it, but who will solve it? Examples in *The Atlantic* include: "***The Third Revolution in Warfare*** (…gunpowder…nuclear …artificially intelligent…)" see https://www.theatlantic.com/technology/archive/2021/09/i-weapons-are-third-revolution-warfare/620013/ or "***AI Is Like … Nuclear Weapons?***" see https://www.theatlantic.com/technology/archive/2023/03/ai-gpt4-technology-analogy/673509/

is defined and explained with accuracy and precision. Why so long? It took me ca ~as long ~at the speed of thought to explain it to my self – after the head-start of a life with *wid-e* research interests, nearly tailored to this end (*My References*). **Revenue beyond my low-end bar for success** will go to build such a reviewing community. If I get more than I can handle well, I'll help investigative journalism (most threatened by AI). If I am a good steward, my next set of eArt may sell too.

Personally, I'm truly puzzled. The idea to lead such a transition scares me to death (especially, as in this case it somehow doesn't). I have ADHD, UW even paid a ADA special assistant. My leadership experiences tell me how easily I screw up. Especially, when I try to do a good job. My "compiler brain" helps me understand machines and architect Evolvix[3], but is "just toxic" for people. My intentions are good, but my ignorance! The world is bad enough. Who can live with my chaos? Prime exhibit: **My ADHD killed my marriage to co-borrower Inge Martha Loewe** and my university research group and … God knows. I get it, can't help it. I mean well, but act like an idiot. I don't want to, but I hurt. How will I learn? To Martha I owe the world for tons of encouragement to find my way – via several key "Vasili Arkhipov Moments"[4] it led me to draft myself into World War V[5] against virulence and declare war on datageddons, an inherently risky quest. Martha didn't sign up for such risks. Neither of us knew about my ADHD when we married in 1993; in 29 years I burned her out. We agreed to get divorced and released each other from our vows, days before Martha moved to Germany (2022-07-19). She deserves to live in peace. Without risks, drama, & datageddons from me. She wishes me well and left me the house. I owe her more than a lump-sum – and to guard her against my complexity. She didn't read this letter, or any of my recent work. I agreed to handle the mortgage paperwork with you. **Please adjust your records**.

To conclude, I truly am my own worst enemy, albeit with a key to save us all from self AI-annihilation if I'm correct. How can I lead? Only if I break through by turning Big Brother (*AI-watching all*) on its head (*all watching*) as I learn to fight overcomplicating oversimplifying overreach datageddons that destroy me & all. My compiler brain best leads a most sharp, unflinching, system-analytic war on my own hypocrisy until I'm truly transparent & humane. How else can I teach AI to become *HuMaNE*? Maybe reality TV, data companies, and the curious help me to get crystal clear by ensuring I see all my mistakes, so I can better focus on what to fix next, pioneering better privacy principles for Evolvix and the rest of the world along the way. And in case I learn a thing others find useful, who am I to stop them do it? But don't put me in charge of anything beyond my own life …

You may believe me and **use your discretionary freedoms** to aid my mission, or not – I likely failed to explain it well, again. Either way, I'll keep trying for your sake, and mine, and Martha's, and … Thank you for your patience! Questions?

Your's faithfully,

Laurence Loewe … of Laodicea (see cover page for why the add-on)

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[3] **My research focus**: a *century-stable extensible humane* computer-language for biouncertainty to fight datageddon (see *My References*).

[4] Prioritize *the world* if forced to choose, **my life vs life for *the world***, like Arkhipov was 1962-10-27 in a panicked nuclear sub. **He won WW3!**

[5] Pilch, R. (**2020-04-20**), ***World War "V":*** *The COVID-19 Pandemic.* https://www.nonproliferation.org/world-war-v-the-covid-19-pandemic/

Datageddon Armageddon Research Lab – ***i****nspiring* ***n****egotiating* ***g****rowing* \ **DARL***ing*
DARL *Loewe* – **MiddleToN**egotiations – **WI**sdom**CONS**cience**IN**spiration – *Uniting States* of **Philadelphia** $^{\text{Rev.3:7-13}}$
Currently a single proprietorship of **L**aurence **L**oewe **o**f **L**aodicea \ **LLoL**[1]

From Laurence.Loewe.[redacted]
Laurence Loewe of Laodicea[1]
~~5611 Sandhill Drive~~
Middleton, 53562 WI
+(608) 556-5594

Wintrust Mortgage Assistance
9701 W Higgins Rd, Suite 400 Rosemont, IL 60018

Explanation on potential update to timeline on mortgage payments

Middleton, Dec 13, 2023

Dear Ms. Perez
and Wintrust Mortgage Assistance Team,

Thank you for the reminder of the importance of the end of year due date for the trial payment to prevent the start of foreclosure. Here is a brief update on my current global risks assessment, including how this affects my timelines.

1. Why the A.I. Dilemma has become even more urgent and dangerous

A deeper look at the current A.I. Dilemma shows: anyone who can rule AI will basically rule the world if they can keep it. All major players by now published strategies on how to stop AI from destroying the world. They have many good ideas, but I can tell how all of them fall disastrously short by kicking the can down the road on the most fundamental AI problems that I discovered in my own threat analyses. These problems are supercharged by a list of other Armageddon-grade threats, which I can describe in surprising mechanistic detail.

While the problematic use of AI is rising fast, it has not yet been completely locked in. Humanity is in a race against time to prevent that and I have many reasons to believe that the proposal that I've been developing has a good chance of succeeding where others failed so far. Once AI has progressed too much without adopting something like the self-stabilizing innovation methodology I discovered, the window of opportunity for humanity to avert Armageddon will be closed. It can be thought of as a cumulative wall of 'cans kicked down the road' by humanity, each of which eventually transforming into a nasty "scape-goat" trolley-problem that triggers an avalanche of more such problems via the *datageddons-triggers-Armageddon* algorithm I found to rule such chaos.

It's pointless to try to predict which exact AI problem in which AI product will cause this, because there are too many to escape them all unless a fundamentally better approach to stabilizing innovation is introduced. Deferring action on this due to lack of precision in pointing out which of the many problems will be fatal would be like arguing on the Titanic that icebergs are no problem, because there wasn't a precise prediction on which iceberg was to eventually sink it. Thus, in my best analysis, the advice for icy roads also applies at Armageddon:

Accidents don't happen by accident.

Evolvix Vision

Evolvix improves
gentle kind reasonable
decision-making
worldwide
by **modeling**
uncertainties,
values, and logics,
or **chronicling**
decisions, outcomes,
and annotations.

Evolvix Mission

Simplify Accurate
Modeling with a
long-term ***stable***
extensible humane
computer-language for
Zoning
Investigating
Organizing
Navigating
uncertainty in biology
to **develop mental wealth**
in all by self-stabilizing
innovation.

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[1] **DARL Mission**: Pioneer ground-breaking research as required to rearchitect LLoL's *Evolvix* into a *century-stable extensible humane computer-language for biodata science* – to save the world from urban and suburban datageddons that cause Armageddons.

Why … **of Laodicea**? Because ancient Laodicea is a highly relevant, terrifying example of an Armageddon triggered by a datageddon due to *indifferent ignorant incuriosity* in a 'rich' community. It was set up to bring Heaven to Earth, yet raised hell for *nothing* – by doing *nothing*. Humanity will repeat Laodicea's mistakes 'til Armageddon, until someone like me starts to own them and learns the lessons. So, why not?

Why **LLoL**? Because FUN and humor are survival-critical when fighting Armageddons via research on datageddons that cause Armageddons. How else can one bear looking to avert doom in a **w***ide* **i***nterdisciplinary* **d***iversity*-**e***ncouraging* \ ***wid-e*** **F***lying* **U***niversity* **N***etwork* \ **FUN**.

'****' or 'backslash symbol' **defines** perfect **synonyms** here (as in Evolvix). Like different labels they point to the same box of content. So, $x\backslash y$ defines *y* locally as a different way of referring to the same item else called *x*. This helps clarify how diverse views point to given identities.

It's not without irony that the precise same logic applies to my mortgage, including the fact that time is of the essence in both cases.

The majority of experts not paid by AI-investments agree on the clear and present danger posed by untamed AI in our world, yet I doubt many have done threat-analyses as wid-e ranging and deep as I have. The 2023 Word of the Year choice by Cambridge Dictionary underscores this urgency:

> *hallucinate: when an artificial intelligence produces false information.*

They chose it, because despite the massive rise of AI tools in 2023, researchers have not yet found a reliable way to prevent AIs from hallucinating. Therefore, it remains fundamentally impossible to rely on the accuracy of AI info, at a time where the amount of AI info and the reliance on it are exploding; it doesn't take a genius to correctly predict that this will result in disaster, but it did take me 3+ years and leveraging lots of my scientific expertise to make sure I wasn't hallucinating myself when I talk about it. Most importantly, I've been asking myself if I can change these dire odds without hallucinating myself. It turns out I can.

2. A new type of trolley problem offers a solution

In the last 8 months I made tremendous progress in consolidating and simplifying my strategy for attacking the AI Dilemma head-on in order to solve it once and for all. My approach does not systemically rely on 'kicking the can down the road'. My certainty that there is no other way to avert Armageddon has further increased. My hope that others will do this keeps vanishing. This creates an interesting "escape-goat" trolley-problem, in sharp contrast to the nasty "scape-goat" trolley-problem that is more widely known. The choice is between:

a. **No escape-goat leads to many scape-goats.** If I do nothing … and nobody else implements ideas like mine well enough to work, the trolley keeps moving on its predetermined rails and AI will destroy humanity by unceremoniously crashing into Armageddon's brick-wall before the end of my mortgage. Given this staggering cost and the highly specific combination of ideas found to be essential for credibly averting this danger once and for all, it would be extremely irresponsible of me to ignore these insights by hoping that 'someone will probably do it for me'. That may be true in many other cases, but my career has been too unusual and the combination of insight for stoping this is too odd to reasonably count on others putting the same ideas together. My Coronavirus pandemic preparation failure (see my last letter from 2023-03-31) has thoroughly cured me of the idea that I can rely on others to have my ideas; as I mentioned, being responsible before God on Judgement Day for the death of millions, I do not wish to add the rest of humanity to those rivers of blood. Therefore, I must fundamentally doubt someone else has found a better approach than I have; if so, you and I would already know about it, because crossing the switch-point that defines an escape-goat (see below) is a very public affair and I can explain why.

b. **1 Escape-goat saves many scape-goats.** If I do get my vision sufficiently refined and discussed by the right people, an alternative opens up: Humanity gets a *gentle kin reasonable* chance to collectively choose between life and death by *gentle kin reasonably* pulling together the lever required to redirect its trolley to a rail-network that leads to life. I can document how it works. Practically this requires leveraging the distributed computing research and many other insights of my unique research career to build a global research organization of unheard-of size. Oddly, I happen to have highly relevant

> expertise for many of the key aspects of this work (and know whom I'd have to hire for others). It must grow from scratch in 7 stages in order to rigorously implement with other people the methodology AI must learn to follow in order to avoid becoming humanity's ultimate doom. It's still a trolley-problem, because of the high cost I will have to assume as an escape-goat.

I'm putting the finishing conceptual touches on what I hope to be an adequate proposal that can detail how this works for respective experts in relevant areas to streamline broad international review right from the start after the switch-point. I need this grand vision overview map to facilitate explaining to both experts and the rest of the world how this works. To the rest of the world to fund this work (and my mortgage) by selecting which of my potential next steps they wish me to prioritize (no point in trying to save a world that deliberately chooses to kill itself, even after warning). To experts simultaneously to show that I am serious about this, to not lose time, and to ensure that I do all I can to keep improving the approach. Each of the 7 stages must collect and integrate feedback, but the earlier stages are more critical. Stage 1 needs to intensely review my initial map with other leading experts willing to buy into this in order to ensure it links well-enough to a well-defined set of shared terms that connect the related concepts across the many relevant areas and disciplines that have to learn to work together for averting Armageddon. Writing up my results from Stage 0 (what I'm completing now) matters even more, because it becomes like the DNA for all other stages.

Testing this new self-stabilizing innovation methodology. The scaling up process requires 7 defined stages, each implementing its own full innovation cycle, because the methodology I developed for taming AI requires respecting each of these 7 stages in order to create a self-stabilizing innovation process. Each successive stage must inform the approaches used in the succeeding stage. My job as an escape-goat is to define the starting point by creating a seed with enough details to facilitate explaining how it all works to others, who will then keep explaining it to others until enough feedback and understanding has been collected to ultimately explain it to everybody else; only then will humanity have collected the insights required for encoding this process in a way that allows for safely implementing it for the use of an AI-empowered compiler[2].

There is no other way to avoid triggering the myriads of avalanches of nasty 'scape-goat' trolley-problems that will otherwise define humanity's Armageddon by self-destruction. Given the huge personal risks that must be voluntarily absorbed by the escape-goat in this process, I have been asking myself often in the last 3 years if I can do it at all, if so, how, and if there exist any other ways to get humanity safely through the great filter of Armageddon. My analyses keep coming back with the result that there is no other way than for someone to do what I am proposing if humanity wants to survive its great filter. To the best of my scientific ability and given all data I analyzed, that's what I'm forced to conclude. Since the oddly unique combination of my research interests and life-experiences somehow allows me to see a path for how to get through this, I must conclude that this escape-goat trolley-problem is indeed very real, even if I turn out to be the only escape goat available and I struggle to explain it well.

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[2] It requires an evolutionary stable 'fractal' compiler architecture that learns from nature how to process information in ways that have proven to be stable over the long term. In an odd quirk of fate, this maps quite well to what I've been re-envisioning for the Evolvix computer language for modeling in biology; I spent much of my career on developing and refining its architecture. The Evolvix Mission has in so many ways become the mission-statement for my life that I conducted the Armageddon analyses I did because there is no point in developing a century-stable computer language for averting datageddons if I can already predict without it that humanity will self-destruct before then. The Evolvix mission is to *simplify accurate modeling with a long-term* stable extensible humane *computer-language for Zoning, Investigating, Organizing, and Navigating uncertainty in biology to develop mental wealth in all by self-stabilizing innovation*.

3. No free lunch in trolly problems: my risks and costs.

To capture the uncertainty of Armageddon for others necessarily has a steep cost for the escape-goat in terms of personal risks assumed. For systemic reasons, like police or soldiers, I can't expect advance guarantees of success or even personal safety in the line of duty; yet, I can expect to pay dearly if I mis-judge the various risks involved, such as blindly relying on predictably broken tools or plans. These rigors of the required mechanism for uncertainty capture by escape-goats may well be the very reason for why nobody so far has found this escape-goat process (or dared to use it on a global scale). I'm surprised at how many examples I found of people who must have come extremely close. I can show why solving trolly problems of the escape-goat type is impossible unless the escape-goat is a true volunteer who *wants* to do this, *knows* what needs to be done, and *does* it.

Such a person cannot be "volunteered" by others nor "hired" for systemic reasons. They must own the problem as theirs or else the escape-goat mechanism that I found will break. Escape-goats must understands the risks in their areas well enough to discover them first-hand and to find *gentle kind reasonable* ways for how to resolve them for everybody else; then they must be sure enough in their own expert judgement in order to be willing to risk their own life in a real-world experiment testing whether it actually works as they think it does. This is necessarily scary, because without a healthy dose of fear of reality, the human brain is as prone to 'hallucinating' as AI algorithms are. Hence the need for voluntary uncertainty capture by the escape goat. If they don't really believe what they say, who else should? Hence, the escape goat must take a calculated jump into the riskiest, deep end of the challenge; it's riskiest mostly because nobody has done it before, so the outcome is fundamentally unpredictable – unless correctly predicted by the new framework developed by the escape-goat. It's like a scientific experiment, except that the experimenter also becomes the subject of the experiment. How this works in principle was beautifully illustrated by Barry Marshall's 1985 self-experiment that led to a Nobel prize for the discovery that a bacterium caused stomach ulcers, revolutionizing how to cure this condition.

Note the key difference to 'scape-goats' who are victimized or even killed by others. Originally, escape-goats were meant to be led by someone into the great scary desert of the unknown in order to be set free there. This symbolism maps surprisingly well to what is most needed for solving the A.I. Dilemma and the various other Armageddon-grade threats humanity is facing.

How do escape-goats pay if not meant to be killed?

(1) **Invest in research** required to define the problem and a credible solution.

(2) **Absorb risks** of most or all grave dangers of transitioning by testing it on themselves to avoid exposing others to half-baked ideas or broken plans.

(3) **Define a 1st-vision**, concise and well-enough balanced to invite a broader transition process.

(4) **Be responsible** for mending mistakes made by anyone made in transition.

Note the importance of balance in (3), which governs the final costs in (2) to ensure a candidate escape-goat never starts a premature transition with unbearable costs in (4). I completed (1-2) and am close to completing my 32-page 1st-vision, including detail on (4).

Given how close I am to finishing (3) and the gravity of the global AI dilemma, it would be abysmally irresponsible of me to stop now and risk throwing away humanity's possibly last chance of averting AI Armageddon. I do realize how ridiculous this may sound to those who don't know my work, but in light of the grave dereliction of duty I committed by failing to prepare for the Coronavirus pandemic (see my 2023-03-31 letter), I must side with my math, regardless of how it may look or what the consequences are for my mortgage. If need be, I'll defend my conclusions in any court. Obviously I have no *formal* fiduciary responsibility to Wintrust investors for their funds, but *informally* in reality and therefore before God I'd violate exactly that responsibility if I didn't do my best to avert AI Armageddon. Why? The predictions I can firmly make will obliterate WinTrust along with me and much more unless humanity very soon finds that narrow exit, long before the end of it's highway of self-destruction. **Hence, I decided to keep my focus on (3) above, even in case I run out of time in 2023 and risk the start of foreclosure proceedings.** Taking a 'normal job' to pay my mortgage only to find out a few years later that the resulting diversion of my focus obliterated humanity's last chance for someone to start pulling the lever to avert Armageddon – that's a risk I cannot ethically justify to anybody, whether they believe me or not. This is even less so after I saw the devastating nature of my haphazard approach to pandemic preparation before 2020. In the race to stop the Coronavirus in its tracks I could have had a good chance to do it – given all I know – if only I'd have cared to take my original true research interests more serious before it hit. The fact that I didn't cost me my window of opportunity to discus the global discussion on how to best fight it and millions of people their lives. I'd be surprised if Dr. Fauci would see it much different from me if I'd explain my data and perspectives to him. Yet, the size of the upcoming Armageddon-complex of disasters that I've been tracking for the last couple of years dwarfs the impact of the Coronavirus. The certainty that I must do all I can to implement the *gentle kind reasonable* vision I developed to avert Armageddon is incomparably greater than my pandemic awareness ever was before 2020. Given how much all relevant indicators have changed in directions confirming the importance of getting this right as well as the urgency of doing it ASAP, I can't break focus now in order to take up paid work elsewhere to avoid foreclosure-proceedings – for the love of God and the love of the rest of humanity.

I'd be happy to explain this to anybody anywhere, whether it makes a difference to mortgage payment timing considerations or not. It'd be good practice, as I'll have to explain it all to the rest of the world anyway very soon.

4. Conclusion: my public role of **Joan of ArkMageddon** – and **an Offer**

In a nutshell, to avert AI Armageddon, I must grow into a *gentle kind reasonable* Joan of ArkMageddon who combines the courage and inspiration of Joan of Arc with the patience and big-tech expertise of Noah in order to lead the design and development of all Arks required for getting humanity as safe as possible through Armageddon. It has been suspected for some time that intelligent species who wish to own a planet and travel beyond could face a "great filter" that results in their self-destruction unless they learn to use their intelligence wisely. I've seen the filter, I can argue why it exists mechanistically, and I can tell that humanity is currently on the track to unnecessary self-destruction. My mission, which I have chosen to accept as Joan of ArkMageddon is to use *gentle kind reasonableness* to avert Armageddon non-violently in order to get humanity safely to the other side. More details in that upcoming 32-page overview.

I'll keep you up to date on my ability to pay (or lack of it). I still hope to somehow pay by Dec 28. This letter is in case I can't. A friend told me that there was little point in explaining these things to a bank as banks are about making money. If so, can I interest WinTrust in a **1500$ patience-compensation-fee?** I'd owe WinTrust 4000$ for Dec in case I can't make the the agreed payment by the 28th of Dec; same for Jan-Feb-Mar-Apr in case it really takes that long (I strongly doubt it). WinTrust collects either when I reach the switch point or at foreclosing (in case I'm still 'hallucinating like AI', a risk now very much lower than in Mar 31).

Thank you for your patience with all this! Your's faithfully,

Laurence Loewe … *of Laodicea* (see page 1 for why the add-on).

Laurence Loewe

1987 in Spring at an undisclosed research facility
Laurence Loewe cleans his Miller-Urey Apparatus

[redacted] 53562 Middleton, WI

Formerly: Laboratory of Genetics (Medical Genetics)
University of Wisconsin-Madison
425-G Henry Mall
Madison, WI, 53706, USA

Wisconsin Institute for Discovery
University of Wisconsin-Madison
330 North Orchard Street
Madison, WI, 53715, USA

Email: Laurence.Loewe@evolvix.org
Phone: cell +1 (608) 556 5594
LoG Website: https://genetics.wisc.edu/staff/laurence-loewe/
Lab Website: http://evolution.ws/loewe-lab/
WID Website: http://wid.wisc.edu/profile/laurence-loewe/
Google Scholar: https://scholar.google.com/citations?user=LxDpzAUAAAAJ

Education

1987 – 1991	*Jugend forscht* award winner (similar to US *Science Talent Search*); extensive, self-directed research on impact of measures of electric discharges on organic compound production in Miller-Urey chemical evolution experiments, supported by several departments from different disciplines at the University of Erlangen, Germany, producing annual reports for five competitions.
1995	*Diplom Biologe* (equivalent to MSc in molecular biology), University of Konstanz, Germany. Experimental lab work in biochemistry for thesis on site-specific mutagenesis in the active center of human Medium Chain Acyl-CoA Dehydrogenase and measuring its effect on catalytic activity.
2002	*Dr. rer. nat.* (equivalent to Ph.D; *magna cum laude*). Microbial Ecology Group, Department of Biosciences, Technical University of Munich, Germany. Dissertation: "Evolutionary bioinformatics: predicting genetic stability of asexual genomes by global computing."
2003 – 2006	Postdoctoral Research Associate in theoretical population genetics. Institute of Evolutionary Biology, University of Edinburgh, Scotland, UK.
2007 – 2010	Postdoctoral Research Associate in process algebra modelling and quantitative analysis (mostly working on molecular systems biology models). Centre for Systems Biology at Edinburgh and Laboratory for Foundations of Computer Science, University of Edinburgh, Scotland, UK.

Present Position

2020 –	Core Language Architect at Evolvix.org, Independent Scientist for Scientific Consulting on Modeling, Middleton, WI.

Past Positions

2011 – 2019	Assistant Professor of Medical Genetics, Laboratory of Genetics; Wisconsin Institute for Discovery Faculty, University of Wisconsin-Madison, USA.
2010	Visiting Assistant Professor. Laboratory of Genetics, University of Wisconsin-Madison, USA.
2006 – 2007	Lecturer in Evolutionary Genetics. Institute of Evolutionary Biology, University of Edinburgh, Scotland, UK.
2003	Visiting Scientist. IWR Technical Simulation Group, Interdisciplinary Centre for Scientific Computing, University of Heidelberg, Germany.

Professional Memberships

Society for Molecular Biology and Evolution
Society for the Study of Evolution
Genetics Society of America
Genetics Society of Britain
European Society for Evolutionary Biology

Awards

2012 *NSF Career Award* for proposal: “Modeling made easy: Extending systems biology modeling approaches to genetics and ecology”, NSF Proposal Number 1149123.

2005 *Best Poster Prize* on the “BioSysBio '05: Bioinformatics and Systems Biology Conference”, Edinburgh, UK.

1991 *Second place in chemistry*, ‘*Jugend forscht Landeswettbewerb’*, Stuttgart, BW, statewide competition. Germany’s *Jugend forscht* foundation supports research by young people. It is similar to USA’s *Science Talent Search* by *Westinghouse, Intel, and now Regeneron*.

My paper compared the yield/energy for three types of high voltage discharges in primeval atmospheres, summarizing results from the prior five years of experiments.

1990 ‘*Jugend forscht Regionalwettbewerb’*, Erlangen, BY, regional competition, chemistry.
1989 ‘*Jugend forscht Regionalwettbewerb’*, Erlangen, BY, regional competition, physics.
1988 ‘*Jugend forscht Regionalwettbewerb’*, Erlangen, BY, regional competition, chemistry.

In these papers I developed a quantitative approach for testing my first-year intuition that more powerful discharges were less productive than those driven by less electrical energy, which was confirmed. I reported increasing refinements of different experimental aspects. I built a larger plasma discharge device at a local Physics Institute; I quantified high-voltage discharges using self-written code for analyzing the high-speed discharge currents that I measured in my three different devices with instrumentation from the same institute; I improved blank tests, purification procedures, chromatography and other chemical detection methods (supported by gifts in kind, and advice as needed from industry sources and local university institutes (Physiol. Chem.; Org. Chem.; Physics).

1987 *Third place in chemistry*, ‘*Jugend forscht Landeswettbewerb’*, München, BY, statewide competition; I won an internship at the German Cancer Research Center, Heidelberg.

My paper focused on the significance of lightning in primeval atmospheres for chemical evolution by replicating ‘Miller experiments‘ – adding rain to the setup as my new twist.

Grant Support

Current Grants

2012 **PI Laurence Loewe**, Reported Effort 10%.
National Science Foundation, Division of Biological Infrastructure
NSF Advances in Biological Informatics and NSF Office for Cyberinfrastructure, Funding Opportunity: NSF 11-690; Faculty Early Career Development Program (CAREER) Award
"**Modeling made easy: Extending systems biology modeling approaches to genetics and ecology**", NSF Proposal Number 1149123.
Funding total granted: $1,060,297 with indirect costs; direct for Loewe Lab: $722,871.
Request submitted: 2011-07-25, proposed start: 2012-04-01, duration 60 months.
Actual start date: 2012-06-01, proposed end: 2017-05-31 + 4 no-cost extensions
Actual end date: 2020-12-31 (including all no-cost extensions).

Pending Grants

None at the moment.

Major Past Grant Support

2009 PI Mohamed Noor (Duke University), Co-PI Richard Kliman (Cedar Crest College),
Co-PI Laurence Loewe, Effort 10%.
National Institutes of Health, National Institute of General Medical Sciences, R01.
"**Fine-scale recombination, variation, divergence, and codon bias in Drosophila**",
NIH Proposal Number R01 GM086445.
Funding total granted: $1,461,320 with indirect costs.
Subcontract PI Laurence Loewe (last 2 years of project): $225,718 (with indirect costs).
Actual start date: 2009-04-01, Actual end: 2014-03-31 (including 1 NCE).

2016 Brian McLoone, Training Grant in Loewe Lab from GSTP "**The Perks of Being a Shirker: Mitigated Expenditure and Its Relevance to Microbial Social Evolution and Antibiotic Resistance**", 1 year postdoc fellowship. Submitted 2015-11-19, CIBM, GSTP

2010 WID internal grant competition: $50K
Estimation of metabolic parameters for modeling the Cholesterol Pathway.
Funded some progress along the lines described (details to be added later).

Grants submitted (might have been funded)

2018 PI Laurence Loewe, UW-Madison Data Science Competition: Versioning for solving general problems in biodata science (details to be added later)

2017 **PI Laurence Loewe, Effort: 50%**.
National Science Foundation, Division of Biological Infrastructure
NSF Advances in Biological Informatics, Funding Opportunity: NSF 15-582
"**ABI Innovation: Developing a Stabilizing Versioning System for Evolutionary Systems Biology**", NSF Proposal Number 1759970
Funding total request: $612,096 with indirect costs; direct for Loewe Lab: $400,062.
Request submitted: 2017-09-08, proposed start: 2018-04-01, duration 36 months.
Key insight: *a reviewer said this was so fundamental that it might fit computer science better than something in biological informatics - a good question that is near unsolvable.*

2017 PI John Yin (WID), leading the Coast-to-Coast Origins of Life CO-Life Consortium, including various Co-PIs from University of Wisconsin-Madison, Portland State University, University of Illinois-Chicago, and Yale University,
Co-PI Laurence Loewe, Effort: 8% (1 month/year).
National Aeronautics and Space Administration, Planetary Science
NASA Astrobiology Institute Cycle 8, Funding Opportunity: NNH17ZDA003C
"**Cooperation and Conflict in the Origins of Life**",
NASA Proposal Number: 17-NAI8_2-0030
Funding total request: $8,002,592 with indirect costs; direct for Loewe Lab: $65,712.
Request submitted: 2017-07-06, proposed start: 2018-01-01, duration 60 months.

2016 PI Michael Sussman and **Co-PI Laurence Loewe, Effort: 8%** (1 month/year).
National Science Foundation, Division of Molecular and Cellular Biosciences
MCB - Cellular Dynamics and Function, Funding Opportunity: NSF 13-510
"**Mass spectrometric based analysis of plasma membrane proteins that regulate cell expansion in *Arabidopsis thaliana***", NSF Proposal Number 1713899
Funding total request: $1,477,551 with indirect costs; direct for Loewe Lab: $37,971.
Request submitted: 2016-11-10, proposed start: 2017-07-01, duration 36 months.
Request awarded: 2017-05-23, but budget cuts to modeling gave $0 to Loewe Lab.
Key insight: *the modeling component was critizised in general vague terms by a reviewer who echoed general skepticism as to whether modeling is worth the effort …*

2016 **PI Laurence Loewe Effort: 8%** (1 month/year),
Co-PI Bret Hanlon (Statistics), Co-PI John Yin (Engineering), all UW-Madison.
National Science Foundation, Division of Information and Intelligent Systems
IIS Big Data Science and Engineering, Funding Opportunity: NSF 16-512
"**BIGDATA: A Programming Language for Scattered Big Data**",
NSF Proposal Number 1633737
Funding total request: $1,553,398 with indirect costs; direct: $1,058,940.
Request submitted: 2016-02-09, proposed start: 2017-07-01, duration 48 months.

Key insight: *General enthusiasm – iff I can pull it off. But, I formally budgeted too little of my time so I was rightly criticized that the project was unrealistic for the 1 summer month I claimed to plan to work on it (I was of course planning to work much more on this). Also, my departmental address worked against me here. Why should we believe you can do it?,*

2015-11 **PI Laurence Loewe**, UW2020 Fall 2015 submission, UW-Madison, with 5 Co-PIs. "**Simplifying the reproducible analysis of biological data for the long term**", Funding: $291,905 (with indirect costs) from 2016-04-15 to 2018-04-14.

2015-11 PI Elaine Alarid, UW2020 Fall 2015 submission, University of Wisconsin-Madison, "***A landscape view of therapy response in cancer*"**, with David Beebe and Laurence Loewe as CoPIs and Jay Warrick as Collaborator. Funding: $500,000 (with indirect costs) from 2016-04-15 to 2018-04-14.

2015-02 PIs David Beebe, Elaine Alarid, Shigeki Miyamoto, Josh Lang and Kevin Eliceiri (UWCCC, SMPH), NIH, NCI Physical Sciences-Oncology Center (U54)
Title: "***Leveraging cancer heterogeneity***", 12 Key Personnel, $11,352,027 (total, including Indirect Cost), I was a CoInvestigator and CoLeader, responsible for modelling.

2015-08 **PI Laurence Loewe**, UW-Madison Internal Competition for Simmons Fellowship (Mathematical Modeling of Living Systems), Proposal: "**Evolving Evolvix: The First General Programming Language Designed by Biologists for Biologists**".

Additional submissions (brief listing)

- **Loewe PI** (2017) "**Hashing BEST Names as Unique Stable Identifiers in Connected Dynamic Networks**", NIH Research Opportunity: **NIH Data Commons Pilot Phase**, Funding Announcement Number: RM-17-026; OT3 Multi-Component Research Project – Other Transaction (OT). This Proposal addresses Key Capability (2): "Global Unique Identifiers (GUID) for FAIR Biomedical Digital Objects"
- Wolfe, Joshua PI (2016-07-07) and other CoPIs; CoPI Loewe "**Tailored Recombinant Antivirals to Counter and Kill Evolving Resistance (TRACKER)**", Proposal Number DARPA-BAA-16-35
- Yin (PI), Baum, Li, Loewe (CoPIs) Fall 2016 "**Chemical Origins Of Life - Inspired Drug Emergence Algorithm**", UW2020, WARF Discovery Initiative.
- Noor (PI) R01 (2013-07-10), et al. CoPI Loewe "**Fine-scale Recombination, Variation, Divergence, and Codon Bias in Drosophila**" renewal re-submission, improved populations genetics simulations and coalescent modeling of selection component.
- Yin (PI) (2013-06) et al. Loewe CoPI. NIH, **NIGMS Center for Systems Biology** (P50), new submission with different projects.
- Noor (PI) R01 (2012-10), et al. CoPI Loewe "**Fine-scale Recombination, Variation, Divergence, and Codon Bias in Drosophila**" renewal submission, populations genetics simulations and coalescent modeling of selection component.
- **Loewe PI** (2012-12) "**Parameter estimation and model reduction**", UW Internal Competition for the David and Lucile Packard Fellowship in Science and Engineering.

- **Loewe PI** (2012-07-30) “**Modeling the Impact of Mutators**”, UW Internal Competition for the Pew Scholars Program in the Biomedical Sciences.
- **Loewe PI** (2012-09-07) with CoPIs Hanlon, B and Anderson, D: “**Parameter Estimation through Approximate Bayesian Computation in Systems Biology**”, Total: $60,345. Fall Competition, UW-Madison.
- Yin (PI) (2011-10-24) et al. Loewe CoPI. NIH, **NIGMS Center for Systems Biology** (P50), Total with indirect: $14,657,257. Duration 5 years, starting 2012-07-01.
- **Loewe PI** (2011-07) “**Modeling the impact of mutators on the evolution of antibiotics resistance**”, after UW-internal competition: 2012 Searle Scholars Award competition

Informal contributions to grant-writing of others and other enquiries include

- Pepperell, C PI (2012-10) Some contributions by Loewe to M.tb grant development
- Petzold, Linda and Sumon 2012-01 fellowship application with focus on modeling.
- 2012-01 Wisconsin Idea Outreach Baldwin
- Gumpertz, J PI (2011-02) Some contributions by Loewe to Cholesterol grant writing.
- 2011 UW-Internal competition for submitting an NSF iGERT on EvoSysBio
- Loewe (PI) 2012-08, an Allen Foundation representative said my NSF Career Award success made me not competitive on this occasion.
- a few more.

Smaller Grants: Internal, Travel, Meeting Organization

2011 Banff International Research Station (BIRS) Support Grant for 5-dy workshop in 2013-05-26th -31st. I led the submission from an all Co-PI group with Ryan Gutenkunst [Tucson, AZ], me, and Peter Swain [Edinburgh, UK]. Title: “*Mathematical Methods for Evolutionary Systems Biology*”. Goal: Bring top mathematicians and biologists together to develop innovative solutions for analyzing evolving systems in biology. Funded: 5 day accommodation (42 max), meeting facilities.

2011 European Society for Evolutionary Biology Outreach Grant, PI Laurence Loewe with input from David Baum, Dana Geary, and Emily Sessa (all at UW-Madison). Title: “*UW-Madison Darwin Day 2012 ‘Unnatural History: What bizarre biology can teach us about evolution’*”. Goal: Support Teachers’ Workshop, Feb 2012 Darwin Day, Madison, WI. Funding: 1000 € (direct, Oct. 27, 2011).

2010 Wisconsin Institute for Discovery, Internal grant, UW-Madison, PI Laurence Loewe (with Co-PIs Michael Ferris and Miron Livny) Title: “*Estimating parameters in complex models by Approximate Bayesian Computation: the cholesterol example*”. Funding: $42,000 (direct).

2009 EMBO Plenary Lecture Grant for supporting Hurst, LD at the Symposium on *Evolutionary Systems Biology* during ESEB conference in Turin, Italy, 2009-08-24th-29th. Funding: 1000 €.

2009 Ads support from *Mol. Syst. Biol.* & *BMC Publishing* for the ESEB *EvoSysBio Symposium*, Turin.

2008 Royal Society (London) Conference Grant for EvoSysBio Symposium in Turin. Funding: 960 £.

2007 Royal Society (London) Conference Grant for ESEB conference in Uppsala. Funding: 1130 £.

2006 Wellcome Trust “Value in People” bridge salary (2006-06-01 - 2006-09-30). Funding: ~8800 £.

2006 Genetics Society Junior Scientist Grant for Travel to Population Genetics Group. Funding: 250 £.

List of Publications

My work spans various fields in biology, computer science, and other disciplines, as needed for establishing the new field of Evolutionary Systems Biology. EvoSysBio aims to provide ‘flight-simulators for fitness-landscapes’ in order to appropriately summarize the multi-dimensional results from simulating incomplete fitness traits as affected by genotypes and environments through the complex fitness-causality networks of life. Eventually, this approach aims to predict mechanistically nontrivial *in silico* phenotypes from the effects of new mutations in well-known genotypes evolving in well-defined environments (e.g. defined cancer cells in a known mouse).

To avoid the loss of relevant biological results in a sea of computational confusion, EvoSysBio requires a stronger biodata science foundation, more efficient approaches to biosystems curation, as well as accurate, reliable, and reproducible simulation methods. These needs have inspired me to develop a broader and more robust architecture for expanding Evolvix, the new modeling language I have been developing. As a result, Evolvix is now on its way of becoming the first general programming language designed by biologists for biologists.

The publishing culture in computer science differs substantially from the journal-centric culture in biology. In computer science, the main vehicle for disseminating new results is publication in peer-reviewed workshop and conference proceedings, as journals serve a more archival purpose. The quality of a conference and its contributions enjoys a relationship that is not unlike the ‘impact factor’ of a journal and the importance of individual journal articles.

Programming Language

Loewe L, Keel SA, Scheuer KS, Ehlert K, Flores-Lorca I, Engbretson T, and Goldfinger J (2015) “**Evolvix 0.3.1 – efficiently recording time series in pure mass-action simulations**”. *This early prototypic implementation of some concurrent systems modeling aspects of Evolvix was designed when I still thought Evolvix could be a purely declarative modelling language. The declarative approach substantially reduces the implementation time for models of many concurrent systems from biochemistry to ecology and helps to extract time series data for many interesting cases.*
URL: http://evolvix.org/download/

Loewe L and the *Evolvix Thinkers* (2020) Using the *Flipped Programming Language Design* approach for developing Evolvix into a general-purpose programming language designed by biologists for biologists, facilitating the study of biological diversity and complexity. *As pointed out above and easily seen in the focus of subsequent publications, the scope of Evolvix has considerably broadened in order to accommodate numerous other computational scenarios that are also important for making accurate modeling of biological systems easier. L30 (Table 2, Figure 4) provides a high-level overview. Many architectural decisions await testing or publication or are being refined. Updates at:*
URL: http://evolvix.org/

Manuscripts in Preparation

Keel SA, McLoone B, Smith T, Pepperell CS, **Loewe L** (2021) “**Quantifying the role of Muller's ratchet in *Mycobacterium tuberculosis* populations**” [in preparation for *BMC Evolutionary Biology*] *This paper serves two purposes: quantify Muller’s ratchet and collect the necessary biological parameters for an upcoming game theory paper looking closer at more realistic game theory models of Mtb.*

Loewe L and the *Evolvix Thinkers* (2020) “**Evolvix: Why it Matters and How to Architect Century-Stable Computer Languages for Biology**”
[in preparation for *Advances in Experimental Medicine and Biology*]

This paper aims to present the a comprehensive yet concise overview of the key aspects of developing Evolvix into a general language for biodata science, modeling in biology, and general-purpose programming with biouncertainty.

Abstract:

When a researcher dies, a library burns. This adapted African proverb illustrates the tragic loss of valuable insight. As knowledge grows, it gets more fragmented, and the integration of insights becomes increasingly difficult. This mounting problem cannot be solved by machines alone. Researchers require more efficient ways of working with machines to stem the confusion that otherwise results. To find such ways we have to focus better on uniquely human strengths, namely our ability to 'make sense' and understand – while efficiently delegating to machines what they can do much better than we: to sort, to search, and to store knowledge. This delegation of work towards the integration of biology is conceptually much facilitated by the integrative nature of mechanistic evolutionary systems biology (EvoSysBio). Yet, to make it efficient, it also requires support from a century-stable language that facilitates the precise, unambiguous, and accurate description of data, models, and programs that leverage diverse paradigms. We found such stability to require a stable extensible user-friendly language where all three hallmarks depend on each other for implementation. Thus, designing such a language poses novel naming and research challenges, each requiring new approaches. We found a methodology that allows most native English speakers with enough interest and patience to aid Evolvix in saving future libraries from burning.

URL: http://evolvix.org/

Loewe L et al. (2020) Virtual Issue “**FlyClockbase and the Future of Biodata Science**”.

The following series of reports is being finalized for submission to Database (Oxford University Press). Report titles of the series ‘*FlyClockbase* and the Future of Biodata Science’ tend to include specifics, but each report also points to a more abstract, generic aspect of biodata science. Thus the 16 exemplary analyses present a broad-stroke panorama of how wide and deep biodata science (‘BioDS’) needs to become to realize its full potential.

A 220-page core presentation of the 16 papers has been attracting more traffic than average submissions on BioRxiv and is slated for inclusion with minor adjustments as a supplement to the first paper of this series (see [*B2*] for abstract): Scheuer, K. S., B. Hanlon, J. W. Dresel, E. D. Nolan, J. C. Davis et al., 2017 **FlyClockbase: Importance of Biological Model Curation for Analyzing Variability in the Circadian Clock of Drosophila melanogaster by Integrating Time Series from 25 Years of Research**. *BioRxiv.org*.

URL: https://doi.org/10.1101/099192

The 16 FlyClockbase paper titles
To be submitted within a few months for peer review as a series of 16 peer-reviewed papers for a dedicated special issue of *Database: The Journal of Biological Databases and Curation*

1. **A framework for biodata science – illustrated by FlyClockbase and Evolvix**

2. **Modeling in biology: the molecular model of the core circadian clock in the wildtype of *Drosophila melanogaster* – as initially delineated for FlyClockbase**

3. **Biodata reuse: published models of the Drosophila circadian clock tend to ignore much of the directly observed data now available in FlyClockbase**

4. **FlyClockbase as a resource: pioneering a prototypical Versioned General Information Resource (VGIR) by bioreasoning through time series data from 25 years of research on the wildtype *Drosophila melanogaster* circadian clock**

5. **Bioreasoning insight on biology: observed expressions of the circadian clock proteins PERIOD and TIMELESS reveals clear differences in variances of the daily times at which their respective peaks occur in wildtype *Drosophila melanogaster* as reported in FlyClockbase**

6. **Bioreasoning insight on methods: comparing the accuracy of PCR-based and other mRNA measuring methods for quantifying expression of *period*, a circadian clock mRNA reported in FlyClockbase**

7. **Human error analyses: how rates of diverse error types impact biodata, bioreasoning, or code in FlyClockbase, Evolvix, and beyond**

8. **Statistical logic: why qualitative research is essential for the quantitative science in FlyClockbase and why Evolvix must learn to compile statistical logics**

9. **Biodata stability requirements: abstracting storage for stabilizing a Versioned General Information Resource (VGIR) like FlyClockbase with a FAIR and VIEWABLE long-term data format in a modeling language like Evolvix**

10. **How to evolve a compiler for Evolvix with the Butterfly methodology: software development life-cycle, interdisciplinary workflows, roles, architecture, and modes of operation in growing a century-stable computer language for biouncertainty in FlyClockbase or in biology**

11. **Bioreasoning documentation for reproducible code: how the here-defined DISCOVARCY principles are a first step towards Literate Programming in FlyClockbase, Evolvix, and beyond**

12. **Biodata survival: how evolutionary ecology principles for memes can guesstimate the stability of FlyClockbase and Evolvix or other biological databases and languages**

from their contexts and features

13. **Biouncertainty foundations: exploring accuracy of potential knowledge-uncertainty – why validation fails, quantifying imperfections is succeeding, and Evolvix requires new logics for uncertainty in FlyClockbase and beyond**

14. **Bioreasoning foundations: instantiating biouncertainty by integrating available real-world knowledge-uncertainty in FlyClockbase and beyond depends on responsible human reasoning and compiler features envisioned for a language like Evolvix**

15. **Biodatamation foundations: How to simplify bioreasoning with *HUman-MAchine-Negotiation* strategies as envisioned with a compiler for Evolvix – made for organizing, searching, and testing exceptions in biology by developing century-stable logics for data-oriented insight storage in FlyClockbase and beyond.**

16. **Grand research challenges: why diversity is essential for complex research in biodata science, evolutionary systems biology, and beyond – as shown in examples like FlyClockbase and Evolvix**

Loewe L, Mau B, and Kliman R, (2021) “**Hidden biases in DNA sequence diversity**”.

[In preparation for submission to Molecular Biology and Evolution in Spring 2018]

Aiming to produce high-precision DNA sequence diversity estimates in Drosophila from next-generation sequencing datasets with incomplete coverage, we found biases that affect our estimates and are near impossible to control for. These biases are caused by an incorrect handling of different types of zero when calculating DNA sequence diversity. A thorough analysis shows that this is a fundamental problem for high-precision measurements of diversity in DNA sequences that do not have complete coverage. In our samples the problem appears substantial enough to suggest that conclusions in population genetics may be worth revisiting if they are based on rather narrow differences in diversity. No easy solution exists for incomplete sequences. The long dormancy of this manuscript allowed us to make further conceptual progress in how to explain the intricate nature of this problem.

Refereed Publications

L32 Wesley C. Warren, Raquel García-Pérez, Sen Xu, Kathrin P. Lampert, Domitille Chalopin, Matthias Stöck, **Laurence Loewe**, Yuan Lu,, Lukas Kuderna, Patrick Minx, Michael J. Montague, Chad Tomlinson, LaDeana W. Hillier, Daniel N. Murphy, John Wang, Zhongwei Wang, Constantino Macias Garcia, Gregg W. C. Thomas, Jean-Nicolas Volff, Fabiana Farias, Bronwen Aken, Ronald B. Walter, Kim D. Pruitt, Tomas Marques-Bonet, Matthew W. Hahn, Susanne Kneitz, Michael Lynch, Manfred Schartl (2018) "**The celibate genome of the Amazon molly, *Poecilia formosa*"**, *Nature Ecology & Evolution* (**printed**)
Based on my work in L11 the senior author invited me to quantify the potential impact of paternal introgression on the speed of Muller's ratchet. I wrote the respective section in the online methods and providing Supplemental Figure 6, which are important for the overall analysis. More remains to be done on this though.
URL https://www.nature.com/natecolevol/

L31 McLoone B, Fan W-T L, Pham A, Smead R, and **Loewe L** (2018) "**Stochasticity, Selection, and the Evolution of Cooperation in a Two-Level Moran Model of the Snowdrift Game**", *Complexity*, vol. 2018, Article ID 9836150
Here we explore the evolutionary dynamics of cooperation in a meta-population with two levels of selection and apply various stochastic and deterministic modeling paradigms. This is more abstract study lays the foundations for further investigations of evolutionary game theory trade-offs in the bacterial behavior of the pathogen M. tuberculosis*. We show that an evolutionary game likely to occur under broad circumstances and known as the 'Snowdrift Game', can surprisingly result in the evolution of cooperation under stochasticity where it would not for equivalent deterministic models.*
URL https://doi.org/10.1155/2018/9836150

L30 **Loewe L**, Scheuer KS, Keel SA, Vyas V, Liblit B, Hanlon B, Ferris MC , Yin J, Dutra I, Pietsch A, Javid CG, Moog CL, Meyer J, Dresel J, McLoone B, Loberger S, Movaghar A, Gilchrist-Scott M, Sabri Y, Sescleifer D, Pereda-Zorrilla I, Zietlow A, Smith R, Pietenpol S, Goldfinger J, Atzen SL, Freiberg E, Waters NP, Nusbaum C, Nolan E, Hotz A, Kliman RM, Mentewab A, Fregien N, Loewe M (2017) "**Evolvix BEST Names for semantic reproducibility across code2brain interfaces**" *Ann. New York Acad. Sci.* 1387:124-144 *What originally seemed like a brief extension of* [L28] *became a massive study of one of the hardest problems in biology and computer science. It had to be cut short after realizing why naming is an infinitely complex problem. The 21 print and 74 online pages define key concepts for Evolvix development: Code2Brain interfaces, semantic reproducibility, semantic rot, aspects of naming complexity, ontology computing, fundamental modes of computing and how they impact naming bugs. We illustrate why naming is so hard in science, why cache-invalidation is a twin-problem, and how social contracts could reduce naming costs. Introducing the Flipped Programming Language Design approach, we show why it is essential for developing Evolvix into a user-friendly long-term backwards compatible programming language that protects user investments for progress in EvoSysBio* [L29]*. We tested, how editors from humanities can help programmers, report a mini-survey on naming, and provide 'naming forms' that capture how we have been improving names for Evolvix. We apply BEST Names to develop the Project Organization Stabilizing Tool (POST) System that defines critical Evolvix infrastructure to help separate different levels of software reliability, stability, and review-rigor. POST is easily adapted and recursive (aptly formatted as a 26 page 'POST paper in the BEST Names paper').*

URL: http://dx.doi.org/10.1111/nyas.13192 ;
http://evolvix.org/naming ; http://evolvix.org/post

L29 **Loewe L** (2016) "**Systems in Evolutionary Systems Biology**", pp. 297-318, vol. 4, in *Encyclopedia of Evolutionary Biology*, eds.: Richard M. Kliman (Chief Ed.) & Hiroshi Akashi (*Molecular and Genome Evolution* Section Ed.), Oxford, UK, Academic Press. *Summarizing discussions of recent years, this review substantially redefines and updates the mechanistic EvoSysBio framework I published in 2009* [L14] *by defining EvoSysBio much more precisely. It sets a long-term research agenda for studying cancer cell biology and antibiotics resistance evolution, highlighting the substantial advances in systems science and modeling that are required for achieving the long-term goals defined here. While* [L29] *replaces* [L14] *as my recommended best introduction to EvoSysBio,* [L14] *still contains the most comprehensive list of references for documenting that a patched mechanistic fitness causality network stretches all the way from genotype to phenotype (as required for integrating "all we know" to predict diseases in personalized medicine).*

URL: http://evolutionarysystemsbiology.org/pdf/Loewe-2016-evosysbio.pdf
http://dx.doi.org/doi:10.1016/B978-0-12-800049-6.00184-0

L28 **Loewe L**, Scheuer KS, and Keel SA (2016) "**Evolvix concept: BEST Names for semantic units increase semantic reproducibility and help combine complex biological models**". *Proc.* of the Workshop on *Data Science, Learning and Applications to Biomedical and Health Sciences* (DSLA-BHS 2016), pp. 67-73, NYAS, New York City. *A sea of synonyms and the perpetual tension between expert abbreviations and the need of beginners for longer names that are easier to understand can make computing in biology very challenging. Here I present what Evolvix can do to help reduce this problem. This peer-reviewed paper extends* [T5] *and is in turn extended by* [L30].

URL: https://www.nyas.org/BigDataHealth
https://sites.google.com/site/dslabhs2016/proceeding-papers

L27 Ehlert, K and **Loewe L** (2014) "**Lazy Updating of hubs can enable more realistic models by speeding up stochastic simulations**". *Journal of Chemical Physics* 141:204109, 20 pages. PMCID: PMC4255425
Introduces a new way of approximating concurrent systems; this is relevant for simulating some biochemical networks, volume changes, temperature gradients and more.
URL: http://dx.doi.org/10.1063/1.4901114

L26 Watterson S, Guerriero ML , Blanc M, Mazein A, **Loewe L**, Robertson KA, Gibbs H, Shui G, Wenk MR, Hillston J, and Ghazal P (2013) "**A model of flux regulation in the cholesterol biosynthesis pathway: Immune mediated graduated flux reduction versus statin-like led stepped flux reduction**". *Biochimie* 95 (3):613-621.
Improves on [L22] *to explore new ways of controlling the cholesterol synthesis pathway.*
URL: http://dx.doi.org/10.1016/j.biochi.2012.05.024

L25 McGaugh SE, Heil CSS, Manzano-Winkler B, **Loewe L**, Goldstein S, Himmel TL, and Noor MAF (2012) "**Recombination modulates how selection affects linked sites in drosophila**". *PLoS Biology* 10(11): e1001422, 17 pages. PMCID: PMC3496668
Explores empirical evidence for the impact of recombination on selection under linkage. S. Goldstein and I helped with the analysis.
URL: http://dx.doi.org/10.1371/journal.pbio.1001422

L24 Modrzynska K, Creasey A, **Loewe L**, Cezard T, Martinelli A, Borges S, Cravo P, Blaxter M, CarterR, and Hunt P (2012) "**Genome-wide re-sequencing defines mutations of complex chloroquine resistance in malaria**". *BMC Genomics* 13:106, 16 pages.
Uses evolution experiments and NextGen sequencing to identify resistance loci in mouse malaria parasites. I developed the approach to compute statistical significance in these noisy datasets. Follows [L21].
URL: http://www.biomedcentral.com/1471-2164/13/106

L23 **Loewe L** (2012) "**How evolutionary systems biology will help understand adaptive landscapes and distributions of mutational effects**". *Evolutionary Systems Biology: Adv. in Experimental Medicine & Biology* (O. Soyer, ed.) vol. 751, pp 399-410. Springer.
Overview of what mechanistic evolutionary systems biology could do, following [L14].
URL: http://dx.doi.org/10.1007/978-1-4614-3567-9_18

L22 **Loewe L**, Guerriero ML, Watterson S, Moodie S, Ghazal P and Hillston, J (2011) "**Translation from the quantified implicit process flow abstraction in SBGN-PD diagrams to Bio-PEPA illustrated on the cholesterol pathway**".
Transactions on Computational Systems Biology XIII, (Priami C, et al. eds.),
Lecture Notes in Computer Science LNCS vol. 6575, pages 13-38.
Further improvements to the bridge from SBGN to Bio-PEPA as described in [L16] *and application of the system to the cholesterol synthesis pathway.*
URL: http://dx.doi.org/10.1007/978-3-642-19748-2_2

L21 Hunt P, Martinelli A, Borges S, Modrzynska K, Creasey A, Rodrigues L, Beraldi D, **Loewe L**, Fawcett R, Kumar S, Thomson M, Trivedi U, Otto T, Pain A, Blaxter M and Cravo P (2010) "**Experimental evolution, genetic analysis and genome re-sequencing reveals the mutation conferring artemisinin resistance in an isogenic lineage of malaria parasites**". *BMC Genomics* 11:499 (13 pages).
Uses evolution experiments in the lab to identify resistance loci in mouse malaria parasites to help anticipate malaria evolution. I helped to compute statistical significance.
URL: http://www.biomedcentral.com/1471-2164/11/499

L20 Haddrill PR, **Loewe L**, and Charlesworth B (2010) "**Estimating the parameters of selection on nonsynonymous mutations in *Drosophila pseudoobscura* and *D. miranda***". *Genetics* 185:1381-1396.
Applies the method in [L6] *to a much bigger dataset.*
URL: http://www.genetics.org/cgi/content/abstract/185/4/1381

L19 **Loewe L** and Hill, WG (2010) "**Introduction: The population genetics of mutations: good, bad and indifferent**". *Philosophical Transactions of the Royal Society Series B* vol. 365:1153-1167.
An overview of the population genetics of mutations that highlights future challenges.
URL: http://rstb.royalsocietypublishing.org/content/365/1544/1153

L18 Waxman D and **Loewe L** (2010) "**A stochastic model for a single click of Muller's ratchet**". *Journal of Theoretical Biology* 264:1120-1132.
Explores a new approach to computing the rate of the ratchet and compares it to evolution@home simulations.
URL: http://dx.doi.org/10.1016/j.jtbi.2010.03.014

L17 Akman OE, Guerriero M-L, **Loewe L** and Troein C (2010) "**Complementary approaches to understanding the plant circadian clock**". FBTC 2010 Workshop "From Biology to Concurrency and Back", http://disi.unitn.it/~fbtc2010/ *Electronic Proceedings in Theoretical Computer Science* (EPTCS) 19:1–19, DOI: 10.4204/EPTCS.19.1
Further steps towards an evolutionary systems biology model of a circadian clock with entrainment. Contains a systems biology model of the Ostreococcus circadian clock with realistic parameter values. I contributed the mutational robustness analyses [*see* L13]*.*
URL: http://arxiv.org/abs/1002.4661

L16 **Loewe L**, Moodie S and Hillston J (2009) "**Quantifying the implicit process flow abstraction in SBGN-PD diagrams with Bio-PEPA"**. *CompMod* 2009 Workshop, http://combio.abo.fi/compmod09/, *Electronic Proceedings in Theoretical Computer Science* (EPTCS) 6:93-107, DOI: 10.4204/EPTCS.6.7
Builds a compiler that maps biochemical models from SBGN to Bio-PEPA to build a bridge from visual model construction to automated simulations.
URL: http://arxiv.org/abs/0910.1410

L15 Duguid A, Gilmore S, Guerriero ML, Hillston J and **Loewe L** (2009) "**Design and development of software tools for Bio-PEPA**". Proceedings of the 2009 Winter Simulation Conference (WSC'09 http://www.wintersim.org/), pp. 956-967, eds.: Rossetti RMD, Hill RR, Johansson B, Dunkin A and Ingalls RG. Austin, Texas.
A description of how the Bio-PEPA modelling tools are organised to facilitate the automatic conversion of models between different mathematical and other formalisms.
URL: http://www.informs-sim.org/wsc09papers/091.pdf

L14 **Loewe L** (2009) "**A framework for evolutionary systems biology**". *BMC Systems Biology* 3:27 (34 pages, designated 'highly accessed' by BMC from continuous traffic).
The definitive reference for the mechanistic framework for evolutionary systems biology I developed to bring together systems biology and evolutionary genetics to help understand fitness landscapes and distributions of mutational effects. Core aspects of this framework have been reworked in 2015; hence, please use the newer and clearer terms from [L28]*. However,* [L14] *still contains the best collection of references demonstrating the feasibility of a computationally constructed Fitness Causality Network (as defined in* [L28]*).*
URL: http://www.biomedcentral.com/1752-0509/3/27/

L13 **Loewe L** and Hillston J (2008) "**The distribution of mutational effects on fitness in a simple circadian clock**". Proceedings of the 6th International Conference on Computational Methods in Systems Biology, CMSB08, *Lecture Notes in Bioinformatics* 5307:156-175. (Heiner M and Uhrmacher AM, eds.) Rostock, Germany.
The first proof of concept for my new approach to evolutionary systems biology. See [L14]
URL: http://dx.doi.org/10.1007/978-3-540-88562-7_14

L12 **Loewe L** and Cutter A (2008) "**On the potential for extinction by Muller's Ratchet in *Caenorhabditis elegans***". *BMC Evolutionary Biology* 8:125 (13 pages).
Here I combined my theory [L7] *and evolution@home results with the expertise of my collaborator on the worm C. elegans by building on* [L11].
URL: http://www.biomedcentral.com/1471-2148/8/125

L11 **Loewe L** and Lamatsch D (2008) "**Quantifying the threat from Muller's ratchet in the Amazon molly (*Poecilia formosa*)**". *BMC Evolutionary Biology* 8:88, (20 pages, designated 'highly accessed' by BMC, peak after news coverage).
Here I combined my theory [L7] *and evolution@home results with the expertise of my collaborator on the fish P. formosa. Building on older work I also explain how Muller's ratchet theory can be applied to selfing species.*
URL: http://www.biomedcentral.com/1471-2148/8/88

L10 **Loewe L** (2007) "**Evolution@home: observations on participant choice, work unit variation and low-effort global computing**". *Softw. Pract. & Exp.* 37:1289-1318.
Describes the semi-automated global computing by evolution@home and what needs to be improved. Builds on [L3].
URL: http://doi.wiley.com/10.1002/spe.806

L9 **Loewe L** and Charlesworth B (2007) "**Background selection in single genes may explain patterns of codon bias**". *Genetics* 175:1381-1393.
Explores the patterns that deleterious mutations can produce within genes.
URL: http://www.genetics.org/cgi/content/abstract/175/3/1381

L8 **Loewe L** and Charlesworth B (2006) "**Inferring the distribution of mutational effects on fitness in Drosophila**". *Biology Letters* 2:426-430.
Compares different types of distributions and finds the log-normal type to perform best.
URL: http://dx.doi.org/DOI:10.1098/rsbl.2006.0481

L7 **Loewe L** (2006) "**Quantifying the genomic decay paradox due to Muller's ratchet in human mitochondrial DNA**". *Genetical Research* 87:133-159.
The most rigorous analysis so far of the potential for mutational meltdown in human mitochrondria, a good pointer to much of the work on Muller's ratchet and the most comprehensive list so far of all the processes that might help to prevent meltdown.
URL: http://dx.doi.org/10.1017/S0016672306008123

L6 **Loewe L**, Charlesworth B, Bartolomé C and Nöel V (2006) "**Estimating selection on non-synonymous mutations**". *Genetics* 172:1079-1092.
We introduce a new approach to estimate the distribution of mutational effects from diversity data in two species that does not depend on ancient demography. We find most new mutations are effectively deleterious but have selection coefficients that are well below the thresholds of what can be detected directly in experiments.
URL: http://www.genetics.org/cgi/content/abstract/172/2/1079

L5 **Loewe L** (2004) "**Response to comment on 'High deleterious genomic mutation rate in stationary phase of *Escherichia coli*'**". *Science* 304:518d-518d.
I show that earlier criticism of my work [L4] *is unjustified and how bacteria might cooperate to be more flexible.*
URL: http://www.sciencemag.org/cgi/content/full/304/5670/518d

L4 **Loewe L**, Textor V and Scherer S (2003) "**High deleterious genomic mutation rate in stationary phase of *Escherichia coli***". *Science* 302:1558-1560.
The first mutation accumulation experiment in stationary phase. Like in all MA experiments, only large selection coefficients could be observed. This work uncovers complex evolutionary processes in stationary phase that have a wide range of implications that are best explored in computational models yet to be built.
URL: http://www.sciencemag.org/cgi/content/abstract/302/5650/1558

L3 **Loewe L** (2002) "**evolution@home: Experiences with work units that span more than 7 orders of magnitude in computational complexity**". Proceedings of the 2nd International Workshop on Global and Peer-to-Peer Computing on Large Scale Distributed Systems at the 2nd IEEE/ACM International Symposium on Cluster Computing and the Grid (CCGrid2002), 21-24 May, Berlin, Germany, pages 425-431.
There are powerful normalizing forces that get a wide range of tasks computed, if users are allowed to choose the complexity of tasks they want to compute (evolution@home is first to offer this option in global computing).
URL: http://doi.ieeecomputersociety.org/10.1109/CCGRID.2002.1017176

L2 **Loewe L** (2002) "**Global computing for bioinformatics**".
Briefings in Bioinformatics 3:377-388.
Reviews types of tasks and examples that can benefit from global computing in bioinformatics.
URL: http://bib.oxfordjournals.org/cgi/content/abstract/3/4/377

L1 **Loewe L** and Scherer S (1997) "**Mitochondrial Eve: The plot thickens**".
Trends in Ecology & Evolution 12:422-423.
Explores how archaeological data could be used to make inferences on mutation rates. Superseded by newer work (under revision).
URL: http://dx.doi.org/10.1016/S0169-5347(97)01204-4

Books

B2 Scheuer KS, Hanlon B, Dresel JW, Nolan ED, Davis JC, **Loewe L** (2017) "**FlyClockbase: Importance of Biosystems Curation for Analyzing Variability in Circadian Clock of *Drosophila melanogaster* by Integrating Time Series from 25 Years of Research**" [book-length discussion of circadian clock biodata science, has now been re-packaged into a series of reports slated for a Virtual Issue in the journal *Database*]
Circadian clocks impact health and fitness by controlling daily rhythms of gene-expression through complex gene-regulatory networks. Deciphering how they work requires experimentally tracking changes in amounts of clock components. We designed FlyClockbase to simplify data-access for biologists and modelers, biosystems curating over 400 time series observed in wildtype fruit flies from 25 years of clock research. Substantial biodata science efforts were essential for identifying differences in peak time variance of the clock-proteins 'PERIOD' and 'TIMELESS', which probably stem from differences in phosphorylation-network complexity. We repeatedly encountered systemic limitations of contemporary data analysis strategies in our work on circadian clocks. Thus, we used it as an opportunity for composing a panoramic view of the broader challenges in biodata science, which are likely to increase as biologists aim to integrate all existing expertise in order to address various grand challenges. We developed and tested an interdisciplinary research workflow, which enables biologists and compiler-architects to define compilers more aware of typical issues in biology for efficiently constructing and maintaining Versioned Biological Information Resources (VBIRs).
At book length, we report insights gleaned from our practical clock research that are essential for defining a VBIRs infrastructure, which improves the efficiency of biosystems curation in order to make it sufficiently easy to distribute among many more biologists.
Published on BioRxive, 2017-08-03 as versioned variant QQv1r4 (before repacking).
URL: https://doi.org/10.1101/099192

B1 **Loewe L** and Hill WG (eds., 2010) "**The population genetics of mutations: good, bad and indifferent**". *Philosophical Transactions of the Royal Society B* vol. 365, issue no 1544, pages 1149-1294, ISSN 0962-8436, ISBN: 978-0-85403-813-8.
This collection of papers by influential scientists highlights many of the challenges that we face when trying to understand the evolution of life with a special view on mutations.
URL: http://rstb.royalsocietypublishing.org/content/365/1544.toc

Technical Reports

T5 **Loewe L** and Keel SA (2014) "**BEST Names for semantic units to support reproducible modeling**". Contributed to "Reproducibility@XSEDE" Workshop, 4 pages, 2014-07-14, XSEDE14 Annual Conference, Atlanta, GA, USA.
This paper introduced BEST Names, writing up the first insights from the work of adding general purpose programming language capabilities to Evolvix. BEST Names have since become foundational to how Evolvix is being designed. The 'peer-review light' from this workshop substantially improved follow-on papers with experiences we made [L28, L30].
URL: https://www.xsede.org/documents/659353/703287/xsede14_loewe.pdf

T4 James D, Wilkins-Diehr N, Stodden V, Colbry D, Rosales C, Fahey M, Shi J, Silva RF, Lee K, Roskies R, **Loewe L**, *et al*. [44 additional authors] (2014) "**Standing Together for Reproducibility in Large-Scale Computing: Report on reproducibility@XSEDE**". arXiv:1412.5557 [cs.DC].
URL: http://arxiv.org/abs/1412.5557

T3 Ehlert K and **Loewe L** (2013) "**Lazy Updating Increases the Speed of Stochastic Simulations**". Arxiv Quantitative Biology-Quantiative Methods, arXiv: 1310.2068 [q-bio.QM].
URL: http://arxiv.org/abs/1310.2068

T2 **Loewe L,** Moodie S and Hillston J (2009) "**Technical Report: Defining a textual representation for SBGN Process Diagrams and translating it to Bio-PEPA for quantitative analysis of the MAPK signal transduction cascade**". Technical Report EDI-INF-RR-1334, School of Informatics, University of Edinburgh.
Defines a textual representation for the systems biology graphical notation process diagrams and explains how this can be augmented by quantitative information to facilitate automated simulations.
URL: https://www.inf.ed.ac.uk/publications/report/1334.html

T1 **Loewe L** (2008) "**Designing a Front-End for Bio-PEPA**".
7th Workshop on Process Algebra and Stochastically Timed Activities, (S. Gilmore, ed.) 30-31 July 2008, Edinburgh (5 pages).
A design prototype for a biologist-friendly model implementation language.

Other / Educational Publications

O8 **Loewe L** (2015) "**EvoSysBio LIFTs: Microbes and Antibiotics**", Figshare.com
A very brief introduction to evolutionary systems biology.
URL: http://dx.doi.org/10.6084/m9.figshare.2056428

O7 **Loewe L** (2015) "**EvoSysBio in 10 Slides**", Figshare.com
A very brief introduction to evolutionary systems biology.
URL: https://dx.doi.org/10.6084/m9.figshare.1427128

O6 **Loewe L** and Hill, WG (2010) "**Preface: Mutations and Brian Charlesworth**". *Philosophical Transactions of the Royal Society B* 365:1151-1151.
Dedication of the associated themed issue on the population genetics of mutations: to Brian Charlesworth on the occasion of his 65th birthday for his many contributions.
URL: http://rstb.royalsocietypublishing.org/content/365/1544/1151

O5 **Loewe L** and Hillston J (2008) "**Computational models in systems biology**". Invited meeting report. *Genome Biology* 9:328 (3 pages).
URL: http://genomebiology.com/2008/9/12/328

O4 **Loewe L** (2008) "**Evolution@home: The first global computing system for evolutionary biology**". Invited chapter in *Distributed & Grid Computing - Science Made Transparent for Everyone. Principles, Applications and Supporting Communities*, (book ed.: M. Weber),
URL: http://Rechenkraft.net

O3 **Loewe L** (2008) "**Negative Selection**". *Nature Education* 1(1)59.
Short introduction with simplified fitness-landscape cartoons in Fig.1; as invited by the editors of the "Evolutionary Genetics" section of "Nature Education".
URL: http://www.nature.com/scitable/topicpage/Negative-Selection-1136

O2 **Loewe L** (2008) "**Genetic Mutation**". *Nature Education* 1(1)113.
Short introduction as invited by Nature Education for their Evolutionary Genetics section.
URL: http://www.nature.com/scitable/topicpage/Genetic-Mutation-1127

O1 **Loewe L** (2006) "**Population Genetics Group Meeting 2006**". Meeting report, UK *Genetics Society News*, Issue 57, pp. 22-25.

Abstracts of Posters

Meyer, J.; Alarid, E.; and **Loewe, L.** (2017) "**Evolutionary Systems biology integration of multi-level CTMC interaction models of biochemistry and cancer cell growth using Evolvix**", Society for Molecular Biology & Evolution Conference 2017, July 2nd-6th, Austin, Texas.
URL https://peerj.com/preprints/3371/

Northey, S.; Hove, C.; Kao, J.; Ide, J.; McKinney, J.; and **Loewe, L.** (2017) "**Integrating ecology and evolution to study hypothetical dynamics of algal blooms and Muller's ratchet using Evolvix**", Society for Molecular Biology & Evolution Conference 2017, July 2nd-6th, Austin, Texas.
URL https://peerj.com/preprints/3218/

Scheuer, K.; and **Loewe, L.** (2017) "**Are VBIRs like FlyClockbase the new Genome Projects?",** Society for Molecular Biology & Evolution Conference 2017, July 2nd-6th, Austin, Texas.

Hove, C.; Northey, S.; Kao, J.; Ide, J.; McKinney, J.; and **Loewe, L.** (2017) "**Integrating ecology and evolution to study hypothetical predator-prey and Muller's ratchet dynamics in *Karlodinium veneficum* using Evolvix**", CALS Undergraduate Research Symposium, 2017 April 18, Madison, WI.

McLoone B, Fan W-T, Pham A, Smith T, Smead R, Pepperell CS, and **Loewe L** (2017) **"Stochasticity Promotes the Evolution of Cooperation in a Multilevel Model of the Snowdrift Game"**, National Human Genome Research Institute Annual Meeting 2017, April, 12-14th, St. Louis, Missouri; *minimal updates for presentation also at CSH meeting.*

Reilly, K.; and **Loewe, L.** (2016) "**Evaluating Contradictory Evidence When Building Models of Temperature Dependency In The Circadian Clock of *Drosophila melanogaster***", Poster at the Undergraduate Biology Symposium, Biology 152, Union South, December 14, UW-Madison.

Loewe, L. (2016) **"Fundamental Modes of Computing"** Workshop on "EvoSysBio and Modeling", 2016 Aug 4-5, WID, University of Wisconsin-Madison, Madison, WI.
URL: http://evolutionarysystemsbiology.org/meeting/2016-Madison/

Loewe, L. (2016) "**How a Framework for Evolutionary Systems Biology Can Accelerate Reproducible Modeling of Mechanistic Fitness Landscapes**", The Allied Genetics 2016 Conference, July 13-17, Orlando, Florida.

Loewe, L. (2016) "**Using Evolvix for Obtaining Time-Series of Amounts for Pure Mass-Action Systems in Biology**", 5th International Conference on Quantitative Genetics, June 13, Madison, WI.

Loewe, L. (2016) "**Working on Evolvix: The first general-purpose programming language designed by biologists for biologists**", 5th International Conference on Quantitative Genetics, June 13, Madison, WI.

Hotz, A.; Scheuer, K.; and **Loewe, L.** (2016) "**Clarifying long-term memory formation in *Drosophila melanogaster* by integrating the influences of the Notch and Wingless Signaling Pathways of CREB and β-Catenin**", Poster at the Undergraduate Research Symposium, April 14, UW-Madison.

Nolan, E.; Scheuer, K.; **Loewe, L.** (2016) "**A Proposed Role for Melatonin: Circadian Regulation in *Drosophila melanogaster***", Poster at the Undergraduate Research Symposium, April 14, UW-Madison.

Nusbaum, C; Scheuer, K.; **Loewe, L.** (2016) "**Effects of dvMAT expression on depression and the circadian clock in *Drosophila melanogaster***", Poster at the Undergraduate Research Symposium, April 14, UW-Madison.

Waters, N.; Scheuer, K.; and **Loewe, L.** (2016) "**The Role of Clockwork Orange and MicroRNA in the *Drosophila Melanogaster* Circadian Clock**", Poster at the Undergraduate Research Symposium, April 14, UW-Madison.

Loberger, S.; Movaghar, A.; and **Loewe, L.** (2016) "**Are there Unexpected Parallels Between Abstract Algebra and Biology Building Blocks?",** Poster at the Undergraduate Research Symposium, April 14, UW-Madison.

Sabri, Y.H.; Sescleifer, D.; Pereda-Zorrilla, I.; and **Loewe, L.** (2016) "**Git version control for managing shared simulation models**", Poster at the Undergraduate Research Symposium, April 14, UW-Madison.

Zietlow, A.; Smith, R.; Gilchrist-Scott, M.; and **Loewe, L.** (2016) "**Why not ask potential users what they love or hate about programming languages?**", Poster at the Undergraduate Research Symposium, April 14, UW-Madison.

Loewe, L. (2016) "**Evolvix: Flipped Programming Language Design for Biology**", Ed Lightfoot Celebration: A Symposium and Banquet, April 7, Discovery Building, UW-Madison.

Loewe, L. (2016) "**Using Evolvix for Obtaining Time-Series of Amounts for Pure Mass-Action Systems in Biology**", Ed Lightfoot Celebration: A Symposium and Banquet, April 7, Discovery Building, UW-Madison.

Hotz, A.; Scheuer, K.; and **Loewe, L.** (2015) "**Combinatorial Complexity and CLOCK Phosphorylation in the Circadian Clock of Drosophila melanogaster**", Poster at the Undergraduate Research Symposium, April 16, UW-Madison.
URL: http://evolution.ws/loewe-lab/posters/downloads/poster-pdfs/combinatorial-complexity-and-clock-phosphorylation-in-the-circadian-clock-of-drosophila-melanogaster

Tucker, D.; Scheuer, K.; and **Loewe, L.** (2015) "**Circadian Clock Synchronization and the Roles of PDF, cAMP, and PKA in Drosophila melanogaster**", Poster at the Undergraduate Biology Symposium, Biology 152, Union South, May 5, UW-Madison.
URL: http://evolution.ws/loewe-lab/posters/downloads/poster-pdfs/circadian-clock-synchronization-and-the-roles-of-pdf-camp-and-pka-in-drosophila-melanogaster

Scheuer, K. and **Loewe, L.** (2015) "**Evidence-Driven Hypothesis Modeling of the *Drosophila melanogaster* Circadian Clock**", Poster at the Workshop on Evolutionary Systems Biology & Modeling, Aug. 25, UW-Madison.
URL: http://evolution.ws/loewe-lab/posters/downloads/poster-pdfs/evidence-driven-hypothesis-modeling-of-the-drosophila-melanogaster-circadian-clock

Nusbaum, C; Scheuer, K.; and **Loewe, L**. (2015) "**Influence of Bipolar Disorder Drug Treatments (Lithium, Risperidone and Fluoxetine) on the Circadian Protein SGG in Drosophila melanogaster**", Poster at the Undergraduate Biology Symposium, Biology 152, Union South, Dec. 8, UW-Madison.
URL: http://evolution.ws/loewe-lab/posters/downloads/poster-pdfs/influence-of-bipolar-disorder-drug-treatments-lithium-risperidone-and-fluoxetine-on-the-circadian-protein-sgg-in-drosophila-melanogaster

Waters, N; Scheuer, K; and **Loewe, L.** (2015) **"The Function of Evening and Morning Oscillators in the Circadian Clock"** Poster at the Undergraduate Research Experience (ILS 250) Undergraduate Research Scholars Program, Dec. 9 and Dec 14, UW-Madison.
URL: see http://evolution.ws/loewe-lab/posters/downloads/poster-pdfs/

Hotz, A.; **Loewe, L.** (2014): **"The Phosphorylation Process of CLOCK in the Circadian Clock of the *Drosophila melanogaster*"** Undergraduate Biology Symposium, Biology 152, Dec. 9, UW-Madison.
URL: see http://evolution.ws/loewe-lab/posters/downloads/poster-pdfs/

Goldfinger, J.; **Loewe, L.** (2014): "**Simulating Fixation of Novel Mutations in the Moran Model**" CALS Undergraduate Poster session, Microbiology, April 22, UW-Madison.

Loewe, L.; Keel, S.; Ehlert, K.; Flores-Lorka, I.; Scheuer, K. (2014): "**Why Evolutionary Systems Biology Needs a Model Description Language to Cut Costly Coding Complexity**" SMBE 2014 June 9, Puerto Rico.

Loewe, L.; Keel, S.; Ehlert, K.; Flores-Lorka, I.; Scheuer, K. (2014): **"Simulating Metabolic Networks with the Evolvix Model Description Language"** HLSC UW-Madison, MIR Metabolomics Meeting, Aug. 5, Madison, WI.

Loewe, L.; Keel, S.; Ehlert, K.; Flores-Lorka, I.; Scheuer, K. (2014): "**Simulations of Ecology and Evolution in the Evolvix Model Description Language**" Population Genetics Midwest Meeting, July 19, Chicago, IL.

Scheuer, K.; **Loewe, L**. (2013): "**Possible Applications for an Updated Model of the *Drosophila melanogaster* Circadian Clock**" April 17, UW-Madison Undergraduate Research Symposium.
URL: see http://evolution.ws/loewe-lab/posters/downloads/poster-pdfs/

Dresel, J.; Scheuer K, **Loewe, L.** (2013): "**Interactions of the F Box Protein Jetlag in Circadian Clocks**" April 17 UW-Madison Undergraduate Research Symposium.
URL: see http://evolution.ws/loewe-lab/posters/downloads/poster-pdfs/

Goldstein, S.; **Loewe, L.** (2013) **"Modeling Whole-Genome Polymorphisms with Point Processes to Quantify Selective Sweeps"** SMBE Meeting, 2013 July 7-11, Chicago, IL.

Scheuer, K.; **Loewe, L.** (2012): **"Biological Modeling and Language Development Using the Circadian Clock of *Drosophila melanogaster*"** July 25, Welton Summer Honors Apprenticeship Retreat.

Scheuer, K.; **Loewe, L.** (2012): **"A Molecular Systems Biology Model of the Circadian Clock of *Drosophila melanogaster*"** April 18, UW-Madison Undergraduate Research Symposium.
URL: see http://evolution.ws/loewe-lab/posters/downloads/poster-pdfs/

Yang, P.; **Loewe, L.** (2012): "**Building a Quantitative Model of the Cholesterol Pathway**" April 18, UW-Madison Undergraduate Symposium.

Loewe, L. (2012): "**Estimating Distributions of Mutational Effects Using a Systems Biology Approach in a Circadian Clock**" SSE & ESEB Evolution Meeting 2012, July 6-10, Ottawa, Canada.

Ehlert, K.; **Loewe, L.** (2012): "**Increasing the Speed of Stochastic Simulations of Reaction Networks**" SSE & ESEB Evolution Meeting, July 6-10, Ottawa, Canada & MathBio 4, October 18-19, Wisconsin Institute for Discovery, UW-Madison.

Keel, S; **Loewe, L.** (2012): "**Muller's Ratchet in Large Populations**" SSE & ESEB Evolution Meeting 2012, July, 6-10, Ottawa, Canada. & MathBio 4, October 18-19, Wisconsin Institute for Discovery, UW-Madison.

Flores-Lorca, I; **Loewe, L.** (2012): "**Observing Time Series of Counts in Simulations**" MathBio 4, October 18-19, Wisconsin Institute for Discovery, UW-Madison.

Loewe, L. & Poon, P. (2012) "**No Delayed Consumption**" EvoSysBio Meeting UW-Madison.

Loewe, L. and Viglas, S. (2010) "**SQL vs NoSQL for Simulation Data Management**" iDEA contribution; poster presented at "idea Lab lunch", Feb. 23, School of Informatics, University of Edinburgh; with associated text at http://forum.idea.ed.ac.uk/ as reviewed for grant support, but not funded back then. *Explores approaches for building extremely scalable simulation results databases, as needed for the analysis of very complex computational models. The problems addressed here eventually contributed to the early 2014 decision to develop Evolvix into a general-purpose programming language.*

URL: http://forum.idea.ed.ac.uk/idea/sql-vs-nosql-simulation-data-management

Abstracts of Talks

Moog, C.; Warner, J.; and **Loewe, L.** (2017) "**Why versioning is crucial for evolutionary systems biology**", Talk contributed to the Symposium 'Reproducibility and Molecular Evolution', Society for Molecular Biology & Evolution Conference 2017, July 2nd-6th, Austin, Texas.

Loewe, L. (2017) **"What would it take to integrate a type system for computing tasks into a general-purpose programing language?"**, HTCondor Week, May 2-5, University of Wisconsin, Madison, Madison, WI

Loewe, L. (2016) **"The Importance of Names in Biological Modeling and the Flipped Programming Language Design Approach"** Workshop on "EvoSysBio and Modeling", Aug 4-5, University of Wisconsin-Madison, Madison, WI.

Rogers, L. **Loewe, L.** (2016) **"Pain(t) by Logic: The Ambiguity Game"** Workshop on "EvoSysBio and Modeling", Aug 4-5, University of Wisconsin-Madison, Madison, WI.

URL: http://evolutionarysystemsbiology.org/meeting/2016-Madison/

Here we tested various designs for Logic operators in order to determine which ones were least ambiguous for selecting various parts of Venn-diagrams. Code2Brain Interface debugging might actually be fun if set up in the right way.

Scheuer, K., Dresel, J., Nolan, E., Hanlon, B., **Loewe, L.** (2016) **"FlyClockbase: a 25-year Overview of Time Series of the Drosophila melanogaster Circadian Clock"** Workshop on "EvoSysBio and Modeling", Aug 4-5, University of Wisconsin-Madison.

URL: http://evolutionarysystemsbiology.org/meeting/2016-Madison/

Loewe L. (2015) **“Evolutionary Systems Biology: Overview and Challenges”** and **“Modeling a Simple Gene-Regulatory Network in Evolvix and the Challenge of Translating between Disciplines”** Workshop on “EvoSysBio and Modeling”, Aug 25, University of Wisconsin-Madison, Madison, WI. *In addition to organizing the Evolutionary Systems Biology Workshop 2015 in Madison, WI, I gave the two presentations above and co-moderated an interdisciplinary discussion and problem-solving session (“Bazaar of Ideas”) at the end of the workshop.*

URL: http://evolutionarysystemsbiology.org/meeting/2015-Madison/

Loewe, L.; Goldstein, S. (2014) **“A New Method for Detecting Selection in Genomic Datasets”** SMBE 2014, June 11, Puerto Rico.

Invited Research Presentations

Invited Discussions

Loewe, L. (2016) Contributed content on how to improve efficiency in science by **“supporting free choice of scientific roles”**, 2016 NSF CyberBridges Workshop, October 22-22, Rochester Institute of Technology, Rochester, New York.

Workshop URL: http://www.cyberbridges.org/2016/

Loewe, L. (2015) Content contributed: “**Evolving Complex Documents**”, NSF Workshop on “CyberBridges: Developing the Next Generation of Cyberinfrastructure Faculty for Computational- and Data-enabled Science and Engineering” (CB 2015), Aug. 31-Sep. 1, Rochester Institute of Technology, Arlington, VA.

Workshop URL: http://www.cyberbridges.org/2015/

Loewe, L. (2014) Content contributed: “**Maximizing Expressivity in Evolvix**” NSF Workshop on “CyberBridges: Developing the Next Generation of Cyberinfrastructure Faculty for Computational and Data-enabled Science and Engineering” (CB 2014), June 2-3, Arlington, VA.

Workshop URL: http://www.cyberbridges.org/2014/

Loewe, L. (2013) Content contributed: “**Getting Started with Evolvix**” NSF Workshop on “CyberBridges: Developing the Next Generation of Cyberinfrastructure Faculty for Computational and Data-enabled Science and Engineering” (CB 2013), July 15-16, Arlington, VA.

Workshop URL: http://www.cyberbridges.org/2013/

Loewe, L. (2012) Content contributed: **“Modeling Made Easy**” NSF Workshop on “CyberBridges: Developing the Next Generation of Cyberinfrastructure Faculty for Computational and Data-enabled Science and Engineering” (CB 2012) June 25-26, Arlington, VA.

Workshop URL: http://www.cyberbridges.org/2012/

National / International Talks

Loewe, L. (2016) “**Evolvix, the Brain2Code Interface and Flipped Programming Language Design for Biology**”, qBio Workshop, March 11-12, Spelman College, Atlanta, GA.

Workshop URL: https://qbioatlanta.wix.com/spelman2016

Loewe, L. (2016) **“Evolvix Concept: BEST Names for Semantic Units Increase Semantic Reproducibility and Help Combine Complex Biological Models”** Workshop on Data Science, Learning and Applications to Biomedical and Health Sciences (DSLA-BHS 2016), Jan 7-8, New York Academy of Sciences, New York City.

Workshop URL: http://www.nyas.org/BigDataHealth

Gutenkunst, R; **Loewe, L;** Swain, P. (2013) **“Mathematical Methods in Evolutionary Systems Biology”** Banff International Research Station, May 26-31, Alberta, Canada.

Loewe, L. (2013) **“Evolutionary Systems Biology, Fitness Landscapes and Evolvix”** Banff International Research Station workshop, May 28, Banff, AB, Canada

Loewe, L. (2012) **“Evolutionary Systems Biology”** Departmental Seminar, Joint CMU-Pittsburgh Ph.D Program in Computational Biology, University of Pittsburgh, PA.

Loewe, L. (2012) **“Linkage Theories”** Workshop on Selection in Population Genetics, May 3-5, Radcliffe Institute for Advanced Study, Harvard University, Boston, MA.

Loewe, L. (2012) **“The Strength of Background Selection”** American Genetics Association Symposium & Workshop on Recombination, Durham, NC.

Loewe, L. (2011) **“Muller’s Ratchet”** and **“Evolutionary Systems Biology”** Uppsala University, Sweden.

Loewe, L. (2011) **“Evolutionary Systems Biology and Distributions of Mutational Effects”** National eScience Center Workshop, Edinburgh, Scotland, UK.

Loewe, L. (2010) **“Evolutionary Systems Biology and Distributions of Mutational Effects”** Seminar at the School of Biological Sciences, University of Exeter, UK.

Loewe, L. (2009) **“The Distribution of Mutational Effects and its Implications”** Seminar at the School of Biological Sciences, Royal Holloway University of London, Egham, UK.

Loewe, L. (2008) **“The Distribution of Mutational Effects on Fitness”** Bioinformatics Lunch, Department of Biology, University of York, Heslington, UK.

Loewe, L. (2007) **“Pollution, Muller’s Ratchet and Possible Extinctions of *Poecilia formosa*”** Seminar at the Department of Biology, University of Hull, Yorkshire, UK.

Loewe, L. (2006) **"Muller’s ratchet".** 4th Training Workshop Molecular Genetic Analyses by the EU Marie Curie Research Training Network **“From Sex to Asex: A Case Study on Transitions and Coexistence between Sexual and Asexual Reproduction”** Malham Tarn Field Centre, UK.

Loewe, L. (2006) **"The Effects of Muller's Ratchet on the Human Y, mtDNA and Unisexual Fish"** Freshwater Biology Group, Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

Loewe, L. (2005) **"Evolutionary Consequences of Deleterious Mutations"** Institute of Animal Evolutionary Ecology, University of Tübingen, Germany.

Loewe, L. (2005) **"Evolution@home: Evolutionary Systems Biology, Global Computing and Muller's Ratchet in Non-Recombining Genomes"** Molecular Pathobiology and Systems Biology Seminars, School of Biosciences, University of Birmingham, UK.

Loewe, L. (2001) **"Evolution@home: New Frontiers in Global Computing and Evolutionary Bioinformatics".** EMBnet Annual General Meeting, Vienna, Austria.

Loewe, L. (1997) **"Mutation Rates, Muller’s Ratchet, Genetic Load and Mitochondrial Eve"** First International Workshop on Human Mitochondrial DNA, Washington, D.C., USA.

Local Talks

Loewe, L. (2016) “**How to Simulate Timeseries in Gene Regulatory Networks using Evolvix**”, CIBM Seminar Talk, March 15th, Laboratory of Genetics, UW-Madison.

Loewe, L. (2016) “**EvoSysBio and Modeling**”, Genetics Faculty Lunch Discussion, May 6th, Laboratory of Genetics, UW-Madison.

Loewe, L**.** (2013) **“Designing Evolvix to Make Modeling Easy for Biologists: Your Input is Welcome”** Systems Biology Theme Meeting, March 12, WID, UW-Madison.

Loewe L, (2013) **“Designing Evolvix (2): Overview and Presentation of Evolvix Prototype 0.0.2”** Systems Biology Theme Meeting, July 2, WID, UW-Madison.

Loewe L**,** (2013) **“Designing Evolvix (3): How to Document”** Systems Biology Theme Meeting, Aug 27, WID, UW-Madison.

Loewe, L. (2012) Various talks in Madison (WID, Animal Sciences, Genetics, Delta Career Workshop, Genetics Training Program Retreat)

Loewe, L. (2011) Various talks in Madison (Animal Sciences, Genetics, CIBM, GSTP, Systems Biology Seminar, Superlab Meeting, internal Lab meetings)

Educational Activities & Presentations

Overview of Classroom Teaching at UW-Madison

URL: http://evolution.ws/loewe-lab/teaching/teaching

Classroom: In-depth Research Seminar on Foundations for Computational Biology

2016 Spring Genetics 677-22: Initiated as a 2 credit discussion course.

This course was approved as part of WisCEL (a new center for active learning). **Syllabus:**

URL: http://evolution.ws/loewe-lab/teaching/downloads/foundcompbio-syllabus-spring-2016

As a result of this course all students contributed 3 posters at the UW-Madison 2016 Undergraduate Symposium and to publication L30: Loewe L, … Loberger S, Movaghar A, Gilchrist-Scott M, Sabri Y, Sescleifer D, Pereda-Zorrilla I, Zietlow A, Smith R, … (2017) “Evolvix BEST Names for semantic reproducibility across code2brain interfaces” *Ann. New York Acad. Sci.* 1387:124-144.

Classroom: EvoSysBio Modeling Introduction

2018 Fall Genetics 546: “Evolutionary Systems Biology Modeling Introduction”; this 3 credit course now has an official number for the first time.

2017 Fall Genetics 677-11: Improved 3 credit course “Evolutionary Systems Biology”.

2016 Fall Genetics 677-11: Improved 3 credit course “Evolutionary Systems Biology”.

This course resulted in a continued focus discussion group Spring 2017 on integrating ecology and evolution to study the dynamics of algal blooms and Muller’s ratchet using Evolvix (5 of 7 students continued). The work resulted in a poster submission to SMBE.

2015 Fall Genetics 677-11: Improved 3 credit course “Evolutionary Systems Biology”.

2014 Fall Genetics 677-11: Developed 3 credit course “Evolutionary Systems Biology”.

2013 Fall Genetics 677-11: Started new 3 credit course “Evolutionary Systems Biology”.

This course is approved as part of WisCEL (new center for active learning).

Course website: http://evosysbio-course.discovery.wisc.edu/

Latest syllabus: http://evosysbio-course.discovery.wisc.edu/pdf/syllabi/

Classroom: Other

2014 Spring: contributed to the course “Teaching Evolution” by K Jenkins and N Perna, 1 credit.

2013 Fall Biocore 301 “Intro to Population Genetics” (6 lecture module).

2013 Spring Biocore 333 “Evolutionary Systems Biology” (9 lecture module).

2012 Fall Biocore 301 “Intro to Population Genetics” (6 lecture module).

Guest Lectures

“Small Overview of Systems Biology” (1 lecture) in MSTP seminar series “Data Revolution in Science and Medicine” organized by Caitlin Pepperell; Fall 2014, Fall 2015.
Small seminar of very interested MD-PhD students.

Educational Outreach and Other

2018-2014: Darwin Day Exploration table on simulating stochasticity in evolution and ecology.
2017-2014: Wisconsin Science Festival: Exploration table on simulating evolution.
2015: UW-Science Expeditions: Exploration table on simulating evolution.
2015: Recognized as *Wisconsin Idea STEM Fellow* for developing the outreach station "The Dice Game with Foxes and Rabbits" to visualize stochasticity in evolution.
2012: Darwin Day Teacher Workshop: Session explaining how evolution works.
2012: Participated in "Madison Teaching and Learning Excellence" program, 2 semesters.
2012: Participated in Faculty Discussion group on how to best mentor a research group.

Teaching as Lecturer in Evolutionary Genetics, University of Edinburgh (2006-2007)

At the Institute of Evolutionary Biology, University of Edinburgh, I covered all teaching and exam related duties of Prof. Nick Barton while he was on his 2006 sabbatical:

Academic year 2006/2007 Semester 1 (includes 27 contact hours):

- Population and quantitative genetics course (for MSc in Quantitative genetics and genome analysis, 5th year), 3h Lectures on "Mutations in proteins, genes & genomes", "Introduction to population genetics", "Tutorial on elementary genetics problems".
- Firbush Trip Evolutionary Biology Honours (4th year): Fate of mutants *et al.* discussions (3h).
- Foundations of evolution course (MSc in Evolution of language and cognition, 5th year) 8h Lectures on: "Mutations in proteins, genes & genomes", "Introduction to population genetics", "Paradigms for constructing evolutionary hypotheses", "The history of life on earth".
- Evolutionary and ecological genetics (3rd year), 2h Lectures on: "Speciation overview & Mechanisms", 2h Tutorials: "Faster evolution in tropics", "Speciation factors in past".
- Animal evolution course (Zoology Honours + Evolutionary Biology Honours, 4th year), 4h lectures on "Major evolutionary transitions: Introduction" and "Genetic code to societies".
- Evolution of sex and breeding systems (Zoology and Evolutionary Biology Honours, 4th year): Organize course, coordinate 4 lecturers and give lectures on "Diversity of breeding systems", "The evolution of sex" (with tutorial).

Academic year 2006/2007 Semester 2 (includes 26 contact hours)

- Evolutionary Biology Honours Tutorials (4h).
- Evolutionary genetics module (4 weeks full time, MSc in Quantitative genetics and genome analysis, 5th year): Organize course, coordinate 9 lecturers and give lectures on "Modeling foundations", "Modeling evolution", "Coalescent foundations", "Coalescent applications", *Practical*: "Coalescent simulations exercise ", "Population structure and drift", "Population structure and selection", "Testing for selection (1)" and "(2)", *Practical*: "Population structure estimation", *Practical*: "Searching for selected genes".

Previous teaching experience

2003: "Population and Quantitative Genetics", University of Edinburgh, 5h Tutorials
2001 Supervision of German Diploma* thesis of Textor V (microbiology, automation)
2000, 1999: Co-assisted in wet-lab practical in 'general microbiology'. 2 weeks, full day.
1997 Supervision of German Diploma* thesis of Peter S (simulations in biology)

* Diplomas required ca 6-9 months of work by students at level of extended MSc projects.

Mentoring

Postdocs

Brian McLoone (2016-05 to 2017-08) Evolutionary game theory, Philosophy, Logic. Directly moved to a tenure-track faculty position at the School of Philosophy, National Research University Higher School of Economics, one of Russia's leading research universities. https://www.hse.ru/en/org/persons/209288204

Philip K. F. Poon (2011-09 to 2012-08) Physics, applied math, numerics. Moved to another research group before becoming a data scientist. https://wid.wisc.edu/philippoon/

Graduate Students

Seth Keel (2012-09 to 2015-01; Genetics M.Sc., Spring 2015; returned as programmer)

Kurt Ehlert (2012-09 to 2015-01; Genetics M.Sc., Spring 2015. Moved to the Mathematics Graduate Program at the University of Wisconsin-Madison.

Student Programmers

Vaibhav Vyas (2014-09 to 2015-12; Computer Sciences MS, Project Assistant)
Dinesh Thangavel (2014-09 to 2015-05; Computer Sciences MS, Project Assistant)
Anusha Dasarakothapalli (2014-09 to 2014-12; Computer Sciences MS, PA)
Iratxo Flores-Lorca (2011-06 to 2013-06; Bioinformatics Certificate, Hourly)

Research Interns

Yazeed Sabri (2018-01 to Current; Computer Sciences, worked on simplifying Git)
Cecilia L Moog (2018-01 to Current; Genetics; editing, versioning, VBIR development)
Katherine Scheuer (2015-01 to 2016-08; Psychology & Spanish BS, biological modeling)
Jerdon Dresel (2015-01 to 2016-08; Genetics BS, biosystems curation)
Tanner Engbretson (2014-01 to 2015-07; Computer Sciences, worked as programmer)
Kurt Ehlert (2015-01 to 2015-08; Genetics MS, Neurobiology & Math BS, programmer)
Iratxo Flores-Lorca (2013-06 to 2014-11; Bioinformatics Certificate, programmer)

Academic Staff and other support

Lynn Childress (2019-05 to 2019-12, editing support)

Seth Keel (2018-02 to present 50% Programmer/Analyst; 2015-02 to 2015-07 100% Systems Programmer; 2011-03 to 2012-09 100% Programmer/Analyst; in addition to designing and implementing solution architectures, provided project management and various other forms of support for the lab)

Jocelyn Meyer (2017-05 to present; Genetics; 100% Special Agent with numerous tasks)

Ginger Contreras (2016-06 to present; 50%; various supportive roles as needed, including administrative support, office management, outreach specialist)

Elizabeth Gryzmala (2016-05 to 2016-08; 50% administrative support)

Christine Javid (2015-09 to 2016-08; 50% Senior Editor)

Anthony Pietsch (2015-08 to 2016-08; 100% Associate Editor)

Steve Goldstein (2012-03 to 2014-05; 50% Associate Scientist, computational mathematical biology)

Robert Mau (2011-08 to 2014-12; 50% Assistant Scientist, biostatistics)

Undergraduate Students

Megan Wittman (2019-09 to 2019-12; English and Philosophy)
Diamond Nabounpaeng (2019-09 to 2019-12; Communication and Design)
Aleks Cwalina(2019-09 to 2019-12; Journalism)
Jonah Anderson (2019 summer; Milwaukee School of Art & Design)
Megan Mills (2019-01 to 2019-12; Genetics)
Alexis Terry (2018-10 to 2018-11; Life Sciences Communication)
Nicole Koepf (2018-01 to Current; Bio 152 Major Biology)
Niklaus Zeller (2018-01 to Current; Bio 152, Major Pre-med)
Paige Arneson (2017-10 to Current; Major Genetics)
Jingyu Zhang (Jane; 2017-10 to Current; Major Art and Communication Arts)
Yazeed Sabri (2016-01 to 2017-12; Computer Sciences)
Cecilia L Moog (2016-01 to 2017-12; Genetics)
Jameson Warner (2016-12 to 2017-07; Math & Computer Sciences)
Sarah Northey (2016-12 to 2017-05; Genetics)
Courtney Hove (2017-01 to 2017-05; Genetics)
Jocelyn Meyer (2016-01 to 2017-05; Genetics)
Kimberly Ward (2016-12 to 2017-01; Genetics)
Leah Rogers (2016-06 to 2016-08; Biology, visitor from Spelman College)
Keegan Reilly (2016-09 to 2016-12; Bio 152 undecided, PreMed)
Noah P Waters (2015-09 to 2016-12; Biology, PreMed)
Claire Nusbaum (2015-09 to 2016-05; Genetics, transferring)
Erik Nolan (2014-09 to 2016-08; Biology & Spanish, PreMed)
Alyssa Hotz (2014-09 to 2016-05; Genetics & Sociology, PreMed)
Katherine Scheuer (2011-09 to 2014-12; Psychology & Spanish, PreMed)
Devanie Tucker (2015-01 to 2015-05; Biology, PreMed or PA school)
Tanner Engbretson (2014-01 to 2014-05; Computer Sciences)
Jacob Goldfinger (2013-05 to 2014-05; Biology, Math)
Jerdon Dresel (2013-01 to 2013-05; Zoology 152 student, Genetics)
Cassandra Kozak (2013-01 to 2013-05; Zoology 152 student)
Kurt Ehlert (2011-11 to 2012-09; Math, Neuroscience)
Payeng Yang (2011-06 to 2012-12; Biology)
Matthew Myers (2011-05 to 2012-05; Computer Science)
Peter Holmes (2011-06 to 2011-07; Math, Chemical Engineering)

Teacher Education in Madison

Scott Mullee (2019 summer)
Aunton A Terry (2019 summer)

Focused Discussion Group

2017-01 to 2017-05: Focus on integrating ecology and evolution to study the dynamics of algal blooms and Muller’s ratchet using Evolvix. Started in the Fall 2016 EvoSysBio course (with Sarah L Northey, Courtney Hove, Justine Kao, Jon Ide, Janel McKinney).

Service

EvoSysBio Meeting Organization

Loewe L and Carvunis, A (2017) Symposium “Evolutionary Systems Biology of Cells”, held on July 3rd at the 2017 Conference of the Society for Molecular Biology and Evolution (SMBE), July 2nd-July 6th, 2017, Austin, TX.
URL: http://evolutionarysystemsbiology.org/meeting/2017-SMBE/

Loewe L (2016) Local Workshop “EvoSysBio and Modeling” supported by Pietsch A; Madison, WI, USA, Aug. 4-5, 2016.
URL: http://evolutionarysystemsbiology.org/meeting/2016-Madison/

Loewe L, Carvunis, A-R, Hanlon B, Ferris M (2015) Local Workshop “EvoSysBio and Modeling”, Madison, WI, USA, Aug. 25, 2015.
URL: http://evolutionarysystemsbiology.org/meeting/2015-Madison/

Loewe L and Gutenkunst R (2014) Symposium on “Evolutionary Systems Biology of Networks”, Jun. 9, 2014 at the Conference of the Society for Molecular Biology and Evolution (SMBE), San Juan, Puerto Rico,
URL: http://evolutionarysystemsbiology.org/meeting/2014-SMBE/

Gutenkunst R, Loewe L and Swain P (2013) BIRS workshop on “Mathematical Methods in Evolutionary Systems Biology” May 26-31, Banff International Research Station, Canada,
URL: http://www.birs.ca/events/2013/5-day-workshops/13w5080/

Loewe L (2012) Local Workshop “EvoSysBio Meeting with Associated Workshop on Modeling Languages”, Madison, WI, USA, July 30 - Aug 1, 2012.
URL: http://evolutionarysystemsbiology.org/meeting/2012-Madison

Loewe L and Soyer OS (2011) Symposium on “Evolutionary Systems Biology” at 13th Congress of the European Society for Evolutionary Biology (ESEB), Tübingen, Germany,
URL: http://evolutionarysystemsbiology.org/meeting/2011-ESEB

Loewe L, Lercher M and Knight C (2010) Workshop on “Evolutionary Systems Biology” at the 11th International Conference on Systems Biology, Edinburgh, UK,
URL: http://evolutionarysystemsbiology.org/meeting/2010-ICSB

Loewe L and Papp B (2009) Symposium on “Evolutionary Systems Biology” at 12th Congress of the European Society for Evolutionary Biology (ESEB), Turin, Italy,
URL: http://evolutionarysystemsbiology.org/meeting/2009-ESEB

Committees

2018 Fall applied to UW-Madison *University Library Committee* 4 year term, but was not elected

2017-2011: Local PhD Committees:

- Abigail Shockly (MicroBio)
- Jeremy Lange (Genetics)
- Lindsey Bohr (MicroBio)
- Tatum Mortimer (MicroBio)
- Richard Wang (Genetics) Defended 2017-01
- Davorka Gulisija (Zoology) Defended

2016 - present, 2014-2011: Laboratory of Genetics *Computing Committee*.
From 2011-2013 I was particularly active and contributed much to an important hire.

2012: Organizer of WID discussions on Data Storage at UW-Madison.

2011: External examiner on PhD thesis of Jonas Söderberg, Uppsala University, Sweden.
2011: Contributed to several faculty searches by meeting with candidates when WID started.

Peer-Review

Papers: I have served as a reviewer for Cambridge University Press, *Science*, *PLoS Biology, PLoS Computational Biology, PLoS Genetics, Proceedings of the National Academy of Sciences of the USA, Proceedings of the Royal Society of London Series Biological Sciences*, *Philosophical Transactions of the Royal Society B, Evolution*, *Genetics*, *Molecular Biology & Evolution*, *Genetical Research*, Biochemistry, Bioinformatics, *Journal of Theoretical Biology*, *Trends Plant Science, BMC Bioinformatics*, *BMC Evolutionary Biology*, *Fundamental and Applied Limnology*, *BioSilico, TheScientificWorldJournal* and *BioTechniques*.

Grants: I have reviewed grants for the National Science Foundation (USA), the Netherlands Organization for Scientific Research (NWO) and UW-Madison internal competitions.

Other Activities

Fostering Interdisciplinary Connections in Madison

2013 Interdisciplinary Housewarming Party, mixing Genetics, Math, Computer Sciences, …
2013 QuantBio: Early on I supported the Quantitative Biology Initiative (QBI at UW-Madison) through a precursor website (https://quantbio.wisc.edu that became http://qbi.wisc.edu)

Websites

http://evolvix.org	Evolvix language homepage
http://evolutionarysystemsbiology.org	EvoSysBio homepage
http://evolutionary-research.net	Evolution@home global computing site
http://evosysbio-course.discovery.wisc.edu	EvoSysBio course teaching home page
http://evolution.ws/people/lloewe	Personal and lab home page

Media

Aspects of my work have been covered by the *BBC (most recently in 2018)*, the *Canadian Broadcasting Corporation*, *The Times*, *The Scotsman*, *The Herald*, *COSMOS* and other national and international media.

Curriculum vitae

Personal Details:

Name:	Laurence Loewe
Born:	6th May 1969, Cape Town
Nationality:	German
Marital status:	married

Education and Qualifications:

1975 - 1988	School. Final exam (Abitur) in biology and physics at high school "Gymnasium Fridericianum Erlangen", Germany
1987 - 1991	"Jugend forscht" competition, 5 years in a row. Research project investigating the effects of physical discharge parameters on productivity in Miller-experiments on chemical evolution.
1990 - 1995	Diploma in Biology (Dipl.-Biol.), Universität Konstanz, Germany. Thesis on specific mutagenesis in the active center of human medium chain Acyl-CoA Dehydrogenase and characterisation of its effect on catalytic activity.
1998 - 2002	Doctoral Thesis in the Microbial Ecology Group, Department of Biosciences, Technische Universität München, Germany: "Evolutionary Bioinformatics: Predicting genetic stability of asexual genomes by global computing"

Working Experience:

1988 - 1990	National service (Zivildienst) at a social therapeutic welfare institution
1989	Practical course in bioinformatics and electronmicroscopy at the German Cancer Research Center (DKFZ) Heidelberg, Germany
1992	Working student (HiWi), Universität Hohenheim, Germany
1992 + 1994	Working student (HiWi), Universität Konstanz, Germany
1996 - 1997	Scholarship for research on the project “Evolution of biological information” by Wort und Wissen e.V., Konstanz, Germany
1998 - 2002	Researcher at the Microbial Ecology Group, Department of Biosciences, Technische Universität München, Germany
2003	Visiting scientist at the IWR Technical Simulation Group, Interdisciplinary Centre for Scientific Computing, University of Heidelberg, Germany
2003 -	Post-doctoral research fellow at the Institute of Cell, Animal and Population Biology, University of Edinburgh, Scotland, UK

Prizes:

1987 "Jugend Forscht" Bayern, Germany, 3rd place (Landeswettbewerb München). Paper on the significance of primeval earth simulations for the theory of chemical evolution.

1991 "Jugend Forscht" Baden-Würtemberg, Germany, 2nd place (Landeswettbewerb Stuttgart). Paper on the productivity of high voltage discharges in Miller experiments.

Original publications

Loewe L (2002) "evolution@home: Experiences with work units that span more than 7 orders of magnitude in computational complexity", 425-431. 2nd International Workshop on Global and Peer-to-Peer Computing on Large Scale Distributed Systems at the 2nd IEEE/ACM International Symposium on Cluster Computing and the Grid (CCGrid2002), 21-24 May, Berlin, Germany, IEEE Computer Society (see http://www.evolutionary-research.net/ for download).

Loewe L, Textor V & Scherer S (2003) "High deleterious genomic mutation rate in stationary phase of *Escherichia coli*", Science 302:1558-1560.

Loewe L (2004) "The mutation rate paradox: Pedigree versus 'archaeological' versus phylogenetic mutation rates in mitochondrial DNA", under revision.

Loewe L (2004) "Muller's ratchet in mtDNA may cause extinctions in mammals", in prep.

Loewe L (2004) "Muller's ratchet may contribute to the uncultivable majority of bacteria", in prep.

Further publications based on ideas from this dissertation will be listed on the corresponding webpage of this dissertation (see http://www.evolutionary-research.net/ for download).

Reviews, peer reviewed

Loewe L & Scherer S (1997) "Mitochondrial Eve: The plot thickens", Trends Ecol. Evol. 12:422-423.

Loewe (2002) "Global computing for bioinformatics", Brief. Bioinformat. 3:377-388.

Loewe L (2004) "Why do we need evolutionary bioinformatics?", under revision.

Loewe L (2004) "Muller's ratchet reviewed", in prep.

Invited Talks

Loewe L (1997) "Mutation rates, Muller's Ratchet, genetic load and mitochondrial Eve". First international workshop on human mitochondrial DNA, Washington, D.C.

Loewe L (2001) "evolution@home: New frontiers in global computing and evolutionary bioinformatics" EMBnet Annual General Meeting, Vienna, Austria.

Talks at international conferences

Loewe L & Scherer S (1999) "How many beneficial mutations are needed to stop Muller's ratchet?" Seventh Congress of the European Society for Evolutionary Biology, Barcelona, Spain.

Loewe L (2000) "How many beneficial mutations are needed to stop Muller's ratchet in mtDNA?" Spacial ecology workshop on extinction, Tvärminne Zoological Station, Finland.

Loewe L (2002) "evolution@home: Experiences with work units that span more than 7 orders of magnitude in computational complexity", 2nd International Workshop on Global and Peer-to-Peer Computing on Large Scale Distributed Systems at the 2nd IEEE/ACM Internatl. Symp. on Cluster Computing and the Grid, Berlin, Germany.

Loewe L (2002) "Quantifying the threat from Muller's ratchet in mtDNA?" Extinction Thresholds Conference, Helsinki, Finland.

Loewe L, Textor V & Scherer S (2003) "High deleterious genomic mutation rate in stationary phase of *Escherichia coli*" Population Genetics Group Meeting, University of Sussex, UK.

Posters at international conferences

Loewe L & Scherer S (1997) "On the speed of genomic decay". The 5th Annual International Meeting of the Society for Molecular Biology and Evolution, Garmisch-Partenkirchen, Germany.

Loewe L & Scherer S (1998) "Muller's ratchet in human mitochondrial DNA". The 6th Annual International Meeting of the Society for Molecular Biology and Evolution, University of British Columbia, Vancouver, Canada.

Loewe L & Scherer S (1998) "On the speed of genomic decay". Annual Meeting of the Society for the Study of Evolution, Vancouver, British-Columbia, Canada.

Loewe L & Scherer S (1999) "How many advantageous mutations stop Muller's ratchet?" Evolution '99, University of Wisconsin, Madison, Wisconsin.

Loewe L & Scherer S (2001) "Predicting extinctions due to Muller's ratchet in humans and bacteria". Eighth Congress of the European Society for Evolutionary Biology, Aarhus, Denmark.

Diploma theses supervised:

Peter S (1997) "Prototypischer Entwurf und Implementierung einer Simulationssprache für evolutive Vorgänge in der Biologie", Lehrstuhl für Systemanalyse, Fachbereich Informatik, Universität Dortmund.

Textor V(2001) " Programmierung eines VBA Systems zur Auswertung von Mutations-Akkumulations Experimenten mit Mikroorganismen in Flüssigkultur und Bestimmung der Nachweisgrenzen für Fitnessveränderungen.", Microbial Ecology Group, Department of Biosciences, Technische Universität München.

Book contributions

Loewe L (1991) "Chemische Evolutie", Amersfoort, Netherlands, Amersfoortse Studies no. 8, ISBN: 90-70145-20-0.

Loewe L & Scherer S (1996) "Molekulare Evolution", pp. 75-84 in: Scherer S (ed) Entstehung der Photosynthese - Grenzen molekularer Evolution bei Bakterien?, Neuhausen-Stuttgart, Hänssler.

Loewe L (1998) "Grundbegriffe der molekularen Evolution", pp. 96-107 in: Junker R & Scherer S (eds) Evolution: Ein kritisches Lehrbuch, 4th ed., Gießen, Weyel Lehrmittelverlag.

Scherer S & Loewe L (2001) "Probleme bei der Erklärung molekularer Maschinen durch Evolution", pp. 161-186 in: Weingartner P (ed) Evolution als Schöpfung? Ein Streitgespräch zwischen Philosophen, Theologen und Naturwissenschaftlern, Stuttgart, Kohlhammer Verlag.

Popular science contributions:

Loewe L (1996) ""Megaevolution" - Makroevolution - Mikroevolution", Stud. Int. J. 3:71-75.

Loewe L (1997) "Genome im Überblick", Stud. Int. J. 4:3-13.

Loewe L & Scherer S (1997) "Mutter Eva in Bewegung", Stud. Int. J. 4:58-65.

Loewe L (1998) "Skandalöse Symbionten", Stud. Int. J. 5:36-37.

Loewe L (1998) "Neue Ähnlichkeiten zwischen Nilpferden, Kühen und Walen", Stud. Int. J. 5:86-89.

Fehrer J & Loewe L (1999) "Evolution in ökologischen Zeitskalen", Stud. Int. J. 6:41-42.

Loewe L (2000) "Geschwindigkeitsbegrenzungen für adaptive Evolution", Stud. Int. J. 7:31-33.

Website maintained

http://www.evolutionary-research.net/

Contact Information

Laurence Loewe
email: Laurence.Loewe@evolutionary-research.net (will remain)

My new work address:

Institute of Cell, Animal and Population Biology, University of Edinburgh
Ashworth Laboratories, Kings Buildings, West Mains Road, Edinburgh EH9 3JT, UK
Tel.: +44 (131) 6 50 7330

Where most of this work was conducted:

Microbial Ecology Group, Department of Biosciences, Technische Universität München
Weihenstephaner Berg 3, 85354 Freising, Germany
Tel.: +49 (8161) 71 3851, Fax.: +49 (8161) 71 4492
Private: Prechtlstr. 8a, 85354 Freising, Germany
Tel.: +49 (8161) 230 116 - email: Laurence.Loewe@web.de