

CompBio Careers

William Haese-Hill

Research Software Engineer

28/11/2025

MY BACKGROUND

PhD in Mathematical Physics

2015



Loughborough University



Loughborough University Science and Enterprise Park

Software Developer
in Industry
(~7 years)



Nigel Cox / Holborn Town Hall



University
of Glasgow

Research
Software Engineer
From 2021

Maths PhD

2011-2015

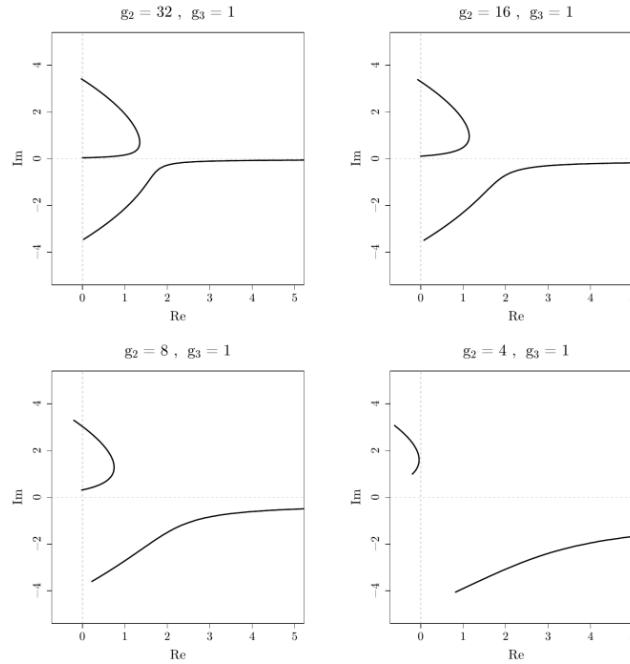
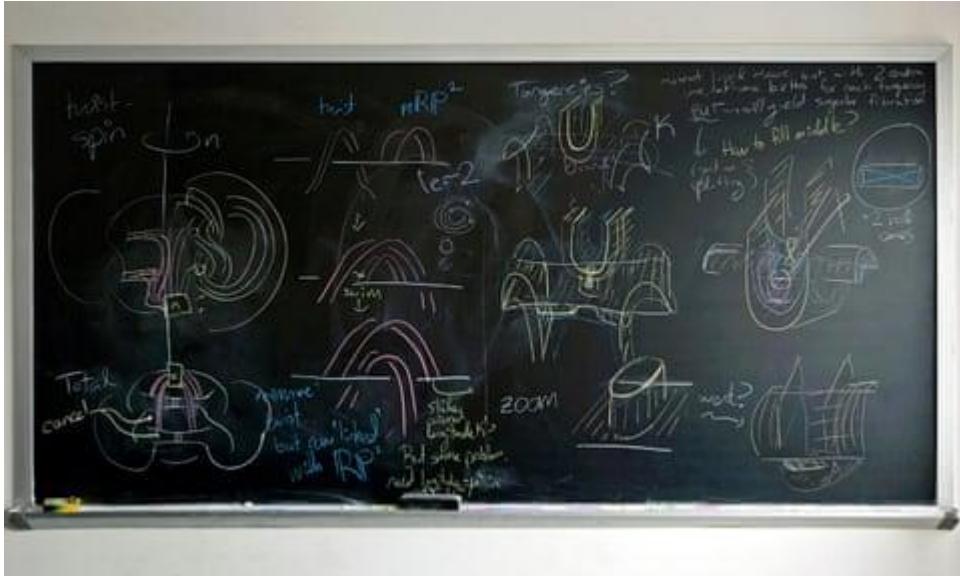


Figure 4. Spectra of the complex Lamé operator (3.1) for rectangular period lattices \mathcal{L} , $m = 1$ and $\omega = \omega_2$.

The Lamé equation

$$-\frac{d^2\psi}{dz^2} + m(m+1)\wp(z)\psi = \lambda\psi,$$

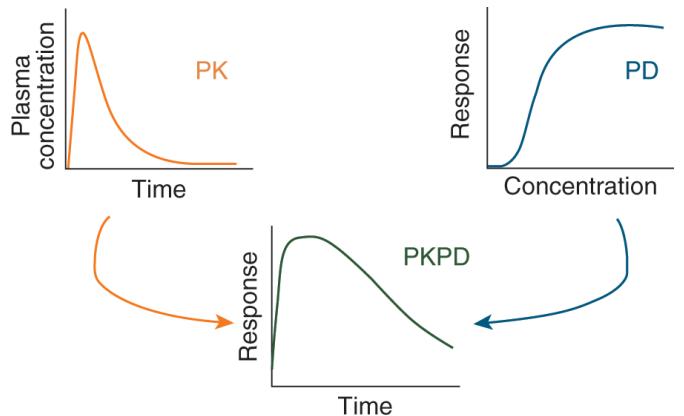


Mathematician Maggie Miller's blackboard at Princeton University. Photograph: Jessica Wynne
[Why mathematicians just can't quit their blackboards](#) | [Photography](#) | [The Guardian](#)

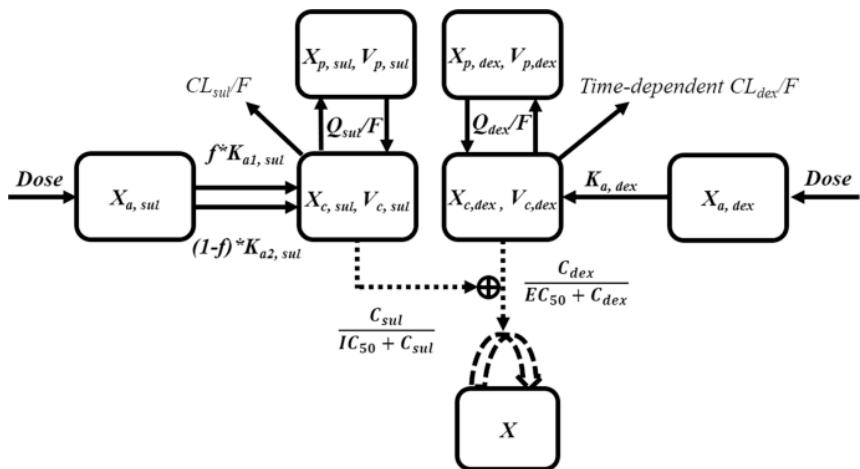


PK/PD modeller

2014-2017



<https://aneskey.com/2-pharmacokinetic-and-pharmacodynamic-modelling-in-anaesthesia/>



<https://doi.org/10.1038/s41401-019-0251-7>



The program for Nonlinear Mixed Effects Modeling

```

$PROGRAM WARFARIN ; Problem title
$INPUT ID TIME AMT RATE EVID MDV MDV 20 ;Column names
$DATA warfarin.csv ignore=C

$SUBROUTINES ADVAN2 TRANS2 ; ADVAN2 is 1st order absorption, one central compartment

$PK
; MU referencing is not required, but can be helpful in evaluating FIM analytically
; providing greater significant digit precision and speed
MU_1=LOG(THETA(1))
MU_2=LOG(THETA(2))
MU_3=LOG(THETA(3))
CL=EXP(MU_1-ETA(1))
V=EXP(MU_2-ETA(2))
KA=EXP(MU_3-ETA(3))
S2=V
F1=1.0

$ERROR
IPRED=A(2)/V
Y=IPRED + IPRED*EPS(1)

$THETA
0.15 ;[CL]
8.0 ;[V]
1.0 ;[KA]

$OMEGA (0.07) (0.02) (0.6)
$SIGMA 0.01 (0.001 FIXED)

;GROUPSIZE is a multiplier to the FIM
;FIMDIAG=1 means to use block diagonal FIM

```

```
C:\Windows\system32\cmd.exe
@ITERATION NO.: 5 OBJECTIVE VALUE: 258.957563934051 NO. OF FUNC.
EQUALS.: 9
CUMULATIVE NO. OF FUNC. EQUALS.: 50
NPARAMETER: 9.1589E+00 1.1372E+01 1.2480E+01 3.6237E+01 8.8238E-02
PARAMETER: 2.0529E-01 2.2898E-01 3.1574E-01 1.3875E+00 1.1987E+00
GRADIENT: 9.5850E+01 -8.2429E+00 3.1222E+00 3.8762E+01 3.2519E+01

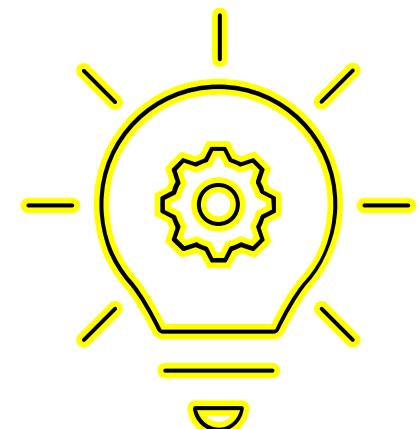
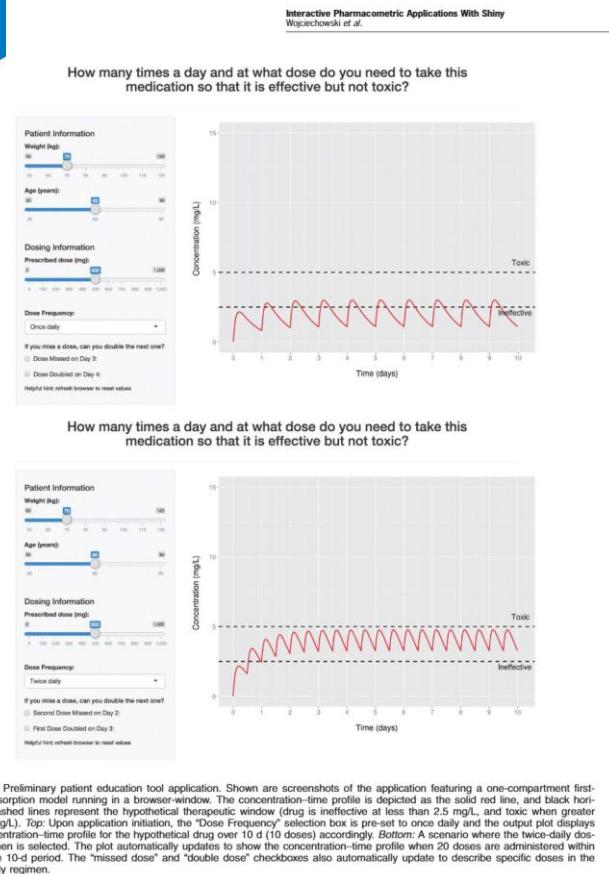
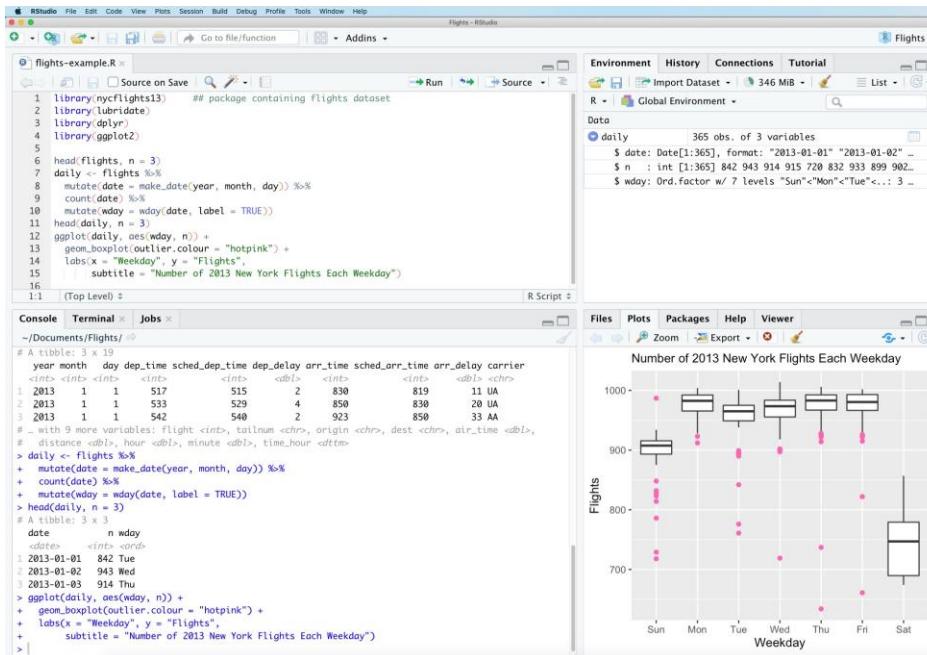
@ITERATION NO.: 10 OBJECTIVE VALUE: 239.964297920093 NO. OF FUNC.
EQUALS.: 8
CUMULATIVE NO. OF FUNC. EQUALS.: 92
NPARAMETER: 8.3274E+00 1.0524E+01 1.1217E+01 2.7445E+01 4.3665E-02
PARAMETER: 6.1011E-01 1.5105E-01 2.1483E-01 1.1996E+00 8.3699E-01
GRADIENT: 5.8991E+00 -1.6976E+00 -5.6022E-01 5.3623E-01 -9.7553E-01

@ITERATION NO.: 15 OBJECTIVE VALUE: 239.944172097418 NO. OF FUNC.
EQUALS.: 10
CUMULATIVE NO. OF FUNC. EQUALS.: 142
NPARAMETER: 8.2732E+00 1.0543E+01 1.1222E+01 2.7704E+01 4.4070E-02
PARAMETER: 6.0358E-01 1.5288E-01 2.1531E-01 1.1190E+00 8.4160E-01
GRADIENT: 1.7927E-02 2.4236E-02 1.4929E-02 2.2920E-03 5.9059E-02
Elapsed estimation time in seconds: 0.13
Elapsed covariance time in seconds: 0.05
Press any key to continue . . .
```

<https://doi.org/10.1002/psp4.12713>

<https://www.pmxsolutions.com/2018/07/01/running-nonmem-models-and-r-scripts-from-batch-files/>

Intro to scripting/coding



cdhowe, CC BY-SA 4.0 <<https://creativecommons.org/licenses/by-sa/4.0>>, via Wikimedia Commons

<https://doi.org/10.1002/psp4.21>

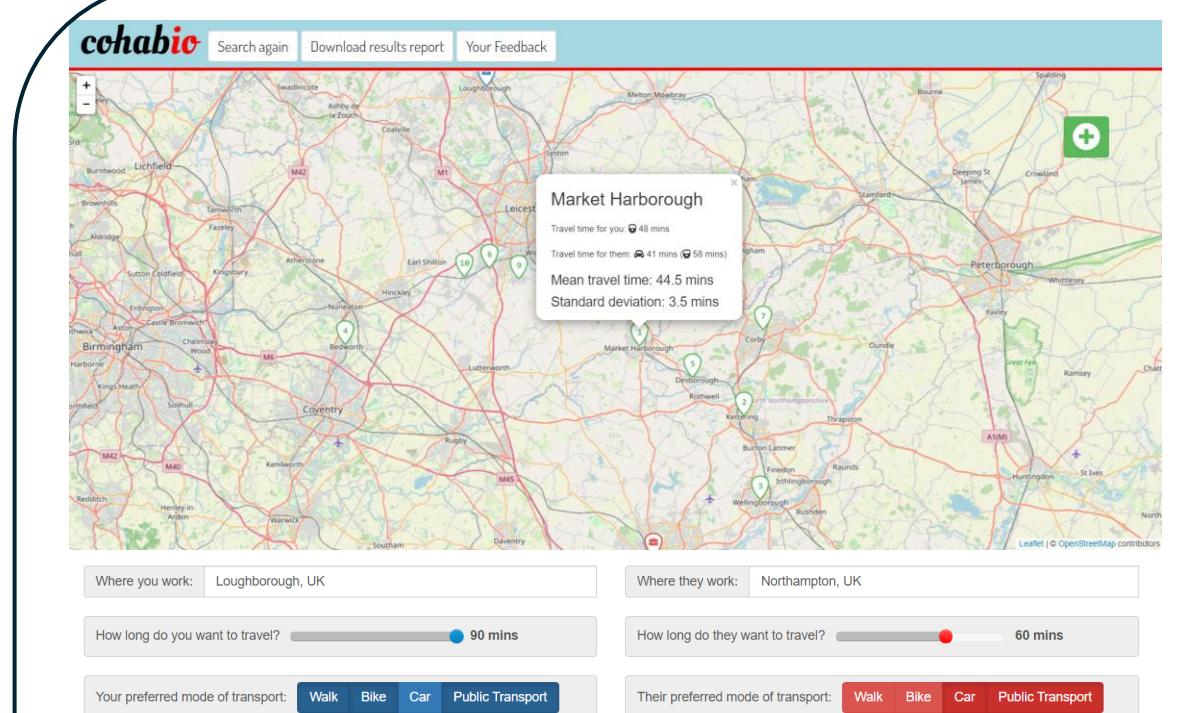
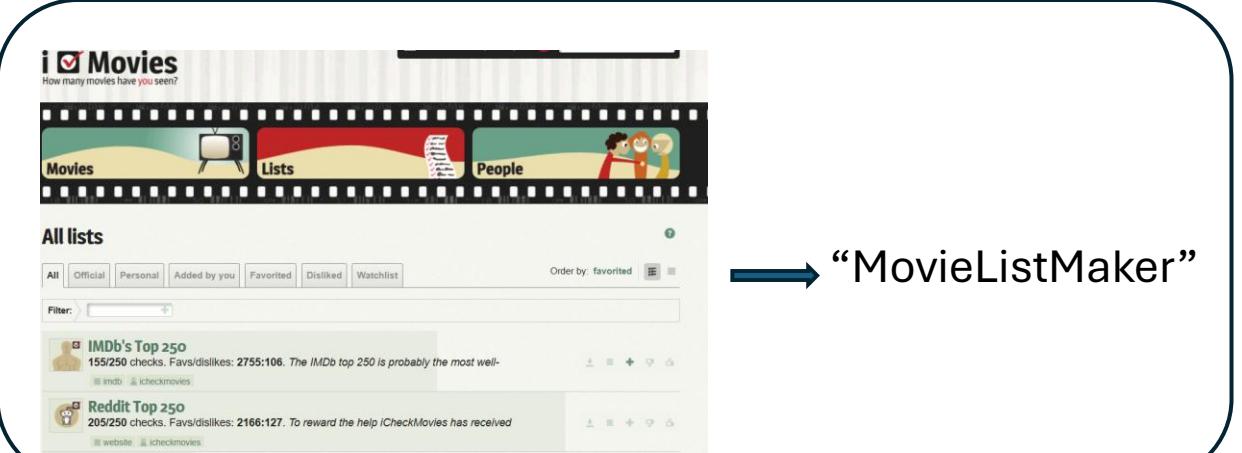
www.wileyonlinelibrary.com/journal/psp

Personal programming projects



django

Copyright © 2000-2025 [JetBrains](#) s.r.o.



<https://cohabio.eu.pythonanywhere.com/>

<https://github.com/haessar/cohabio>

Python dev/analyst in industry

2017 - 2019



Sector	Company	Location	Role	Duties
Digital marketing	Mavens of London (later Kantar)	Holborn, London	Dev team – Python dev	Building scraping and reporting tools
Sustainable energy	Energy Systems Catapult	Birmingham	Interim model analyst	Scripting for data processing and KPI calculation
Finance	JPMorgan Chase	Glasgow	Small cog in a corporate giant	ETL pipelines, Python 2 -> 3 migration



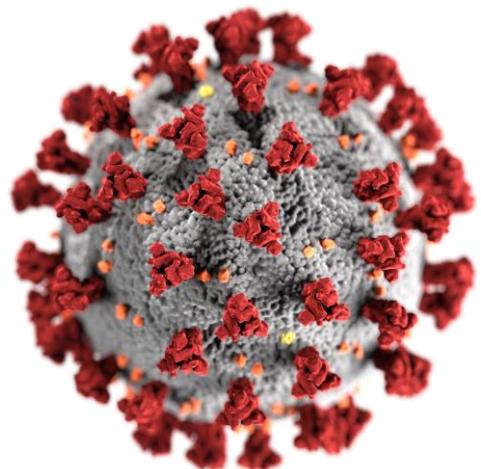
All code proprietary/private



3 months effectively unemployed

Covid and UofE

2020 - 2021



Alissa Eckert, MS; Dan Higgins, MAM, Public domain, via Wikimedia Commons



- Remote role
- Central IT rather than academic
- “People and Money” system - ETL pipelines
- Toxic team culture / worst job yet



- New to parenthood
- Isolation
- Low job satisfaction
- = Depression



Uni payment backlog left staff crying - report



Oliver Coe
BBC Scotland News

8 December 2023
Updated 9 December 2023

<https://www.bbc.co.uk/news/articles/cd1p32pd90po>

Entry to UofG

2021 - 2024



Prof Thomas
Otto's lab



WCIP ISAB/Retreat 2022

A screenshot of the COMPANION genome annotation tool. The interface includes logos for various tools: Tux (Linux), BASH, NGINX, git, GitHub, Ruby (A PROGRAMMER'S BEST FRIEND), nextflow, and Perl. The main title is "COMPANION" with a handshake icon. Below it is the subtitle "Easy and reliable genome annotation." and a blue button with the text "Annotate your sequence!".

COMPANION

Easy and reliable genome annotation.

Annotate your sequence!

Ruby A PROGRAMMER'S BEST FRIEND

nextflow Perl

- Open-source code
- Publications
- Collegiate culture

A screenshot of the peaks2utr tool. It features the Python logo and a DNA helix icon. The title "peaks2utr" is displayed. Below the title is the subtext "Forward-stranded 3' UTRs extended by several tools". A plot shows genomic tracks for various 3' UTR extensions. A legend identifies the tracks: "reference 3' UTR" (red), "extended 3' UTR" (green), "extended 3' UTR with SPAT" (blue), "UTRine extended 3' UTR" (yellow), and "GETUTR extended 3' UTR" (cyan).

peaks2utr

Forward-stranded 3' UTRs extended by several tools

reference 3' UTR
extended 3' UTR
extended 3' UTR with SPAT
UTRine extended 3' UTR
GETUTR extended 3' UTR

A screenshot of the paraCell tool. The interface includes a sidebar with checkboxes for "batch", "celltype", "donor", "tissue", and "tissue". A main panel shows a 3D t-SNE plot of "Human Cell Landscape" with many colored points representing different cell types. To the right are two histograms: "Autosuggest genes" and "Bulk add genes". Logos for R, Bioconductor, scanpy, and Seurat are visible at the bottom right. The paraCell logo is in the top right corner.

cell-gene Human Cell Landscape

batch >

celltype >

donor >

tissue >

AdultAdipose

AdultArenasGland

AdultAterney

AdultAscendingColon

AdultBladder

AdultBloneMarrow

AdultCerebellum

AdultCervix

AdultEsophagus

AdultEpithelium

AdultEsophag

AdultEsophagus

AdultGallbladder

AdultHeart

AdultLithium

AdultJejunum

AdultKidney

AdultLiver

AdultLung

Autosuggest genes

Bulk add genes

R

Bioconductor

scanpy

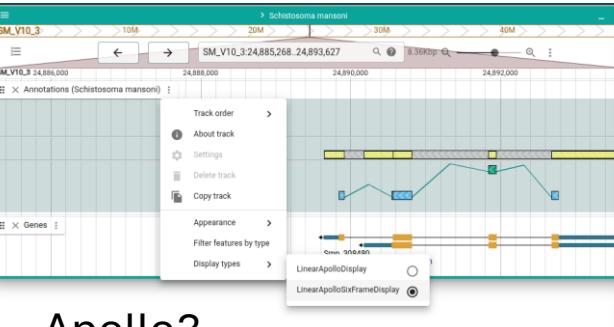
Seurat

paraCell

Current RSE role

2024 - Present

- Academic track – permanent contract
- Lots of autonomy
- Lots of variety
- = Job satisfaction



Apollo3

JBrowse

TS TypeScript

This block contains a screenshot of the Apollo3 genome browser interface, showing a genomic track for Schistosoma mansoni. The interface includes a main plot area with a blue line and yellow boxes, and a sidebar with track order, settings, and display type options. Below the screenshot are the logos for JBrowse and TypeScript.

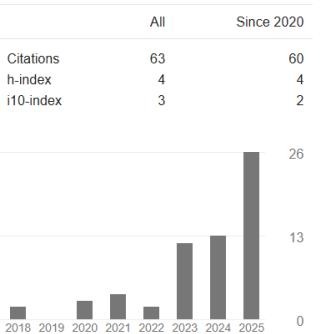


Image credit Ryan Field



Thanks for
listening!

“ *My advice to others: don’t be afraid to try a variety of roles before settling on something that works for you. There will always be opportunities arising in unexpected areas, and doors reopening that once might have seemed firmly shut.* ”

<https://theauditorium.blog/2025/03/12/pathfinder-career-narratives-60-research-software-engineer/>