

Composable disease modelling

An open toolkit in Julia using Applied Category Theory

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on behalf of the Epirecipes team

LSHTM Open Research Awards 2026

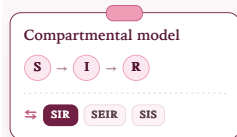
- ▶ Epidemic models are often built to answer specific disease or outbreak questions
- ▶ In that form they are:
 - ▶ **Slow** to adapt/modify during an active outbreak
 - ▶ **Hard to check** as models grow in complexity, we can't easily see how they reach a given conclusion
 - ▶ **Time-consuming** to build from scratch or even to modify for a new question each time

This makes outbreak modelling slower, and harder to validate.

We're building an **open-source, composable toolkit** grounded in Applied Category Theory: a branch of maths for describing how different models (*categories*) relate to one another through structure-preserving maps (*functors*).

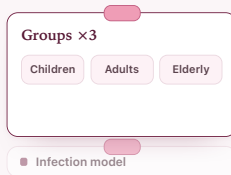
1 Pick the base

Choose a disease model: SIR, SEIR, SIS.



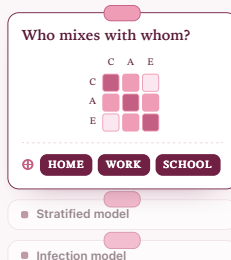
2 Stratify

Repeat the model across groups in one move.



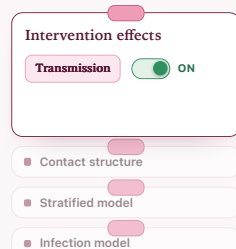
3 Contact structure

Set who mixes with whom between the groups.



4 Intervention

Switch an effect on or off on any variable affected by intervention.



Being open is the whole point: we build on what others share, and share ours back.

- We build on the community's open tools: AlgebraicJulia (model building), Turing.jl (inference), JuMP.jl (optimisation).

Our code is open-source, and can be found in the [epirecipes Github project](#):

Our contribution

Where it's at

Policy optimisation (NLP)

Published, open access, with code

Model fitting to case data (DDSA)

Public repo, paper to follow

Contact structure (ContACT.jl)

In development, public repo

Interventions (CategoricalInterventions.jl)

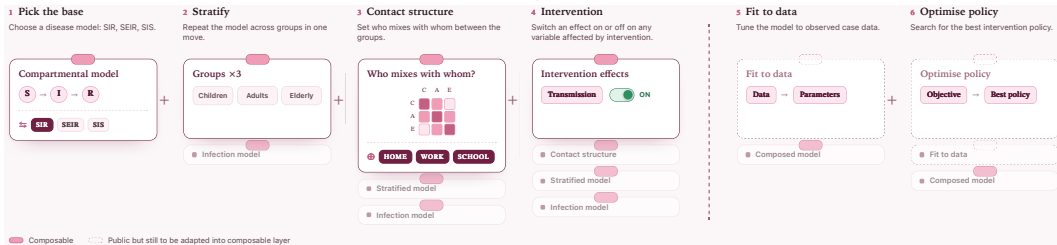
In development, public repo

► Inside the categorical layer:

- Model generation: Using AlgebraicJulia packages
- Contact structure: Using ContACT.jl (in development)
- Interventions: Using CategoricalInterventions.jl (in development)

► Outside the categorical layer:

- Fitting to case data: DDSA (discrete dynamic survival analysis) with Turing.jl
- Optimisation of interventions: JuMP.jl for nonlinear programming



- ▶ ACT and Julia may be unfamiliar to many epidemiologists
 - We bridge this with comprehensive documentation, interactive notebooks, public design, and hands-on workshops
- ▶ Working openly requires documenting our design choices
 - This transparency and visibility makes the toolkit auditable and trustworthy

- ▶ **Useful already:** No need to wait for the full pipeline. The repos are public and each tool stands on its own
- ▶ **Integration:** The community tools exist, but no toolkit yet connects them into a composable outbreak-response system, that's what we're building
- ▶ **Changed how we work:** we design each tool to work on its own *and* as part of the whole
- ▶ **Reach:** openly releasing our code aims to help public health agencies and international partners respond faster to future epidemics

Open from the start

More to come: next workshop introducing Julia modelling, September 2026
(More details coming soon!)

Epirecipes team:

LSHTM

- ▶ Simon Frost (Lead)
- ▶ Sam Abbott
- ▶ Sebastian Funk

Swansea University

- ▶ Ashley Akbari
- ▶ Michael Gravenor

Find it all: github.com/epirecipes · Paper: doi.org/10.1371/journal.pcbi.1014238