

Typed and Stratified Models with Slice Categories

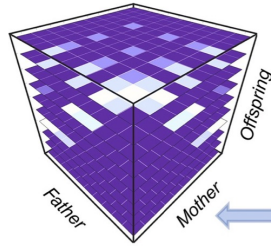
Sophie Libkind, Evan Patterson, James Fairbanks,
Andrew Baas, Micah Halter

ACT 2022

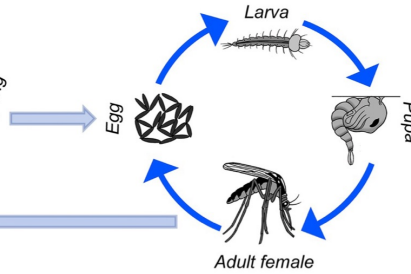
I. Motivation

Stratified Models

A. Inheritance



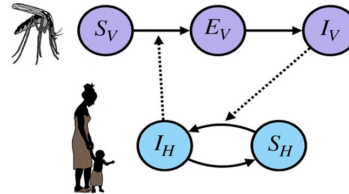
B. Life history



C. Landscape



D. Epidemiology



Wu et al., 2021

I. Motivation

Comparing metapopulation dynamics of infectious diseases under different models of human movement

Daniel T. Citron^{a,1}, Carlos A. Guerra^b, Andrew J. Dolgert^c, Sean L. Wu^c, John M. Henry^a, Héctor M. Sánchez C.^c, and David L. Smith^a

disease models

-SIR

$$\begin{aligned}\frac{dS}{dt} &= -\beta \frac{SI}{N} \\ \frac{dI}{dt} &= \beta \frac{SI}{N} - \gamma I. \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

movement models

-flux

$$\frac{dN_i}{dt} = - \sum_{j=1}^K f_{i,j} N_i + \sum_{j=1}^K f_{j,i} N_j,$$

$$\frac{dS_i}{dt} = -\beta_i \frac{S_i I_i}{N_i} - \sum_{j=1}^K f_{i,j} S_i + \sum_{j=1}^K f_{j,i} S_j$$

$$\frac{dI_i}{dt} = \beta_i \frac{S_i I_i}{N_i} - \gamma I_i - \sum_{j=1}^K f_{i,j} I_i + \sum_{j=1}^K f_{j,i} I_j.$$

$$\frac{dR_i}{dt} = \gamma I_i - \sum_{j=1}^K f_{i,j} R_i + \sum_{j=1}^K f_{j,i} R_j$$

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disease models

- SIR

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$

$$\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I.$$

$$\frac{dR}{dt} = \gamma I$$

$$\frac{dS_{i,i}}{dt} = -\beta_i \frac{S_{i,i} \sum_{k=1}^K l_{k,i}}{\sum_{k=1}^K N_{k,i}} - \sum_{k=1}^K \phi_{i,k} S_{i,i} + \sum_{k=1}^K \tau_{i,k} S_{i,k}$$

$$\frac{dS_{i,j}}{dt} = -\beta_j \frac{S_{i,j} \sum_{k=1}^K l_{k,j}}{\sum_{k=1}^K N_{k,j}} + \phi_{i,j} S_{i,i} - \tau_{i,j} S_{i,j}$$

$$\frac{dI_{i,i}}{dt} = \beta_i \frac{S_{i,i} \sum_{k=1}^K l_{k,i}}{\sum_{k=1}^K N_{k,i}} - \gamma I_{i,i} - \sum_{k=1}^K \phi_{i,k} I_{i,i} + \sum_{k=1}^K \tau_{i,k} I_{i,k}$$

$$\frac{dI_{i,j}}{dt} = \beta_j \frac{S_{i,j} \sum_{k=1}^K l_{k,j}}{\sum_{k=1}^K N_{k,j}} - \gamma I_{i,j} + \phi_{i,j} I_{i,i} - \tau_{i,j} I_{i,j}$$

$$\frac{dR_{i,i}}{dt} = \gamma I_{i,i} - \sum_{k=1}^K \phi_{i,k} R_{i,i} + \sum_{k=1}^K \tau_{i,k} R_{i,k}$$

$$\frac{dR_{i,j}}{dt} = \gamma I_{i,j} + \phi_{i,j} R_{i,i} - \tau_{i,j} I_{i,j}$$

movement models

- flux

- simple trip

$$\frac{dN_{i,i}}{dt} = - \sum_{j=1}^K \phi_{i,j} N_{i,i} + \sum_{j=1}^K \tau_{i,j} N_{i,j}$$

$$\frac{dN_{i,j}}{dt} = - \tau_{i,j} N_{i,j} + \phi_{i,j} N_{i,i}$$

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disease models

- SIR
- SIS
- Ross-Macdonald
-
-
-

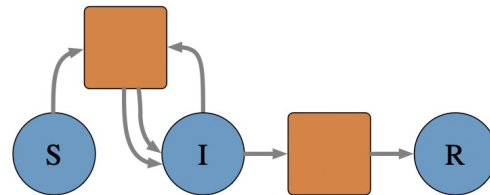
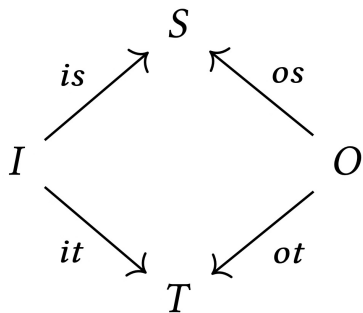
movement models

- flux
- simple trip
-
-
-

II. Typed Petri nets

The category of whole-grain Petri nets (Petri) has

- objects: diagrams of finite sets

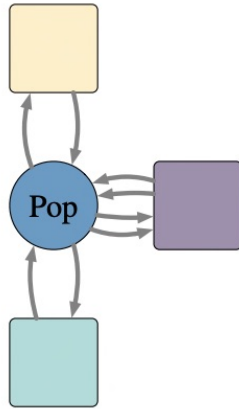


- morphisms: etale maps

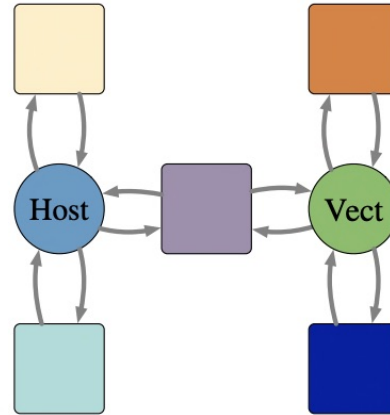
(Kock, 2020)

II. Typed Petri nets

A Petri net can represent a domain-specific type system



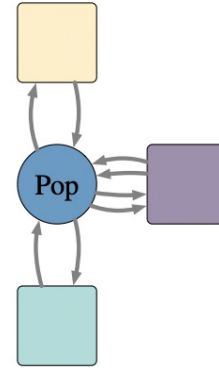
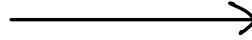
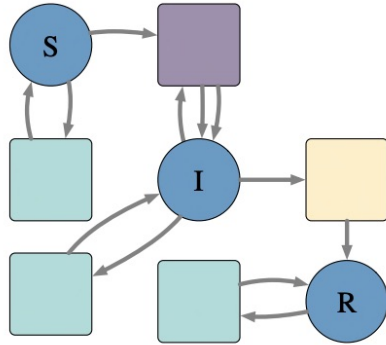
type system for
infectious diseases



type system for
vector-borne diseases

II. Typed Petri nets

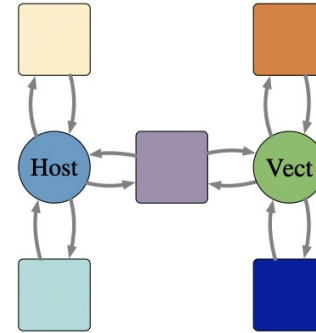
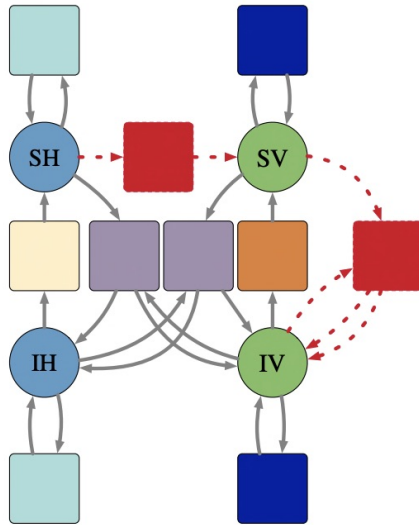
A typed Petri net is an object of the slice category $\mathbf{Petri}/P_{\text{type}}$



$P_{\text{type}} =$ type system for
infectious diseases

II. Typed Petri nets

A typed Petri net is an object of the slice category $\text{Petri}/P_{\text{type}}$

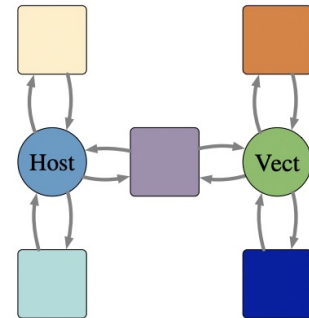
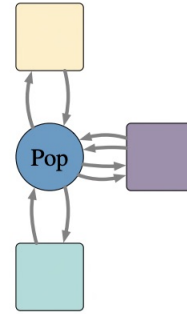


$P_{\text{type}} =$ type system for
vector-borne diseases

II. Typed Petri nets

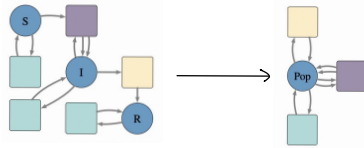
Advantages:

1. model checking
2. facilitate high-level critiques
3. features of type system imply features of model
4. guardrails for composition



II. Typed Petri nets

Implementation of

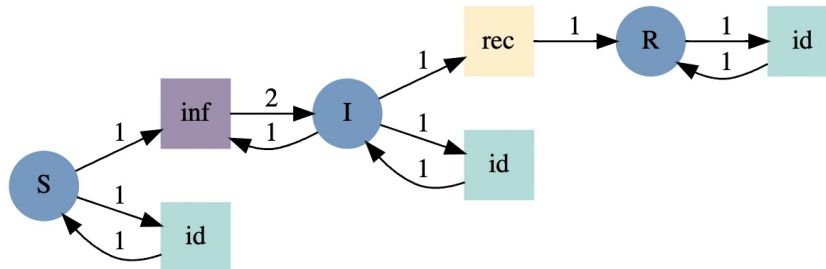


in Algebraic Petri

```
SIR = LabelledPetriNet([:S, :I, :R],
    :inf => ((:S, :I)=>(:I, :I)),
    :rec => (:I=>:R),
    :id => (:S => :S),
    :id => (:I => :I),
    :id => (:R => :R)
)

typed_SIR = ACSetTransformation(SIR, infectious_type,
    S = [s, s, s],
    T = [t_interact, t_disease, t_strata, t_strata, t_strata],
    I = [i_interact1, i_interact2, i_disease, i_strata, i_strata],
    O = [o_interact1, o_interact2, o_disease, o_strata, o_strata],
    Name = name -> nothing
)

@assert is_natural(typed_SIR)
```

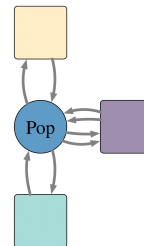
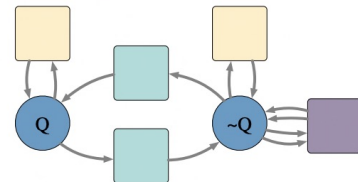
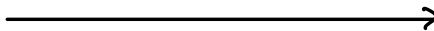
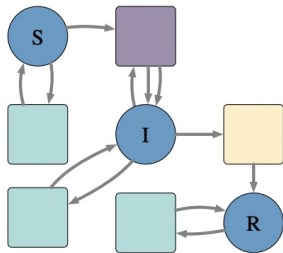


III. Stratified Models

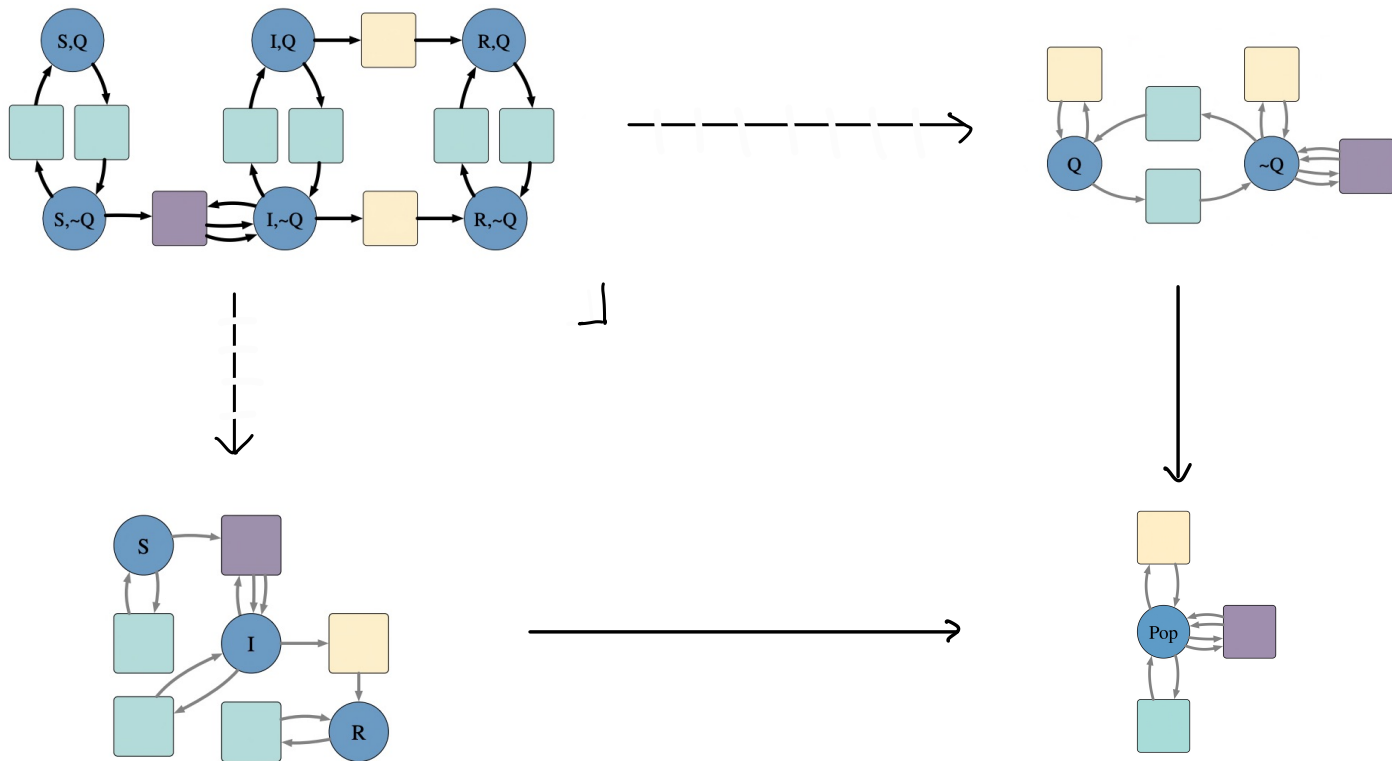
A product in $\text{Petri}/P_{\text{type}}$ is a stratified Petri net

$$\begin{array}{ccc} P_{\text{stratified}} & \dashrightarrow & P_{\text{strata}} \\ \downarrow & \lrcorner & \downarrow \\ P_{\text{disease}} & \longrightarrow & P_{\text{infectious}} \end{array}$$

III. Stratified Models



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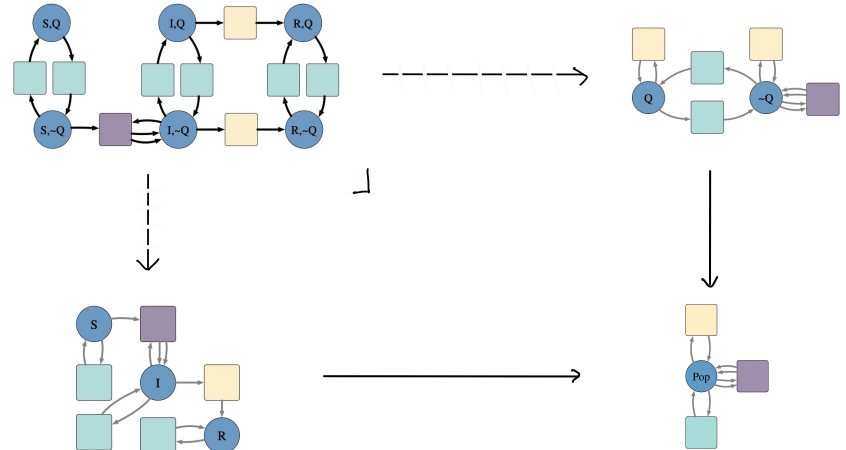


III. Stratified Models

Implementation in Algebraic Julia

```
using Catlab.CategoricalAlgebra
```

```
pb = pullback(typed_SIR, typed_quarantine)  
typed_stratified_model = compose(proj1(pb), typed_SIR)
```



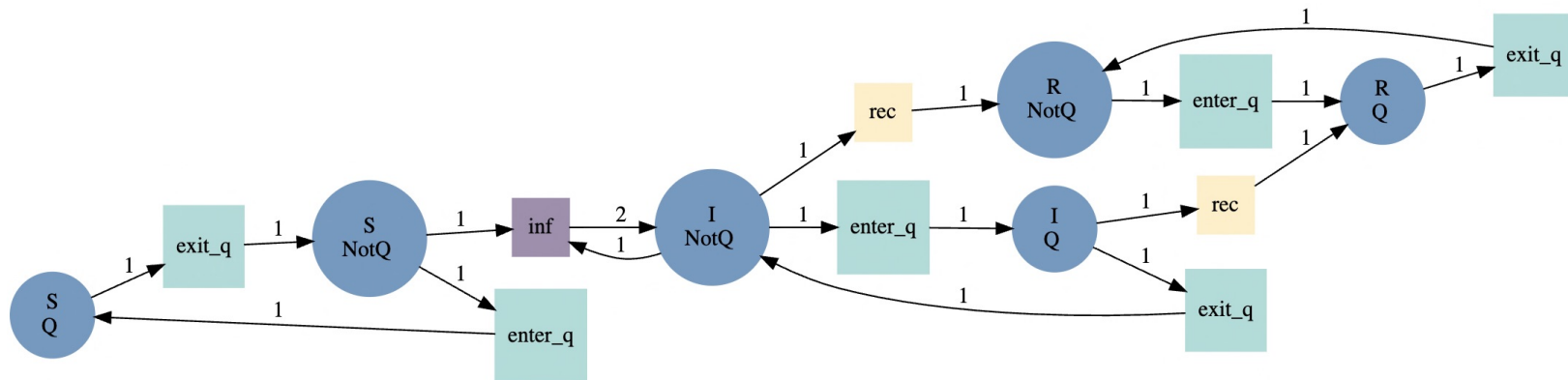
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Implementation in Algebraic Julia

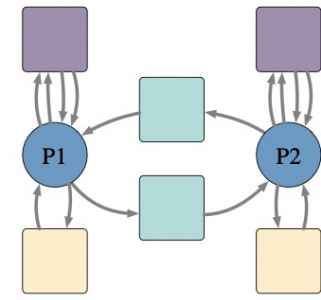
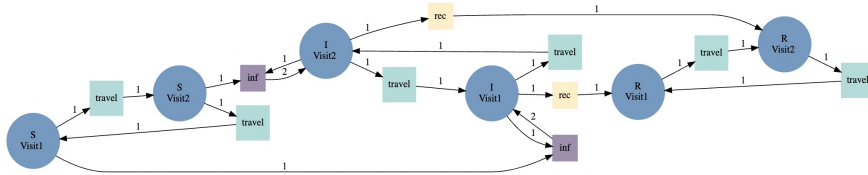
```
using Catlab.CategoricalAlgebra
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```
pb = pullback(typed_SIR, typed_quarantine)
```

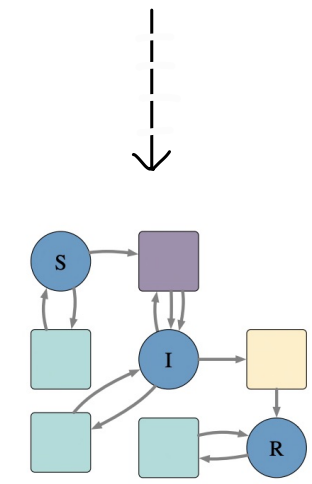
```
typed_stratified_model = compose(proj1(pb), typed_SIR)
```



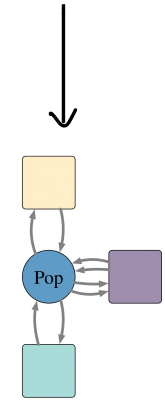
III. Stratified Models



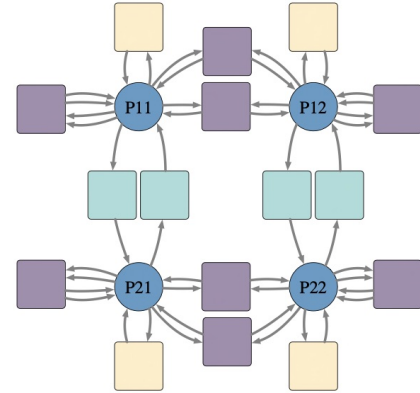
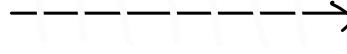
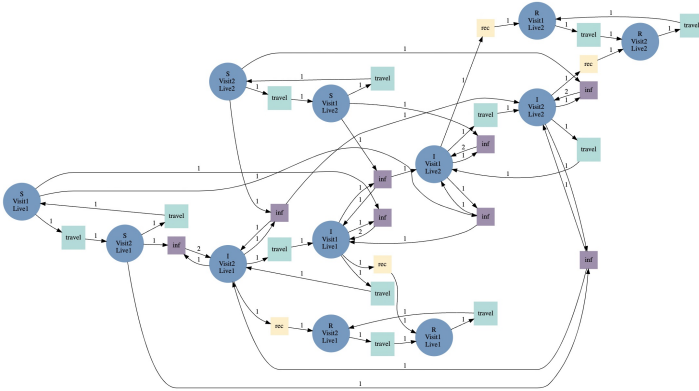
movement model



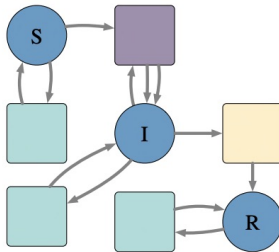
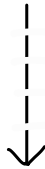
disease model



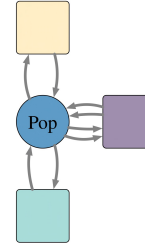
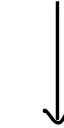
III. Stratified Models



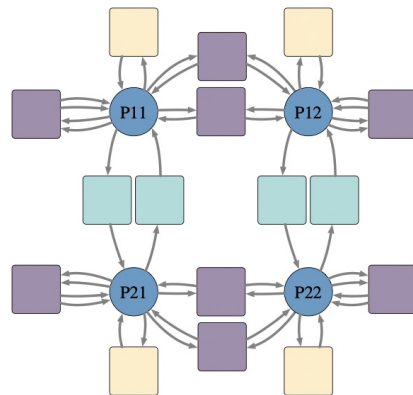
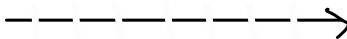
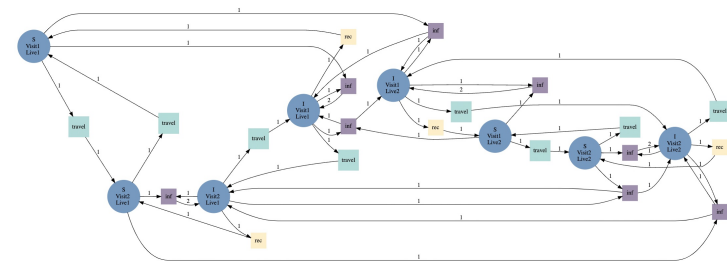
movement model



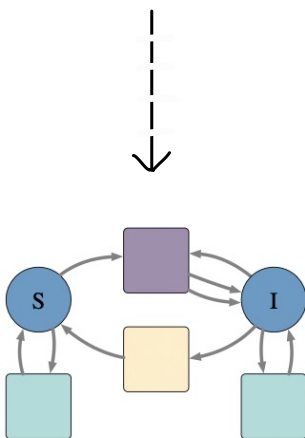
disease model



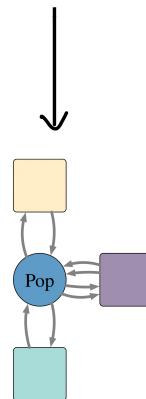
III. Stratified Models



movement model



disease model



Acknowledgements



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GTRI



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University of Florida



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Topos Institute



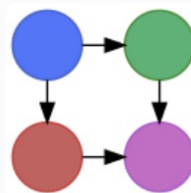
Owen Lynch
Utrecht University



Micah Halter
Balena

Thanks also to

John Baez and Sean Wu



AlgebraicJulia

<https://www.algebraicjulia.org>

Paper

- Libkind, Sophie, Andrew Baas, Micah Halter, Evan Patterson, and James Fairbanks. "An algebraic framework for structured epidemic modeling." *arXiv preprint arXiv:2203.16345* (2022).

Demo

- <https://github.com/AlgebraicJulia/Structured-Epidemic-Modeling>