

Modular construction of compartmental epidemic models

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1 JD: Can we drop “comprehensive” from the title? What about “modular construc-
2 tion of ...”? SW: agreed. done.

3 1 Introduction

4 The COVID-19 pandemic has reemphasized the importance of compartmental epi-
5 demic models (Abou-Ismaïl, 2020; Massonis et al, 2021; Adam, 2020; Currie et al,
6 2020; Lofgren et al, 2014; McBryde et al, 2020; Enserink and Kupferschmidt, 2020)
7 and has resulted in a flood of new compartmental models (e.g., Friston et al (2020);
8 Fields et al (2021); Chang and Liu (2022); Lavielle et al (2020); Balabdaoui and Mohr
9 (2020); Leontitsis et al (2021); Levine and Earn (2022)). This abundance of new model
10 variants is expected given the number of public health modelers trying to use scientific
11 understanding of emerging infectious diseases to contribute to public policy. Modelers
12 must be able to build models rapidly to explore scenarios and generate high quality
13 forecasts; public health recommendations have the biggest impact if they can be acted
14 on promptly. However, the speed at which modelers can develop new models typically
15 trades off with model quality. We therefore need tools that allow modelers to build
16 models more quickly without sacrificing quality.

17 One approach to this speed-quality trade-off is to build infectious disease models
18 incrementally. Information is scarce early in an epidemic, and so early models should
19 be simple to reflect ignorance. As epidemics progress, we learn more about the char-
20 acteristics of the pathogen and its transmission; at the same time the public health
21 landscape becomes clearer but more complex. Because policy choices require fast input
22 from scientists, modelers need to add complexity to their models quickly if they are
23 to be relevant to policy.

24 Proceeding in this way eventually results in complex and fragile models, much of
25 whose complexity is no longer relevant. This sort of complexity also makes it harder

to add additional features to the model. Therefore, modelers need tools that make it easier to flexibly add and remove model structure.

Savageau (1988) and Voit (1988, 1990) made an early attempt to create such a toolbox by recasting the underlying differential equations of a model into a canonical form they call an “S-model”. Unfortunately this effort focused on the model’s differential equations rather than its graphical structure, thus making it unsuitable for less mathematically inclined modelers. It does not seem to have been widely adopted.

Friston et al (2020) describe how the state space of a complex epidemiological model can be constructed from the product of different latent state dimensions (their Figure 1 shows an example with infection status, clinical status, testing status, and location), but the definition of which compartments are connected, and the rates of flow between them, is left up to the modeller.

A promising recent project to formalize the construction of compartmental models employs the language of category theory (Fong and Spivak, 2018; Libkind et al, 2022, 2021; Baez et al, 2023; Baez and Pollard, 2017). This powerful approach addresses many of the concepts we discuss here; however, at its current stage of development it requires considerable knowledge of advanced mathematics to use effectively. An ongoing project to implement the category theoretic approach in the Julia language can be found at <https://github.com/AlgebraicJulia/AlgebraicPetri.jl> (Halter et al, 2022).

Worden and Porco (2017) use the relatively simple language of graph theory to describe common methods of “multiplying” a set of compartmental models (*factor models*) into a new *product model* that incorporates the structure of all of its factors. The current paper is a result of our efforts to build software implementations of the products described by Worden and Porco.

Procedure for Model Multiplication

We view model multiplication as a four-step procedure:

- 52 1. **Generate vertices** of the product model by combining the vertices of the factor
53 models using a Cartesian product (i.e., generate new vertices by choosing one vertex
54 from each factor model, e.g., old susceptible).
- 55 2. **Generate edges** of the product model, typically by taking the Cartesian product
56 of edges in each factor model with the vertices in the other (e.g., we would have an
57 edge from old-susceptible to old-infected). In some cases, we may add additional
58 edges, to allow state changes in multiple strata to occur simultaneously (e.g., a
59 direct flow from medium susceptible to old infected).
- 60 3. **Simplify** by first removing vertices we wish to disallow (e.g., old people with mater-
61 nal antibody protection), with associated edges, and then removing any additional
62 edges that we wish to disallow.
- 63 4. **Adjust flows** by specifying how flow functions should accommodate the presence
64 of additional strata (e.g., spatial structure constrains infection processes).

65 The graph generated by using the default Cartesian products in steps 1 and 2
66 is sometimes called the “box product” (apparently due to Harary 1969, needs to be
67 chased down).

68 Worden and Porco pointed out that flows may need to be adjusted (step 4); for
69 example, when combining a standard SIR model with some other form of structure,
70 we need to decide whether the susceptible population of any particular stratum can be
71 infected by the infectious populations of other strata. In other cases we might prohibit
72 cross-stratum infection, for example by allowing infection within but not between
73 geographic regions.

74 2 What is a Compartmental Model?

75 Figure 1 shows two factor models: the “Epi” model represents individuals in a pop-
76 ulation being infected and then recovering from some infectious disease; the “Age”
77 model represents individuals aging. Our goal is to design an algorithm to generate an

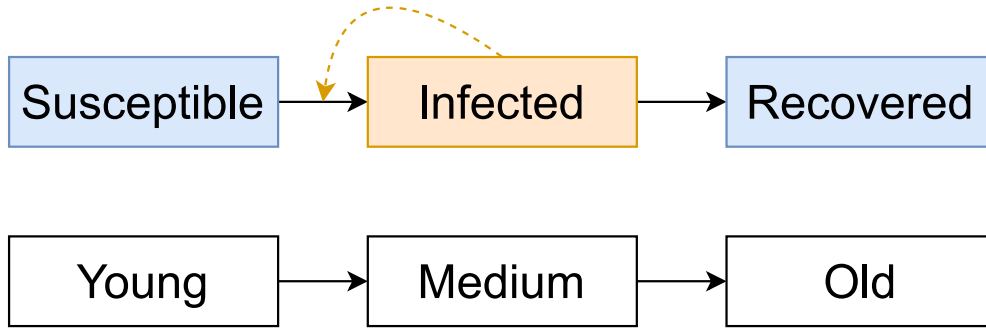


Fig. 1 A standard SIR model and a simple age stratification model. Orange shading denotes the infectious compartment, while blue shading denotes non-infectious compartments.

appropriate product of these two factors (Figure 2). Each compartment in the product model inherits labels from one compartment in each of the factor models (e.g. SY = “susceptible, young”); the flows also typically have two labels (e.g. old infection flow).

Infection flows and infectious compartments

All of the flows in the Age model are constant *per capita* flows; that is, the rate of flow between any two compartments is strictly proportional to the number of individuals in the “from” compartment. The flow from “infected” to “recovered” in the Epi model is also a constant *per capita* flow. In contrast, the *per capita* flow from Susceptible to Infected is typically proportional to the number of Infected – thus, the *per capita* rate depends on occupancy of another compartment, indicated by the dashed arrow in Figure 1. In the specific context of compartmental models for epidemiological dynamics, *per capita* flows that are state-dependent will generally relate to the infection (transmission) process; we will call these flows “infection” flows, and call the compartments that determine their rates “infectious” compartments.

In the SIR model the infectious compartment is the “to” compartment of the infection flow; this is not true for all models. Models may also have multiple infectious compartments — for example the infected population maybe separated on the basis of

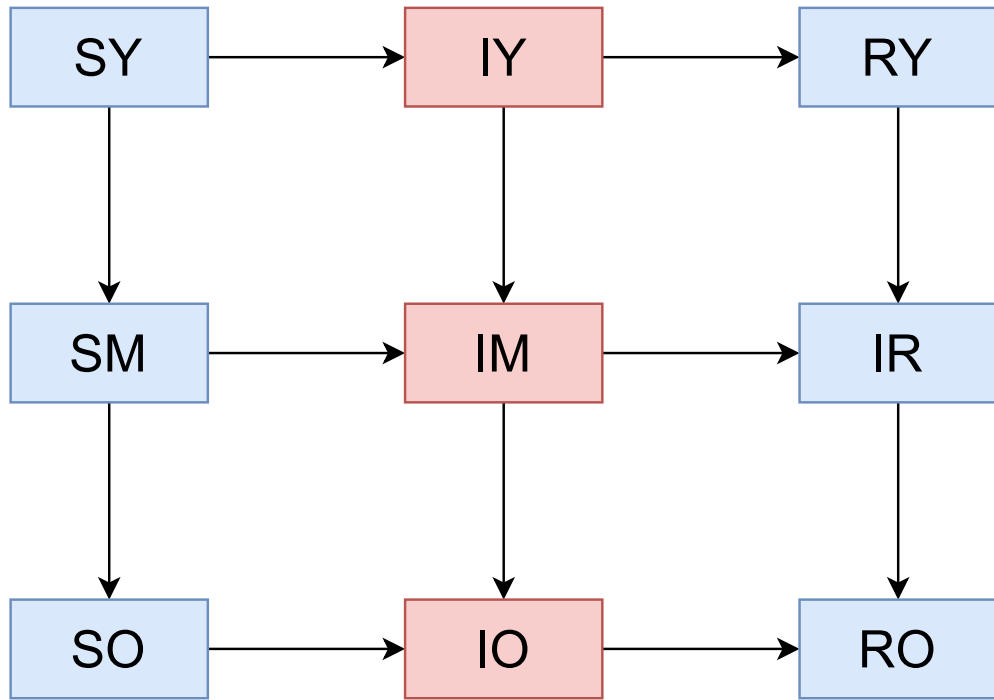


Fig. 2 The product of the two models shown in Figure 1. JD: These two panels should be combined into one Figure for readability, I think.

95 symptom severity. Figure 2 does not include dashed arrows connecting infection flows
 96 with infectious compartments; these relationships will be discussed in Section 3.

97 *Sources and sinks*

98 Consider the long-term outcome of the “Age” model in Figure 1. Since the population
 99 is closed and people only flow from younger compartments to older ones, the entire
 100 population will eventually accumulate in the “old” compartment. If we want to simu-
 101 late the system over time scales comparable to the host lifespan, we need to add and
 102 remove people from the model (“vital dynamics”). This can be done with “sources”
 103 (flows with no “from” compartment”) and “sinks” (flows with no “to” compartment).
 104 We could add a source flow into the “young” compartment and a sink flow out of the

105 “old” compartment (or out of every compartment), representing the effects of birth
106 and death.

107 Sources are also useful in models of viral presence in wastewater. The rate at
108 which new viral particles enter the wastewater compartment is proportional to the
109 number of infected people in the population. But infected people don’t *become* contam-
110 inated wastewater; instead, we add a source whose flow rate depends on the infected
111 population.

112 Multiplying factor models that have sources and sinks may require extra decisions.
113 In most models incorporating vital dynamics, for example, newborns entering the
114 youngest age class are assumed to be susceptible (Earn, 2008), but in cases where
115 vertical transmission or maternal immunity are possible, we might need to consider
116 other possibilities.

117 ***Absolute and per capita flows***

118 Most of the flows discussed above are *per capita* flows, where the total flow between
119 compartments is given by a *per capita* rate multiplied by the population in the “from”
120 compartment (for infection flows, the *per capita rates* depend on the infectious com-
121 partments). In contrast, ***absolute flows*** are specified in terms of the total flow. Source
122 flows, which have no from compartment, can only be implemented as absolute flows
123 (this is how births are typically implemented (Earn, 2008)). If population-level vacci-
124 nation rates are recorded in public health data, it may be simplest to implement these
125 as absolute flows (although specifying an absolute flow from a non-source population
126 may sometimes lead to a mathematically ill-posed model (Gharouni et al, 2022)).

127 ***Implementation***

128 To define a compartmental model, we:

- 129 1. specify compartments (nodes) and flows (edges). A flow is specified by defining:
130 from/to compartments (one of which will be empty for a source or sink flow); a rate

131 type (*per capita* or total); and a rate function that describes how the rate depends
132 on parameters, time and other flows.

133 2. compute the rate vector \vec{r} , based on parameters, time and the state vector \vec{x} . The
134 length of the rate vector is the number of flows in the model.

135 3. compute the flow vector \vec{f} by multiplying each element of the rate vector by a value
136 from the state vector (for *per capita* rates) or by 1.

137 It will sometimes be convenient to have different elements of the flow vector have
138 the same to and from compartments; for example if individuals in one compartment
139 may be subject to infection by individuals in several different compartments. Such
140 flows will typically be added together downstream.

141 JD: Above are the changes that I already wanted to make... I need to try now to
142 read the rest before changing anything. I switched the definitions of \vec{f} and \vec{r} above
143 only, so watch out for that below.

144 JD: Need to add a ¶ about discrete vs. continuous and Markovian vs. deterministic
145 downstream of the flow vectors.

146 2.1 Parameterizing product models

147 In addition to understanding how to construct compartments and flows of a product
148 model from the compartments and flows of its factors, we would like to be able to
149 compute parameter values for the product model using the known values from the
150 factor models. Product model parameters are often related to parameters in the origi-
151 nal model factors in simple mechanistic ways. However, there is an enormous range of
152 possible relationships between the parameters of the factor models and the parameters
153 of their product. Some parameters, such as those relating to aging, may be constant
154 across all strata of a product model. Others, such as recovery time, may be constant
155 with respect to some strata (e.g., location) but variable with respect to others (e.g.,
156 age). In some cases, we may want to simplify relationships due to data constraints —

for example, we may choose to model recovery time as constant across ages for a particular purpose. Ultimately, the question of how factor-model parameters should be generalized to the product model depends on the goals of the model.

If a parameter describes processes that are purely host-dependent it will be constant across strata for different strains of the pathogen. The converse could also occur, if there are parameters that are purely pathogen-dependent. In other cases, the value of a parameter at each stratum in the product model may be derived from factor-model parameters by a simple rule. For example, it might be useful to parameterize the recovery time of hosts in different strata as proportional to some baseline value (e.g., the value in healthy adults). If α is the parameter value in the factor model and $\vec{\beta}$ denotes the values of the derived parameters at each different strata in the product model then $\vec{\beta} = \alpha \vec{w}$ where \vec{w} is a vector of weights.

Relationships among factor-model parameters can be constrained in other ways. When multiple flows emanate from a single compartment, we may want to parameterize them as a partition of the total outflow. For example, an exposed host may have multiple possible fates such as asymptomatic infection, mild infection, or severe symptoms. In that case the factor model in question will have three parameters ($\alpha_i \in (0, 1), i = 1 \dots 3$) that sum to one ($\sum \alpha_i = 1$). Every stratum of the corresponding product model will have three parameters derived from the original α values, but each stratum may have different partitions. For example people in different age groups may be more or less likely to experience severe, mild, or no symptoms.

Different strata of a product model may interact. A standard formulation for the force of infection of a pathogen (i.e., the per-susceptible rate of infection) is $\Lambda = \frac{\beta I}{N}$. Suppose we now stratify this model to represent a scenario where each person lives in one of three different locations but may come in contact with anyone in any location. Our model would then have three infectious proportions ($\vec{\chi} = (I_1/N_1, I_2/N_2, I_3/N_3)$) and three susceptible compartments ($\vec{S} = (S_1, S_2, S_3)$). Using the standard formulation,

we could then calculate the force of infection as:

$$\vec{\Lambda} = B\vec{\chi},$$

178 where B is a 3×3 matrix of transmission parameters $B = (\beta_{ij})$.

179 The generic version of this approach makes the number of required parameters
180 increase quadratically with the number of locations. Epidemiological modelers have
181 devised many ways to add structure B to reduce the required number of parameters
182 [Anderson and May \(1985, 1992\)](#); [Grenfell and Anderson \(1985\)](#). JD: Need recent
183 [cites here](#). For example, the likelihood of a person residing in one location coming
184 into contact with a person somewhere else may be assumed to depend only on the
185 distance between the two locations, allowing the construction of large B matrices with
186 a relatively small number of parameters.

There are, of course, other ways to handle this kind of parameter simplification. Many situations will allow for a mapping that relates the default parameter space generated by model products to a smaller parameter space based on straightforward assumptions. SW: Added the following to this paragraph because it is how I think about β in product models. One useful approach is to decompose β_{ij} into susceptibility, σ_i , and infectivity, τ_j , parameters.

$$\beta_{ij} = \sigma_i p_{ij} \tau_j,$$

187 where p_{ij} is the rate of contact between individuals in i and j SW: Should p_{ij} be
188 considered part of the parameter decomposition or, as I prefer, as additional ‘data’
189 that help put the parameters on a more interesting scale?. If i and j represent age
190 groups, these parameterizations could distinguish between the effects of age on non-
191 contact processes that impact infectivity (e.g., masking SW: something better here?)

192 versus those that impact susceptibility (e.g., age-dependent immunity). **SW: Balancing**
193 **contact rates stuff**

194 3 Cartesian Model Products

195 Returning to Figure 1, recall that the dashed arrow in the SIR model indicates that
196 the flow from S to I is an infected flow and that its magnitude is partly determined
197 by the number of infected people. When we combined the SIR and age models in
198 Figure 2 we omitted dashed arrows. Worden and Porco (2017) describe two separate
199 products, each with the dashed lines drawn differently. In their **naive product**, each
200 susceptible group can only be infected by infectious people in the same group (Figure
201 3). In their **modified product**, each susceptible group can be infected by infectious
202 people in any group (see Figure 4).

203 These two models have the same graph, given by the box product of the factor
204 models. They differ only in the form of the infection flows. The graph underlying
205 a product model is not always the box product (or a subset), though: Worden and
206 Porco's **strong product** adds additional edges. In the model illustrated in Figure
207 2, individuals cannot move directly from the young susceptible compartment to the
208 middle infected one; to make that transition they must take one step first and then the
209 other. If we have strata corresponding to different pathogens, we might use a strong
210 product to allow for the possibility of infection with multiple pathogens in a single
211 event. Strong products might also be preferred for implementations with discrete time
212 steps, where the probability of two independent events in the same time step cannot
213 be neglected.

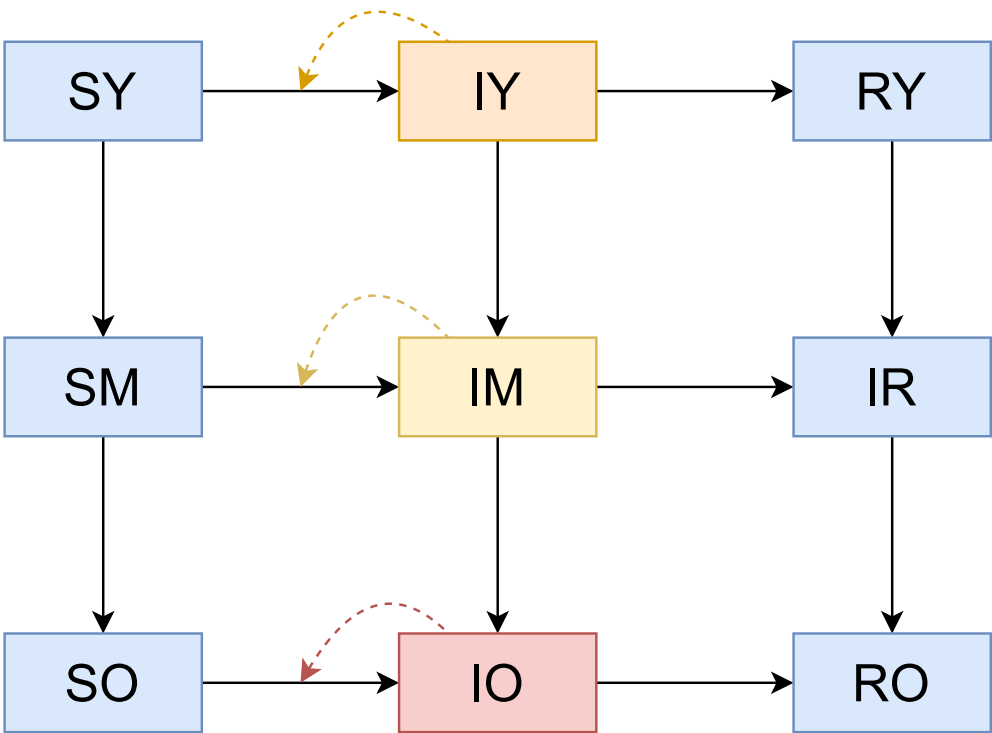


Fig. 3 The naive product of the two models from Figure 1. Blue denotes non-infectious compartments, yellow/orange/red denote infectious compartments. The force of infection is only influenced by the infected population within the same age stratum. In this example, people of different age groups have no contact (or very limited contact) with each other.

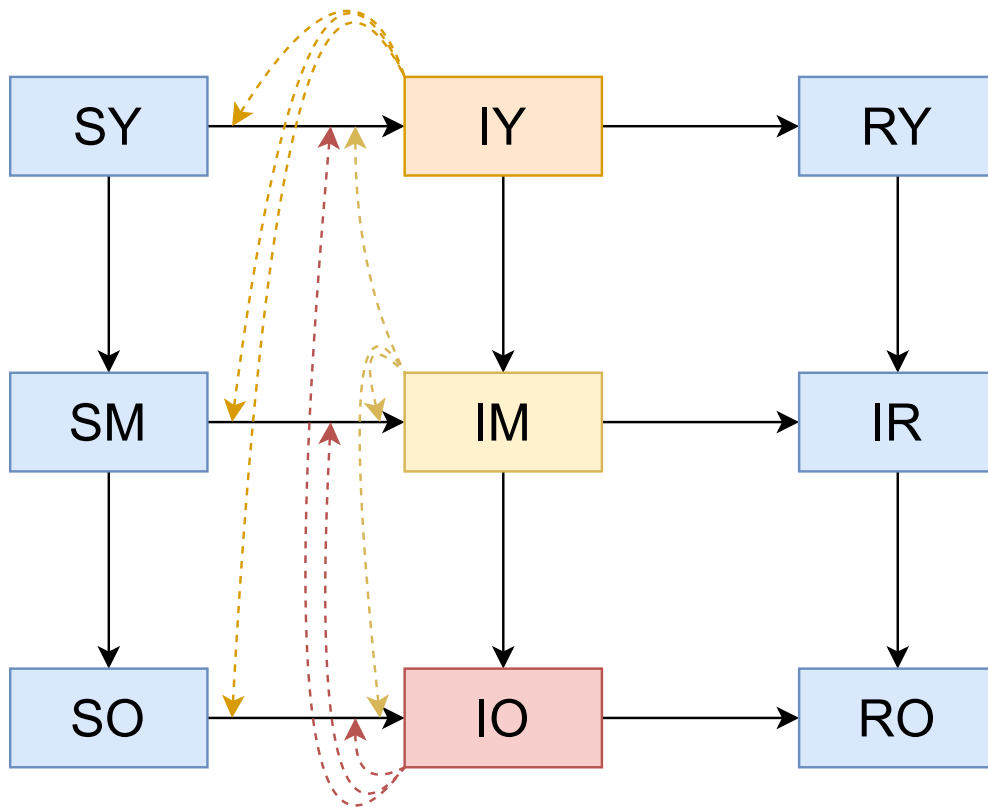


Fig. 4 The modified product of the two models from Figure 1. Unlike in Figure 3, individuals make epidemiological contacts across age strata, so the force of infection for each age stratum is influenced by the infected population in all age strata.

214 Age-stratification will typically use a modified product, because people of all ages
215 commonly interact with each other. Spatial stratification can use different approaches.
216 When movement of individuals is simulated explicitly, (e.g. [Mohammadi et al, 2023](#)),
217 it makes sense to use a naive product, where we assume that people in different
218 locations do not physically interact. Models without explicit movement, (e.g. [Dietz
219 and Sattenspiel, 1995](#)), are more suited to a modified product, which would allow
220 people based in different locations to have some amount of contact.

221 The naive product restricts interaction to people in the same stratum; the modified
222 product allows people in any strata to interact. In many cases, it will be computa-
223 tionally efficient to consider an intermediate “generalized” approach, that allows for
224 people in each stratum to interact with people in “neighboring” strata.

225 Below we show three different ways an SI model could be stratified with location.
226 Figures 5 and 6 show the naive and modified products respectively. Figure 7 shows
227 a generalized product where interactions can only occur within a single geographic
228 region or between neighboring regions. For example, an infected person in the Toronto
229 region could infect a susceptible person in Toronto or Ottawa but not one in Montreal,
230 while the neighbourhood of an infected person in Ottawa includes all three regions.
231 This model is equivalent to, but more efficient than, the modified product with β_{31}
232 and β_{13} set to zero.

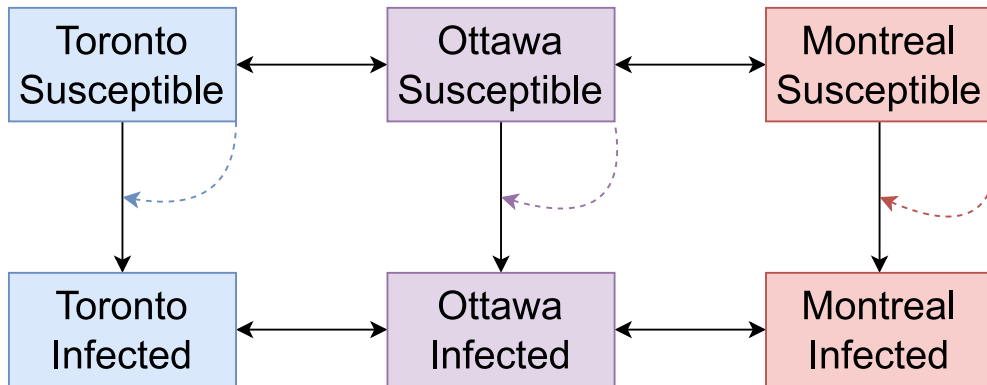


Fig. 5 The naive product of an SI model with location model including Toronto, Ottawa, and Montreal. The force of infection at any given location depends only on the infectious population at that location.

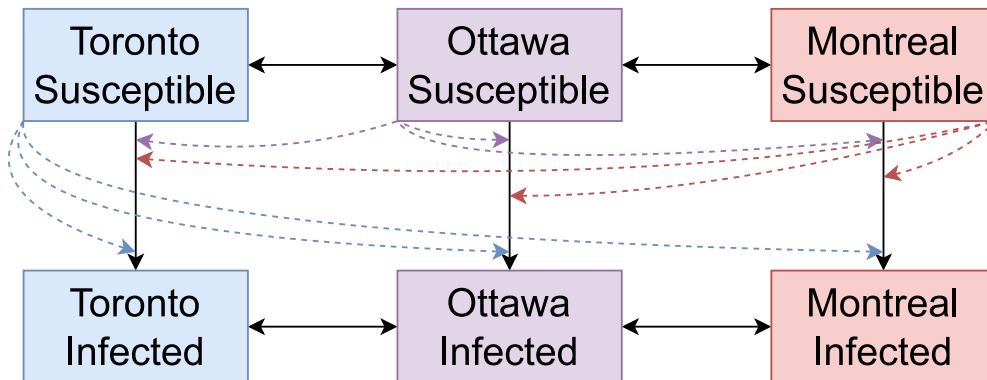


Fig. 6 The modified product of an SI model with location model including Toronto, Ottawa, and Montreal; the forces of infection depend on infectious populations in all three regions.

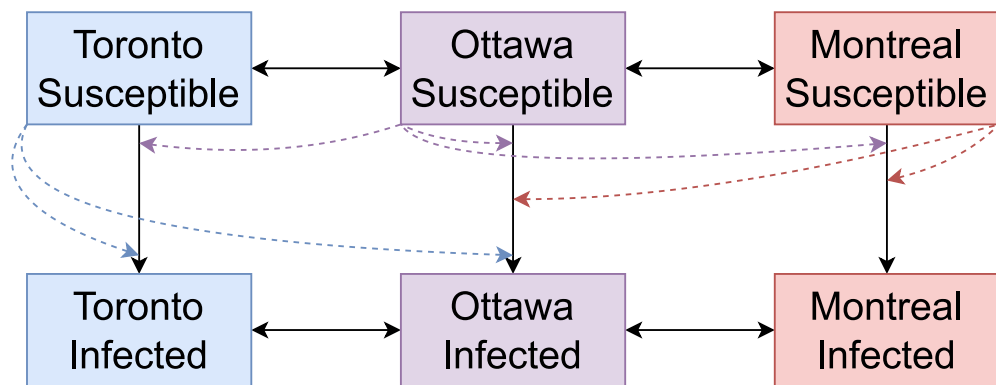


Fig. 7 A generalized product of an SI model with location model including Toronto, Ottawa, and Montreal. The forces of infection depend on the infectious population at the same location and in neighboring locations.

233 4 Examples

234 While Cartesian products allow us to construct a wide range of compartmental models,
235 they cannot account for many useful stratified models. In this section we discuss a
236 number of examples where the model products we have defined so far are insufficient.

237 4.1 Linear Chains

238 4.2 Models with Testing

239 One such example involves modeling the effects of testing for infection, inspired by the
240 dynamics of testing during the COVID-19 pandemic (Gharouni et al, 2022). Consider
241 the epidemiological model in Figure 8 and the testing process depicted in Figure
242 9. The modified product of these two models includes a compartment for untested
243 individuals at the hospital. However, this product is not what we want (Figure 10).
244 The key difference is that untested individuals entering the hospital are typically tested
245 (i.e., moved from “untested” to “awaiting results”); in our model, we will assume
246 that they are always tested. Therefore, the “untested hospitalized” compartment in
247 product model is always empty; the flow that goes to that compartment should instead
248 be directed to the “hospitalized/awaiting test result” compartment. Constructing the
249 desired model would thus require an extra step to redirect this flow and remove the
250 superfluous compartment.

251 BB: can we condense/combine Figs 8-10 without making them impossible to read?
252 (Fig 10 is pretty challenging in any case ...)

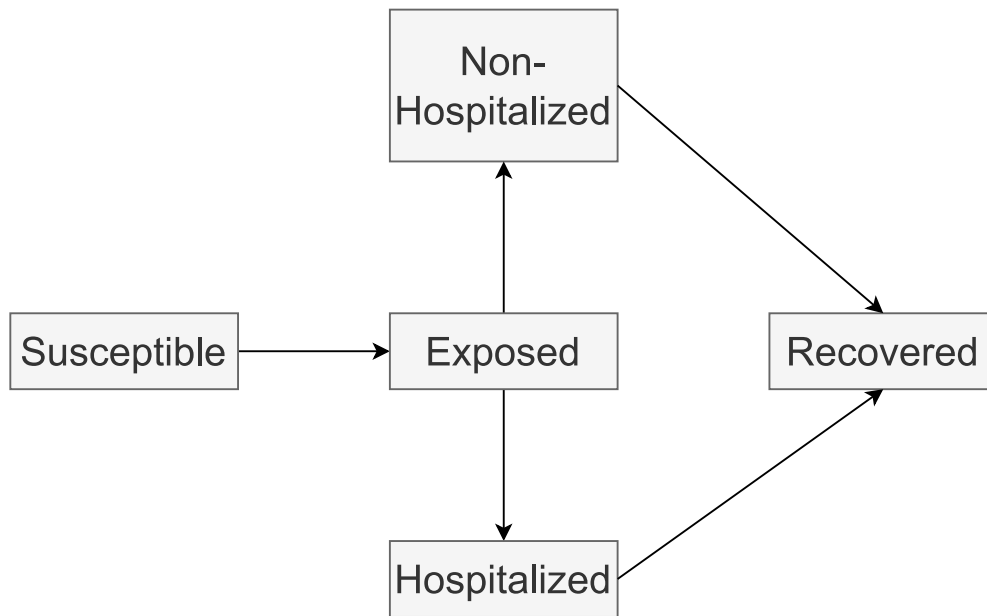


Fig. 8 A simple epidemiological model that we will expand to include testing. In this model, some exposed individuals will develop asymptomatic or mild illness, in which case they stay in the community during their infectious period (and potentially transmit to others); those who instead develop severe illness will be hospitalized. (This model allows neither for within-hospital transmission nor for disease-induced mortality either inside or outside the hospital.)

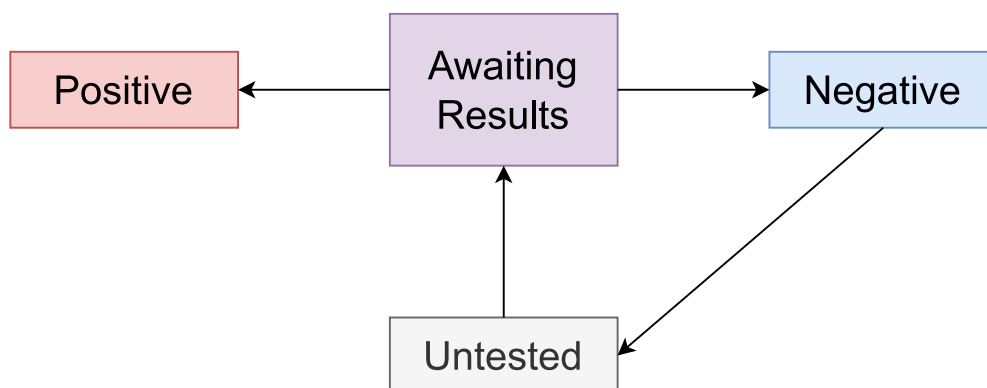


Fig. 9 A simple testing model. Individuals who test negative will, over time, revert back to the “untested” status. This is not the case for those that test positive; at least during the early stages of the COVID-19 pandemic, someone who had tested positive for COVID-19 would assume that they were immune and would not be re-tested even if they developed COVID-like symptoms.

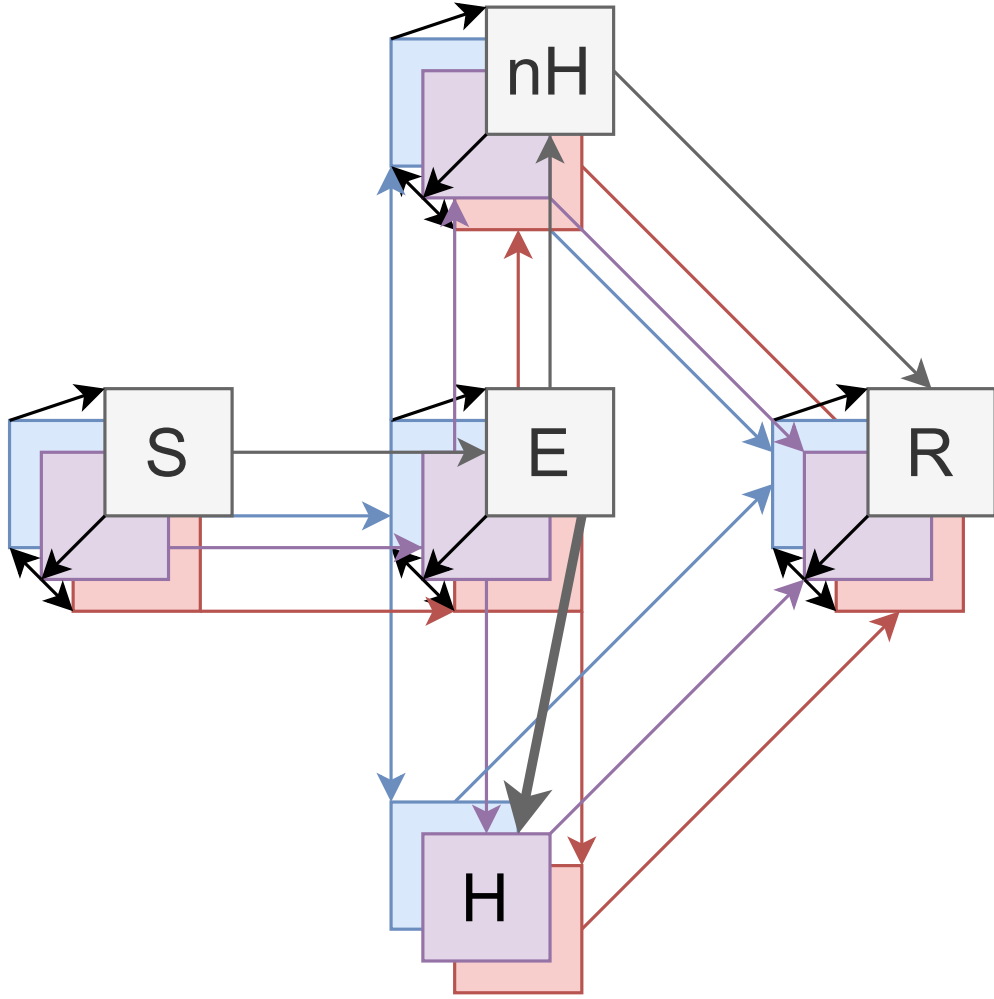


Fig. 10 The desired result of combining Figure 8 with Figure 9. Note the missing grey “untested” box associated with the hospital location; exposed individuals going into the hospital (enlarged, grey downward arrow starting at E) flow into the purple “awaiting results” subcompartment.

4.3 Multistrain Models and a Weak Product

Many epidemics involve multiple co-circulating strains of the same pathogen (Gog and Grenfell, 2002; Williams et al, 2021). In the case of COVID-19 such variants have significant implications for the efficacy of vaccines (Abu-Raddad et al, 2021; Koyama et al, 2020) and diagnostic tests (Vasireddy et al, 2021). In more complex models, including multiple strains rapidly inflates the size of both the state space and the parameter

space (Kryazhimskiy et al, 2007). One way to limit the size of these unwieldy models while continuing to include the effects of multiple strains in our model is to disallow the possibility of superinfection (i.e., an individual being infected with multiple strains at the same time). BB: should we worry about distinguishing superinfection (infection A then B) vs coinfection (simultaneous inf with A and B)? It would therefore be useful to define a weak product similar to the operations proposed by Worden and Porco (2017) but which excludes all states corresponding to a superinfected status. One way to do this, which works well for two-strain models, is to use the standard Cartesian product but include only flows that emanate from compartments with no inflow (**sources**) or enter compartments with no outflow (**sinks**). Flows in this category typically represent initial infection (i.e., flows out of a susceptible class that is a source) or final recovery (i.e., flows into a recovered class that is a sink). In making this restriction, we exclude all the flows within the set of compartments that represent infected states, such as from an exposed to an infected compartment). For convenience we denote this operation by \boxplus and call it the **weak product**.

Figure 11 depicts a two-strain SIR model without superinfection, corresponding to the weak product of two SIR models. Unfortunately, the weak product is not associative! Figures 12 and 13 depict two different results for the weak product of three SIR models with different grouping. If the factor models for the three strains are M_1 , M_2 , M_3 then Figure 12 depicts $(M_1 \boxplus M_2) \boxplus M_3$ and Figure 13 depicts $M_1 \boxplus (M_2 \boxplus M_3)$. Figure 14 depicts the desired result for a three-strain SIR model with no super-infection.

BB: I got a little bit confused by the flow here. The three-strain model, and why the weak product doesn't work in this case, is presented (are there other applications of the weak product other than multi-strain models? Seems a little limited if the *only* thing it is good for is two-strain models without superinfection). Then we say "but we can't do that with these products". Then we talk about labeled partitions. Then

286 we present a *different* two-strain model, which I guess represents another problematic
287 case for the weak product (but which can also be solved with labeled partitions)? The
288 only thing we say about this model (in the last few lines of the body of the paper) is
289 that it’s problematic [and could be solved by labeled partitions?]

290 It is possible to create a version of the weak product defined above that will pro-
291 duce the model shown in Figure 14. However, it requires us to distinguish between
292 compartments that are *global* sources or sinks and compartments that are sources or
293 sinks with respect to one of the three strains specifically. That is to say, while a global
294 sink must have no outflows, a weaker condition says that a compartment is a sink
295 with respect to a specific pathogen if every compartment that can be reached via the
296 outflow has the same infection status with respect to that pathogen as the original
297 compartment. Programmatically we achieve this by introducing a concept of ‘labeled
298 partitions’ which separates the vertices of the model into disjoint sets corresponding
299 to the vertices’ status with respect to a specific pathogen. Each dimension of strati-
300 fication in the model corresponds to a different labeled partition with each stratum
301 corresponding to a different disjoint set. In this way we can define sources and sinks
302 with respect to a specific set of labels rather than globally. For example, we can say a
303 compartment A is a sink with respect to a specific labeled partition if every compart-
304 ment that can be reached after being in A is in the same set as A . Figure 15 outlines a
305 compartmental model with one source compartment but two sink compartments and
306 Figure 16 shows the weak product of two such models. An unfortunate aspect of this
307 construction is that several of the compartments can only be reached by individuals
308 after they are already dead (!). If there are relatively few such compartments a modeler
309 may choose simply to leave them in the model and treat them all as a single com-
310 partment. But if there are many such “zombie compartments”, or if computational
311 efficiency is a pressing concern, they could be removed from the model.

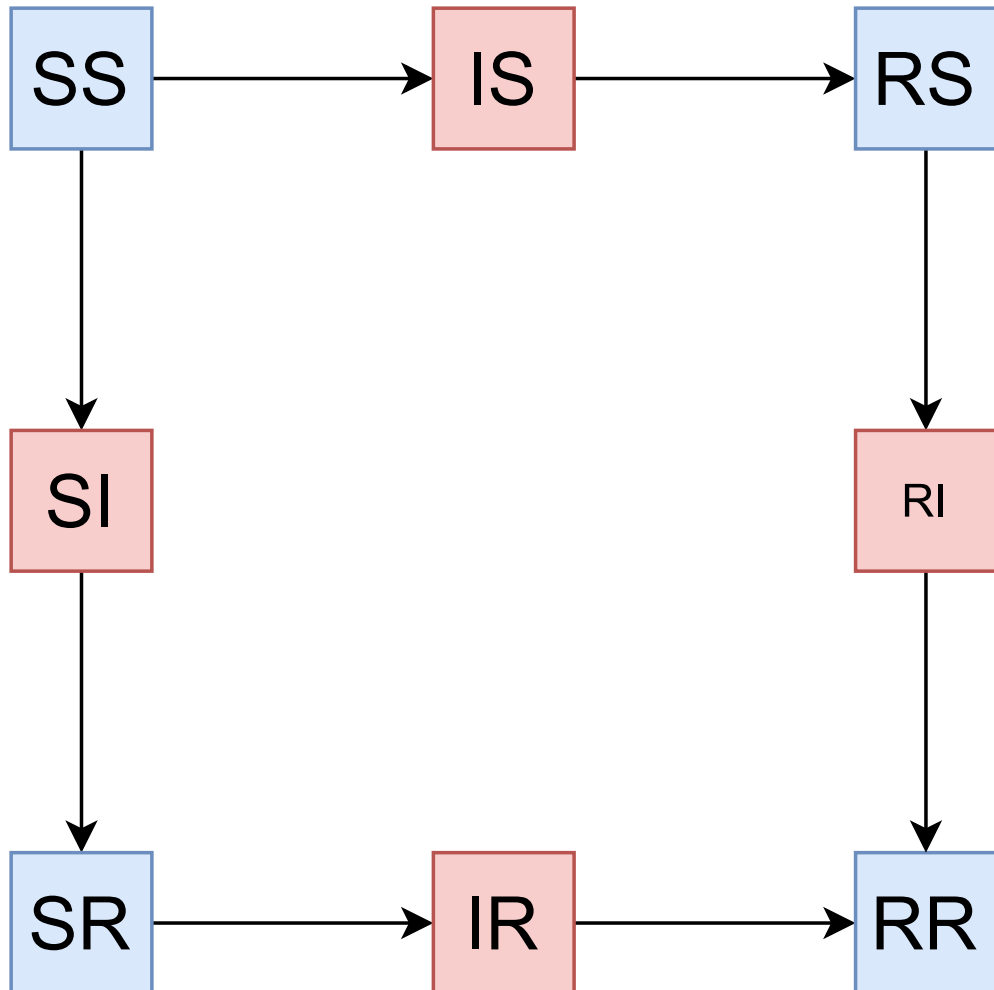
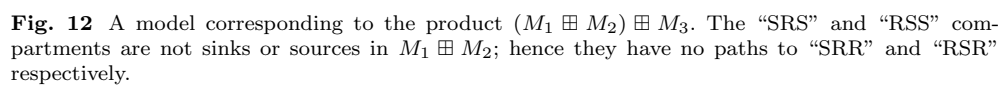
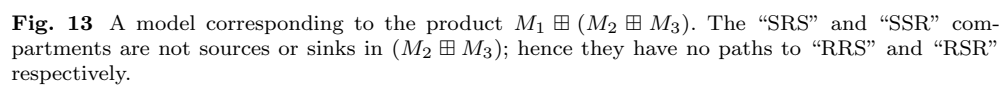
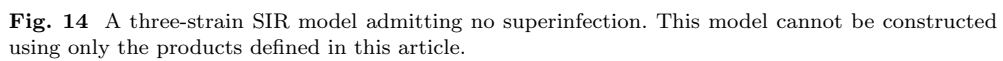


Fig. 11 A two-strain SIR model admitting no superinfection. Red Compartments indicate an infectious population whereas the population in blue compartments are not infectious







312 4.4 Levels of immunity

313 4.5 STD models

314 SW: These are some ideas from Ben about STD models. I've deleted the section that
315 they originally appeared in.

316 STD models with varying mixing rates?

317 Activity-weighted mixing, as in STD models: the relevant value is an activity-
318 weighted average, $\sum_j \beta_{ij} c_j I_j / \sum_j c_j N_j$ (or something like that)

319 5 Conclusion

320 Adding new strata to simple epidemiological models is closely related to taking the
321 Cartesian product of digraphs. Modellers who want to combine sets of simple models
322 into a single large stratified model would benefit from a toolkit based on well-defined
323 mathematical operations. This toolkit must contain a variety of operations represent-
324 ing a useful subset of the numerous ways that separate strata in a model can interact.
325 Ideally, it should also be specified in such a way that it can act *automatically*, once
326 users have clearly specified which set of rules should be used for constructing the
327 model product. We have developed a mathematical formalism for defining such oper-
328 ations and used it to restate two previously proposed model operations, the naive and
329 modified products, which represent extremes of a spectrum of interactions between
330 strata. The naive product corresponds to the case where different strata never interact,
331 while the modified product corresponds to scenarios where any stratum can interact
332 with any other stratum. We generalize these previously proposed operations to a third
333 operation that allows any level of interaction between model strata, for example to
334 construct geographically stratified models where interactions can occur within a single
335 location and its neighbours but not more distantly.

336 BB: this needs to be restated in a more positive and useful way! Ultimately, all we
337 have really done here is discuss ways to reduce the size and complexity of compart-
338 mental model products by eliminating unnecessary flows and compartments. If time
339 and resources were unlimited we could treat every compartmental model as though it
340 was a complete graph with every compartment connected to every other compartment.
341 Doing this would certainly simplify the process of finding the product of two models,
342 but simulating the result would involve spending a lot of time computing things like
343 the probability of someone spontaneously aging thirty years and developing immunity
344 to a pathogen they never actually encountered. Our goal however is not only to pro-
345 duce mathematically accurate models, but also to use those models to provide policy
346 makers with useful and timely advice. This means that finding ways to reduce the time
347 needed create relevant models and generate their output is a highly beneficial exercise.

348 Several challenges remain for anyone wishing to further develop a model construc-
349 tion toolkit. (1) While we have considered the structure of model products in detail, we
350 have been less thorough in building a parallel scheme for the rules used to generalize
351 from factor-model parameters to the parameters of the corresponding product model;
352 a set of product types similar to the naive, modified, weak, etc. products described here
353 would be useful. Many models (e.g., models with infection status testing) also have
354 asymmetries in their structure that cannot be reproduced with Cartesian-like prod-
355 ucts. This suggests the need for additive operations to supplement the multiplicative
356 operations presented here. In fact, such operations already exist in the category-
357 theoretic approach to model operations, one reason why it could be a worthwhile
358 project to unite the category theory and graph theory approaches. This would involve
359 finding “type-graphs” that cause the category theoretic operations known as “pull-
360 backs” and “push-outs” to reproduce the results of graph theory operations (Fong and
361 Spivak, 2018; Libkind et al, 2022, 2021; Baez et al, 2023; Baez and Pollard, 2017).

362 We are heavily motivated by the desire to develop software to facilitate model
363 construction. One insight of our investigations is the utility of a system of so-called
364 “labeled partitions”, which divide the compartments of a model into mutually exclu-
365 sive groups. Each group in such a division will contain all compartments that are
366 in the same level of some dimension of stratification and the groups can be labeled
367 accordingly. By applying several such divisions to a model, one for each dimension
368 of stratification, it becomes possible to specify important subsets of the model com-
369 partments. Using this system of labels and partitions provides an easy way to address
370 issues like the non-commutativity of the weak product and the presence of “zombie
371 compartments” discussed in Section 4.3.

372 Although theoretical and practical challenges with the application of binary oper-
373 ations on model space remain, our approach forms the basis of a powerful toolkit for
374 the construction of complex, stratified, compartmental models.

375 BB: beyond further streamlining and clarification, the two things I might like to see
376 in this paper (if they fit in) are (1) something about the decomposition of transmission
377 matrices into (susceptibility \times contact \times infectivity, as in the [state-dependent rates](#)
378 [vignette](#) . . . and (2) more on labeled partitions, which we introduce at the beginning of
379 the paper and only get back to at the very end, a little bit. Can we add stuff on labeled
380 partitions without driving ourselves crazy or making this take much longer . . . ?

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386 7 Declarations

387 The authors declare that they have no competing interests.

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