Macromodel - *Errata*

To whitepaper printed for the 2024 IDM Symposium

Text formatting	Interpretation
Present	Unchanged text to orient where we are in the document
Added[1]	Add the green text and any footnotes to the document, replacing any text in its place.
[2]	This footnote already existed, but its text has changed
~~Removed~~[3]	Delete struck-through text and any struck-through footnotes
… / ~~…~~	Present or removed text not necessary to list.
Note: This is a note	This will add context.

Paragraph 2: *Risk factors are already integrated into the Macro Model, but are optional.*
…characterized distinctly by those primary factors: geographic location, age, sex, and race/ethnicity~~, and…condition risk factors.~~

Paragraph 3: *The static coupling factors are not limited to a single value; it can even be an asymmetric matrix, although typically it is symmetric.*
…As such, we optionally partially couple their basic reproductive rate numbers and mortality rates. Regular patterns of movement…are ~~currently…between-location mobility data.~~ parameterized through static coupling factors, which can be set by the user or from provided mobility data. Although…

Paragraph 4: *Clarified the relationship between indoor events and other history/plans and that the indoor airborne transmission model is only applied to the indoor events.*
…interaction with others. When ~~we have…where they have been~~ an individual app user provides specifics about their congregations with others indoors (indoor events), we calculate ~~the risk for the individual~~ their event risk using…modeled very similarly to a collection of people, essentially by ~~duplicating~~ cloning the individual…and by making necessary adjustments for that duplication when modeling the individual's interactions.[1]

Paragraph 6: *Age is not the only such risk factor. We have a number of COVID-19 risk factors.*
Finally, within a given node, vaccination and behavioral and disease condition risk factor…if available. ~~Age is currently the only such risk factor.~~

Footnotes page 1:
1. We will handle multiple individuals with other techniques (*i.e.*, subsampling).

Table headers:

Feature	Pandemonium ~~Macromodel~~	~~Covasim~~Starsim	EMOD

Revised: Dec 10, 2024

Table changes:

Feature	Changes (only listed when things actually changed)
Simulation type	Pandemonium: ~~Population-based~~[1] Population/Group/Individual modeling as desired, including simulating at multiple scales within one session.
Availability	Pandemonium: Python library (soon), web app (in user testing) EMOD: C++ library, python library, standalone app
Handling of stochastic variance	Pandemonium: Sampling is handled automatically by Pyro framework Starsim: One sample per simulation run with no built-in variance estimation EMOD: One sample per simulation run with no built-in variance estimation
Parameter inference ~~from data~~	Pandemonium: Yes, uses Pyro library for Bayesian inference from data Starsim: No, must be tuned manually or with external software to fit data EMOD: No, must be tuned manually or with external software to fit data
Compute scaling	Pandemonium: A typical 28-day run…takes 10-20 minutes[3] EMOD:No performance figures given, but explicitly intended to be run on HPC clusters ~~for all but the simplest models.~~
Memory scaling	Pandemonium: Scales quadratically with the number of distinct subpopulations *Note: This is due to the coupling matrix.* Starsim: Appx. 1 GB / 1M agents (linear scaling)
Heterogeneity of infection between regions	Starsim: Officially "possible, but not easy"[4] ~~: must be…~~
Heterogeneity of demographic groups [within regions]	Pandemonium: Yes, through subdivision of geographical nodes into homogeneous subpopulations Starsim: Yes EMOD: Yes
Individual risk assessment support	Pandemonium: Yes[5] ~~(includes subsampling capability)~~
Spatial movement	Pandemonium: Explicitly supported[46]
Applicability to new diseases	Starsim: Relatively easy (directly extensible with Python)
Asymptomatic carriers	Pandemonium: Not currently explicitly modeled (but will be)
Contact networks	Pandemonium: Yes (via coupling factors)
Viral load model	Pandemonium: Yes (only in MicroModel)
Biophysical airborne transmission model	Pandemonium: Yes (via [Bazant & Bush] MicroModel integration)
~~Supports~~ Importance sampling?	Pandemonium: ~~Yes~~ Not Yet (will via Pyro)
~~Interventions (general or targeted)~~	~~Pandemonium: Planned~~ ~~Starsim: Yes~~ ~~EMOD: Yes~~ *Note: all models are able to model interventions via multiple runs with different circumstances or actions taken, hence this row is unnecessary.*
Common Random Numbers technique for intervention impact noise reduction	Pandemonium: Planned but very difficult (would likely require modifying Pyro and/or implementing automatic graph surgery) Starsim: Yes EMOD: No

Footnotes page 2:

~~1.~~ *(deleted)*

2. *(unchanged)*

3. Pandemonium is designed to produce distributions of outcomes to reflect variance/uncertainty, and it can infer latent variables including parameters. As such, one Pandemonium run is equivalent to many Starsim or EMOD simulations for the purposes of statistical analysis, and will fully self-tune to input data.

4. Starsim directly supports only one region per model run. While modeling interactions between regions or expressing heterogeneity is possible through individuals' contact graph, these must be constructed manually or with external automation, making it challenging to implement.

5. We currently provide scaled individual modeling when evaluating risk for a single individual by modeling them as a population without self-interaction and proportionally reduced impact on other populations.

~~4~~6. *(unchanged but renumbered)*

7. caveat: multiple individuals have not yet been tested.

8. Viral load modeling occurs within the integrated MicroModel, specifically during MicroEvents, and is not generalized or directly exposed within the broader MacroModel.