The Reference Model for Disease Progression

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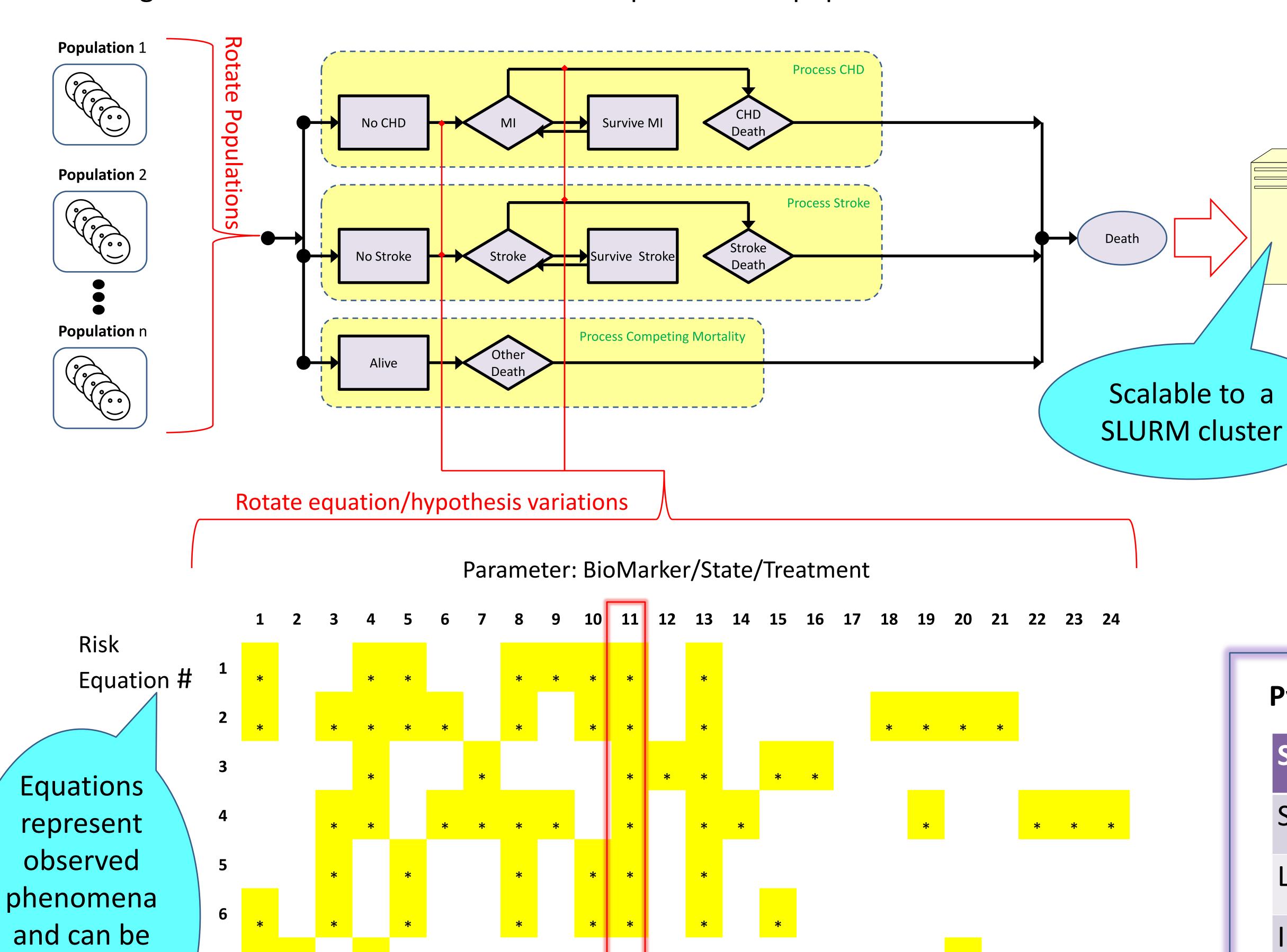
http://sites.google.com/site/jacobbarhak/

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• Built from literature references and hence the name

Designed to serve as a reference for new equations and populations

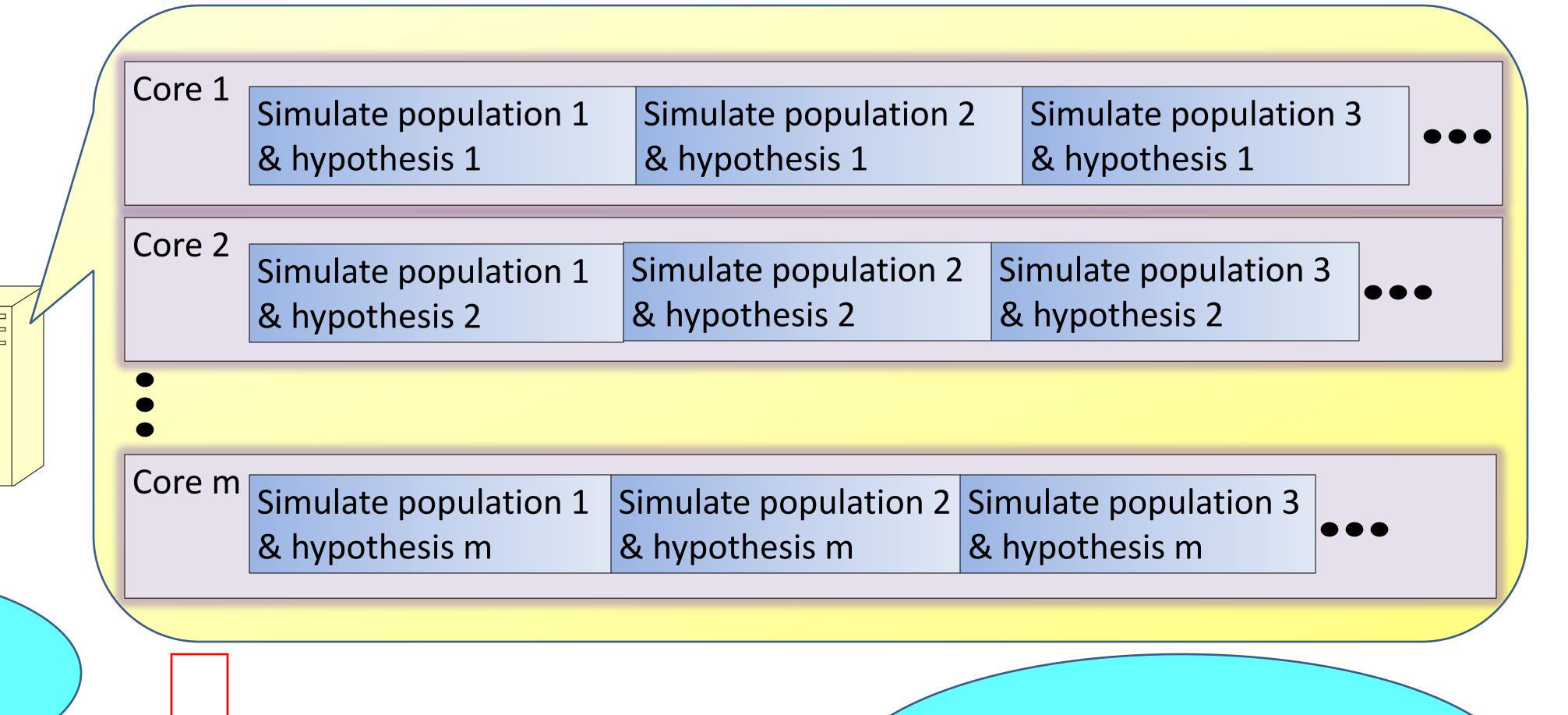


Smoke

Inputs are based on secondary data:

- Published Risk Equations
- Published Clinical Trials, i.e. no real individual data
- Other publications

Allows the model to access more population sets and cover more phenomena



Comparisons improve

understanding of

disease progression

Outputs:

- 1. Clinical outcomes / Deaths
- 2. Costs / Quality of Life
- 3. Population / Equation / Hypothesis fitness

Python provides the following advantages:

| Support | Libraries/commands |
|------------------------------|--|
| Simulation language support | parser, tokanize, re |
| Launching multiple processes | shlex, subprocess, multiprocessing, import |
| Import/export | csv, pickle, zipfile |
| Math/statistics | math, numpy |
| Graphic user interface | WxPython |
| Plots | matplotlib |

Refeencese:

- Barhak J., Isaman D.J.M., Ye W., Lee D.: Chronic disease modeling and simulation software.
 Journal of Biomedical Informatics, Volume 43, Issue 5, October 2010, Pages 791–799,
 http://dx.doi.org/10.1016/j.jbi.2010.06.003
- Barhak J., The Reference Model in the Mount Hood #6-2012 validation challenge and the uncertainty challenge. The Mt hood challenge 6, June 7-8, 2012. Johns Hopkins Mt. Washington Conference Center.

Acknowledgments:

combined

with

hypothesis

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