

Generating Populations for Micro Simulation from Publicly Available Data

Jacob Barhak Ph.D.

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



Populations in the MIST!

In a Nutshell: MIST is a free Micro Simulation Tool

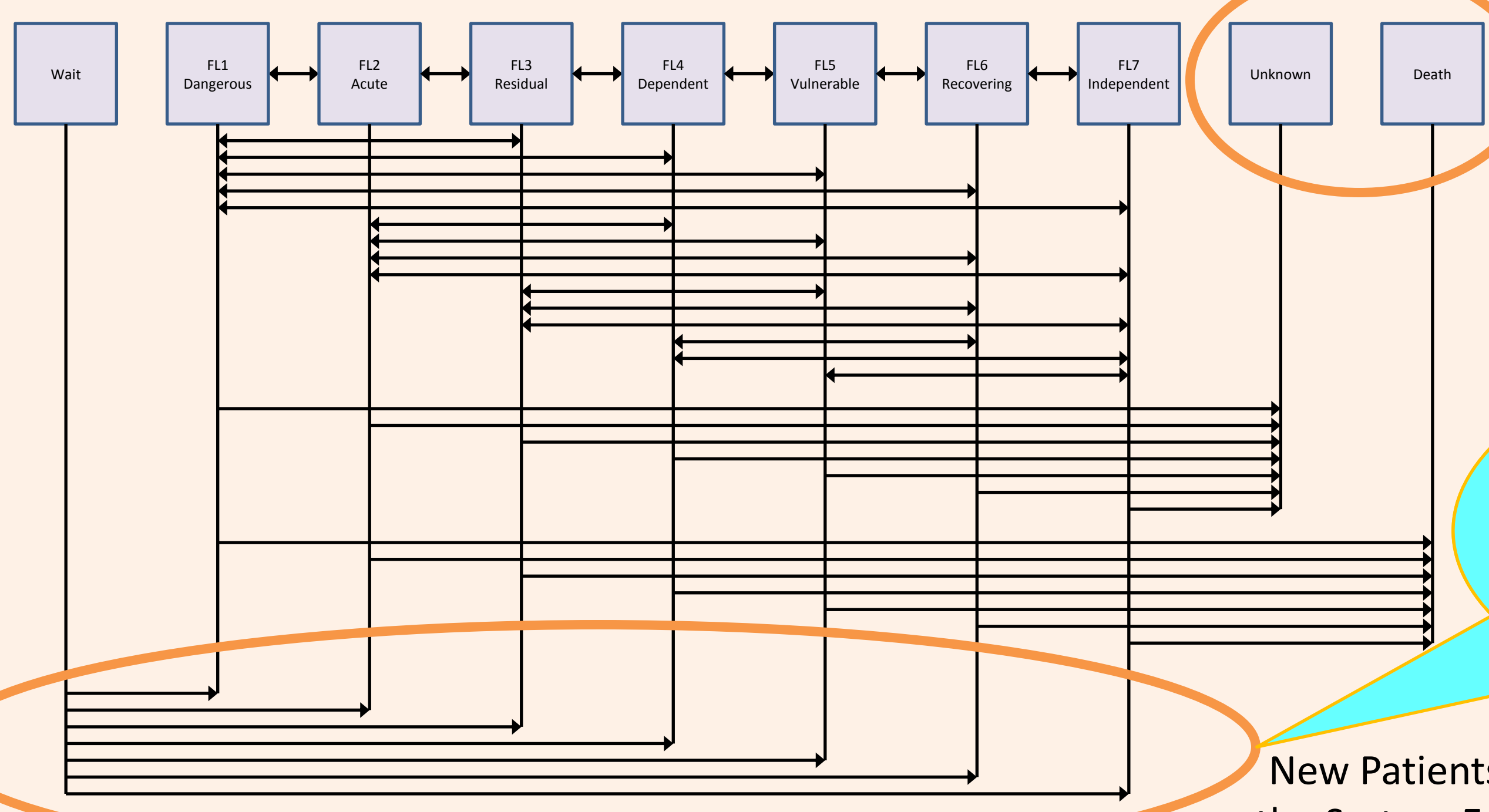
MIST supports several ways of generating and handling populations

IMAG Multiscale Modeling (MSM) Consortium Meeting

3-4 September 2014

Mental Health Model

Developed by Stephen Leff



Patients Exiting the System to Absorbing States

The Mental Health Model Describes Population Flux

New Patients Entering the System Each Month

Reproducibility Info: MentalHealthMist_MIST_2014_08_27.zip

Abstract:

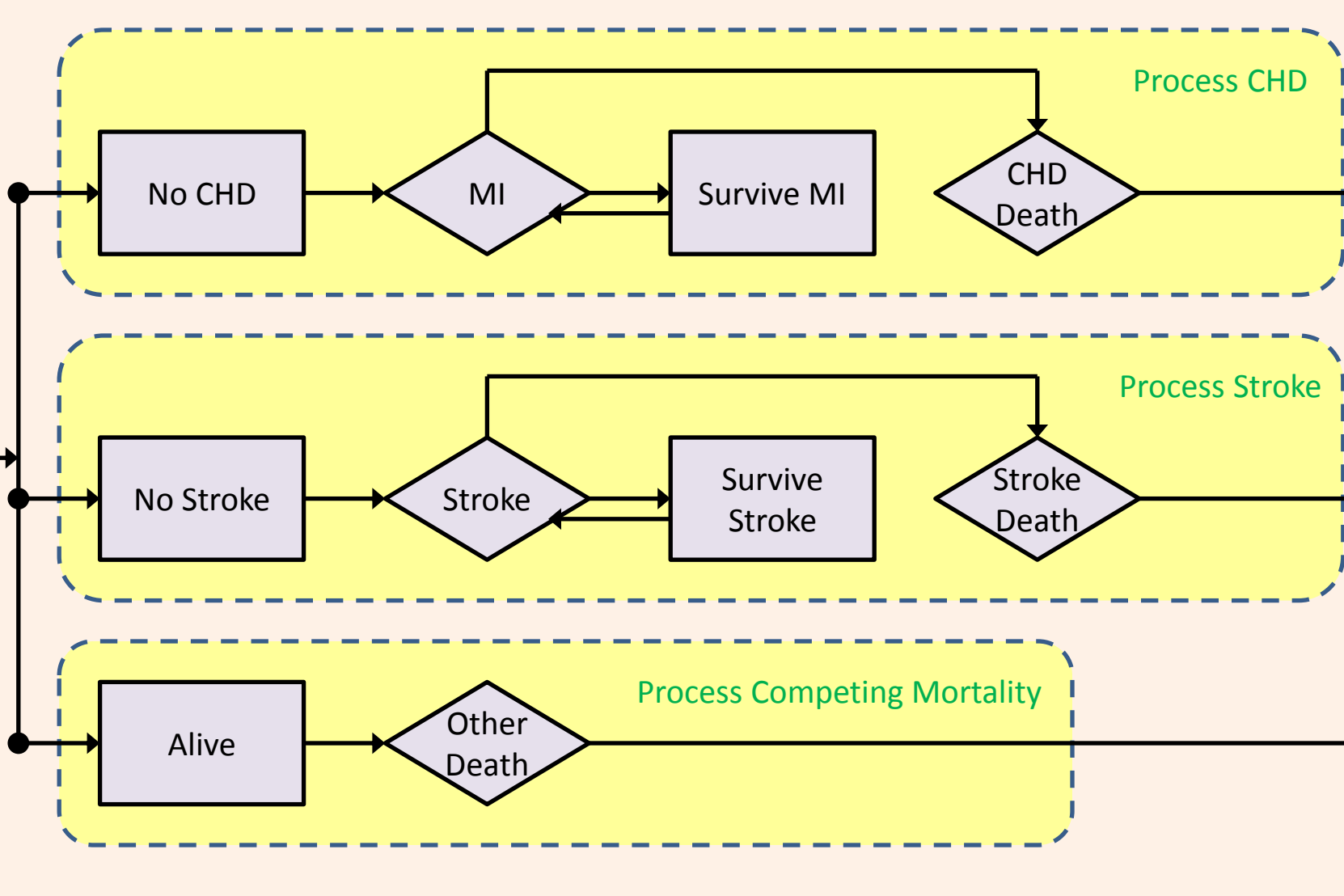
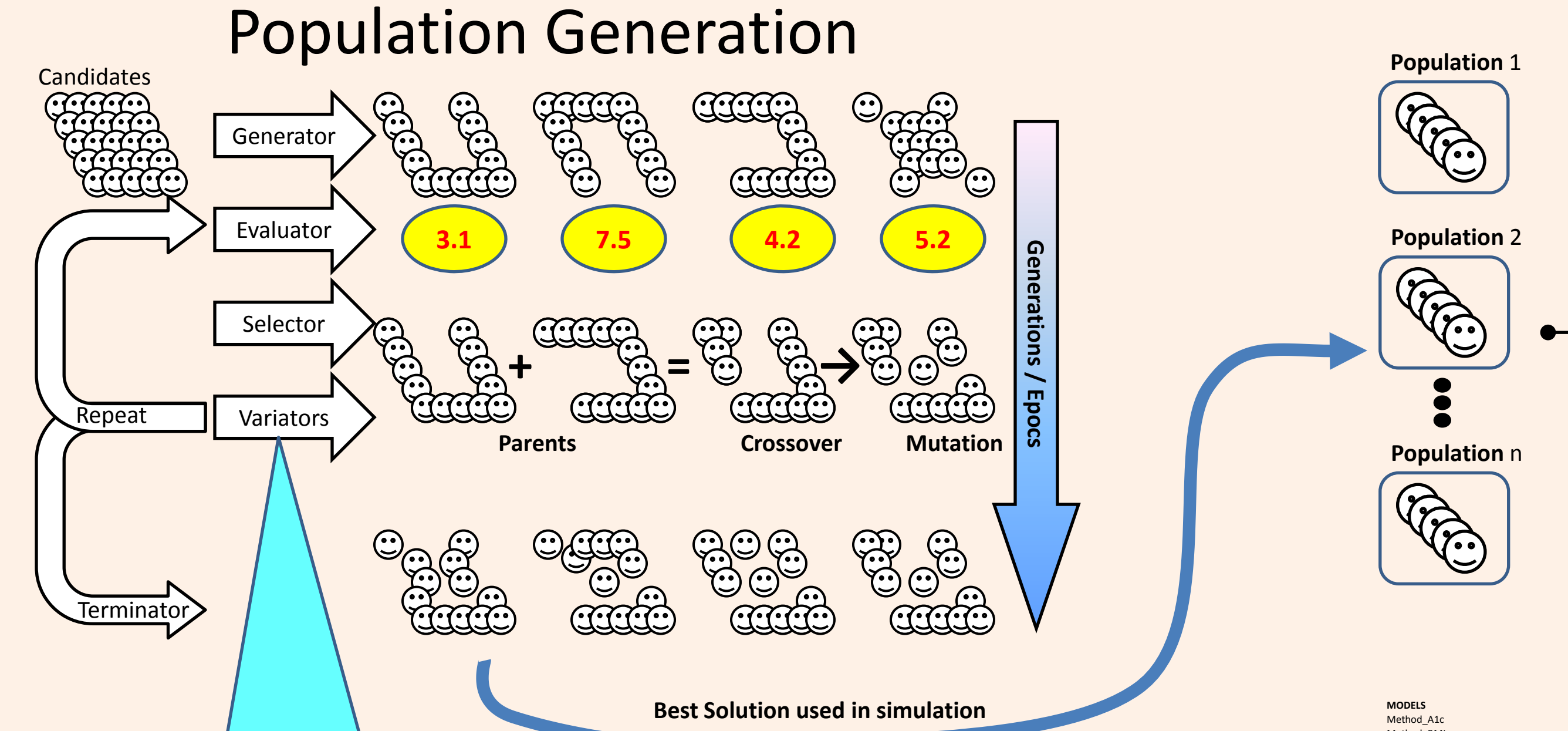
Individual medical data has restricted access. However, a lot of summary data is public through clinical trial results publications or other statistical tables. This summary data is available for baseline inputs for simulation models or for understanding population compositions. There are benefits from generating mock individual populations from the available distribution data:
1) Aggregating public information that otherwise would not be accessible.
2) Studying observed phenomenon under given hypotheses.
3) Micro-simulation at the individual level models non linear model effects.

The Micro Simulation Tool – MIST is free software that has various population generation capabilities. Specifically two techniques to model populations using micro-simulation are presented:

- 1) Mental Health Model: Where population size changes due to incoming and outgoing patients. MIST allows maintaining a wait state where individuals are held before entering simulation and accounting for lost populations using terminal states. MIST reporting system allows following the flowing population in each state. The Mental Health Model implementation is joint work with Stephen Leff from HSRI. A web portal containing the original model that this work re-implements and enhances towards using microsimulation is available in: <http://model.planningbythenumbers.org/>
- 2) The Reference Model for disease progression: In this case populations are generated from distributions. MIST uses evolutionary computation by INSPYRED to match the distribution statistics to given objectives. This allows coping with inclusion/exclusion criteria of clinical trials skewing distributions. The Reference Model uses those populations as input and calculates fitness of different models to those populations. Differences in model fitness are studies when generating the populations with and without evolutionary computation towards objectives. MIST capability of using evolutionary computation is joint work with INSPYRED creator Aaron Garrett from Jacksonville State University: <http://mcis.jsu.edu/faculty/agarrett/>

MIST Runs Over the Cloud!

The Reference Model for Disease Progression



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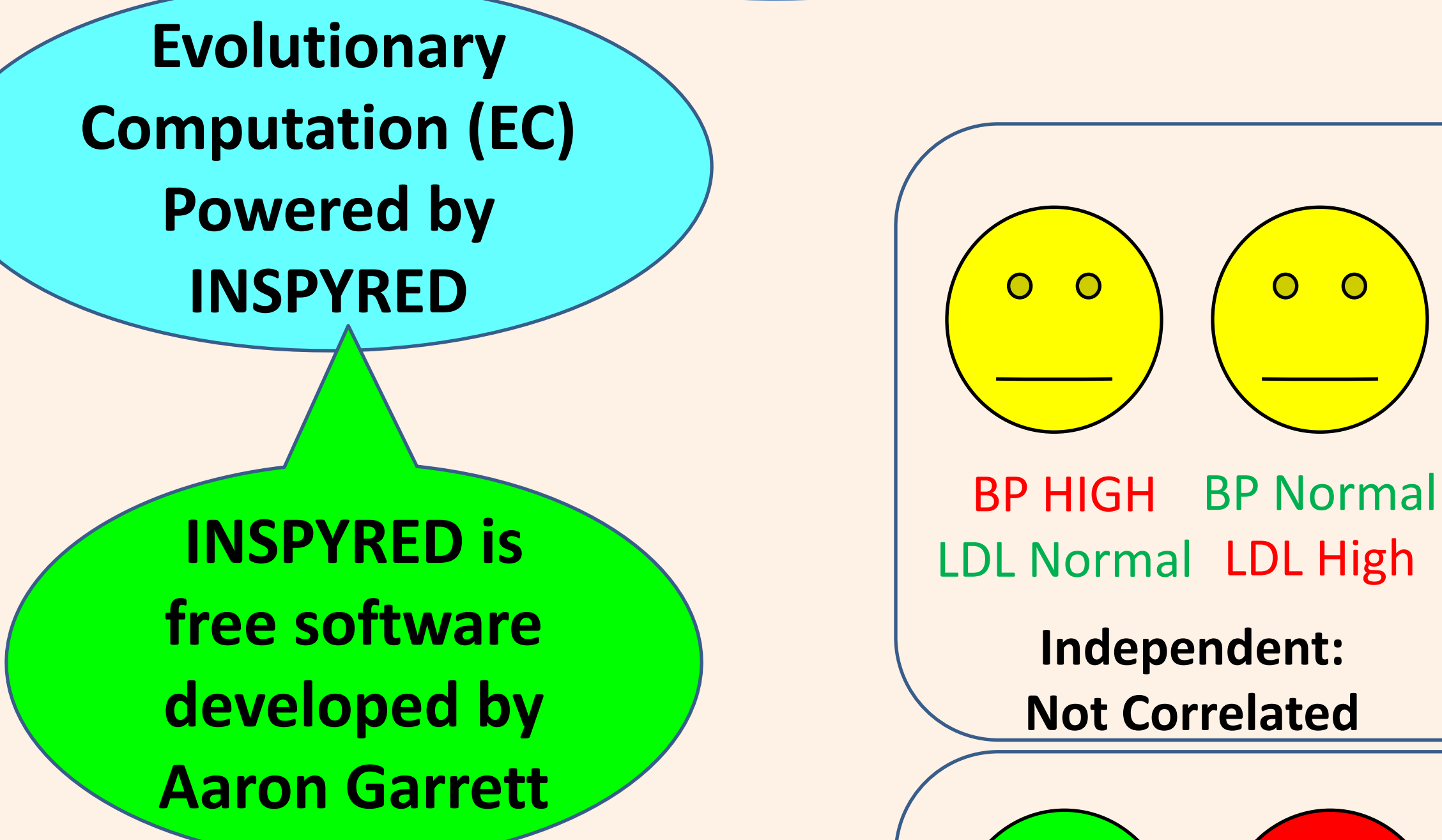


References:

- [1] J. Barhak, The Reference Model for Disease Progression uses MIST to find data fitness. PData Silicon Valley 2014 held at Facebook Headquarters. Presentation: http://sites.google.com/site/jacobbarhak/home/PData_SV_2014_Upload_2014_05_02.pptx Video: <https://www.youtube.com/watch?v=vvxllc5vA>
- [2] J. Barhak, A. Garrett, Population Generation from Statistics Using Genetic Algorithms with MIST + INSPYRED. MODSIM World 2014, April 15 - 17, Hampton Roads Convention Center in Hampton, VA. Paper: http://sites.google.com/site/jacobbarhak/home/MODSIM2014_MIST_INSPYRED_Paper_Submit_2014_03_10.pdf Presentation: http://sites.google.com/site/jacobbarhak/home/MODSIM_World_2014_Submit_2014_04_11.pptx
- [3] J. Barhak, H.S. Leff, Modeling a Chronic Disease Model and a Mental Health Model Using the Same Modeling Tools, MODSIM World 2013, April 30 - May 2nd, Hampton Roads Convention Center in Hampton, VA. Paper: http://sites.google.com/site/jacobbarhak/home/MODSIM_World2013_Submitted_04Apr2013.pdf Presentation: http://sites.google.com/site/jacobbarhak/home/MODSIM_World_Presented_2013_05_2.pptx

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Populations Generated Without Evolutionary Computation

| Model | BP | LDL |
|---------|--------|--------|
| Model_1 | High | Normal |
| Model_2 | High | High |
| Model_3 | Normal | Normal |
| Model_4 | Normal | High |
| Model_5 | High | High |

Populations Generated With Evolutionary Computation

| Model | BP | LDL |
|---------|--------|--------|
| Model_1 | Normal | Normal |
| Model_2 | Normal | Normal |
| Model_3 | Normal | Normal |
| Model_4 | Normal | Normal |
| Model_5 | Normal | Normal |

Fitness Difference = With - Without Evolutionary Computation

| Model | Fitness Difference |
|---------|--------------------|
| Model_1 | 0.00 |
| Model_2 | 0.00 |
| Model_3 | 0.00 |
| Model_4 | 0.00 |
| Model_5 | 0.00 |

Independent: Not Correlated

| Model | BP | LDL |
|---------|--------|--------|
| Model_1 | High | Normal |
| Model_2 | High | High |
| Model_3 | Normal | Normal |
| Model_4 | Normal | High |
| Model_5 | High | High |

Dependent: Perfect Correlation

| Model | BP | LDL |
|---------|--------|--------|
| Model_1 | Normal | Normal |
| Model_2 | Normal | Normal |
| Model_3 | Normal | Normal |
| Model_4 | Normal | Normal |
| Model_5 | Normal | Normal |

The Fitness Matrix is like a score board of a league of disease models

Rows = Populations
Columns = Models

Reproducibility Info: Version 26_MIST_RefModel_2014_05_23_BEST_REPEAT_Trackback.zip

Better Fitness to Known Results

Worst Fitness to Known Results

Best Model