ClinicalTrials.Gov is an NIH project that accumulates clinical trial data

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In a Nutshell: The Reference Model, that accumulates other models and validates them against observed outcomes, can now import data from ClinicalTrials.Gov

models and validates m ClinicalTrials.Gov

Abstract:

The Reference Model for Disease Progression allows merging information from multiple existing disease models and from observed results from clinical trials. This is a powerful way of accumulating clinical knowledge, both cognitive knowledge embedded within computational models, and evidence based knowledge provided by clinical studies. The Reference Model development started half a decade ago and accumulated observed data published in clinical trial reports such as baseline demographics and outcomes. However, entry of such data was tedious and prone to errors since it involved copying printed data manually and transferring it into programmatic modeling code.

Detached from this project, the NIH started accumulating clinical trial data in the last few years in the ClinicalTrials.Gov web site. The web site provides a registry for clinical trials. Recently, the registry was adapted to hold clinical trial results that contain essential information for modeling. The registry web site was designed to be easy to interface with, and it can export data using XML scheme – a widely used data transfer format.

The Reference Model can now interface with ClinicalTrials.Gov allowing it to convert the registered knowledge into modeling code. The work will describe the basics of this interface that will allow the model to accumulate more clinical information in the future to better understand disease progression.

This work builds upon a decade of development with key publications in the following list:

[1] J. Barhak, The Reference Model for Disease Progression uses MIST to find data fitness. PyData Silicon Valley 2014 held at Facebook Headquarters:

Presentation: http://sites.google.com/site/jacobbarhak/home/PyData_SV_2014_Upload_2014_05_02.pptx
Video: https://www.youtube.com/watch?v=vyvxiljc5vA

- [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/iasehbarbak/home/MODSIM2014, MIST, INSPYRED, Paper Submit, 2014, 02, 10 pdf
- Paper: http://sites.google.com/site/jacobbarhak/home/MODSIM 2014 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, Object Oriented Population Generation, MODSIM world 2015. 31 Mar 2 Apr, Virginia Beach Convention Center, Virginia Beach, VA.

 Paper: http://modsimworld.org/papers/2015/Object Oriented Population Generation.pdf

 Presentation: http://sites.google.com/site/jacobbarhak/home/MODSIM2015 Submit Jacob Barhak 2015 03 29.pptx
- [4] J. Barhak, The Reference Model for Disease Progression Combines Disease Models. I/IITSEC 2016 28 Nov 2 Dec Orlando Florida.

 Paper: http://www.iitsecdocs.com/volumes/2016

 Presentation: http://sites.google.com/site/jacobbarhak/home/IITSEC2016 Upload 2016 11 05.pptx

What is novel?

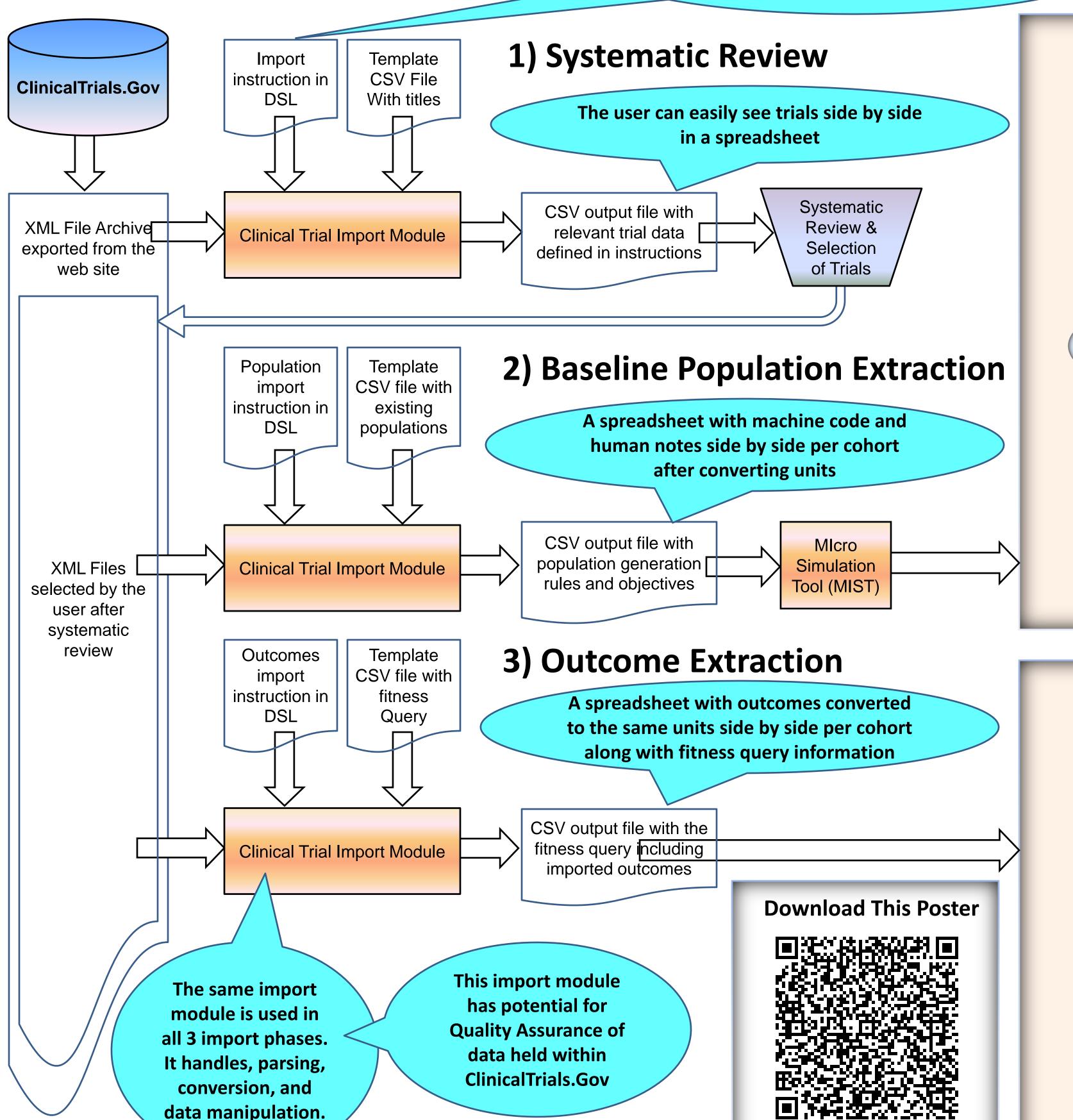
Clinical Trials from all around the world. On 12-Feb-2017 there were 236,687 trials registered in this database where 24,251 reported results. This database keeps on growing. The Reference Model new interface with this database provides an essential modeling capability that is traceable and reproducible.

Key Points

- Ensemble model
- Accumulates knowledge from:
 - Existing models
 - Observed outcomes
- Modeling at the population level
- Simulation at the individual level
- Focuses on summary data
 - Avoids individual data restrictions
 - Larger merged population base
- Flexible Import from ClinicalTrials.Gov
- Applicable for other disease processes
- Traceable and reproducible

3 Phases of Import

DSL = Domain Specific Language that is dedicated to extract data from ClinicalTrials.Gov



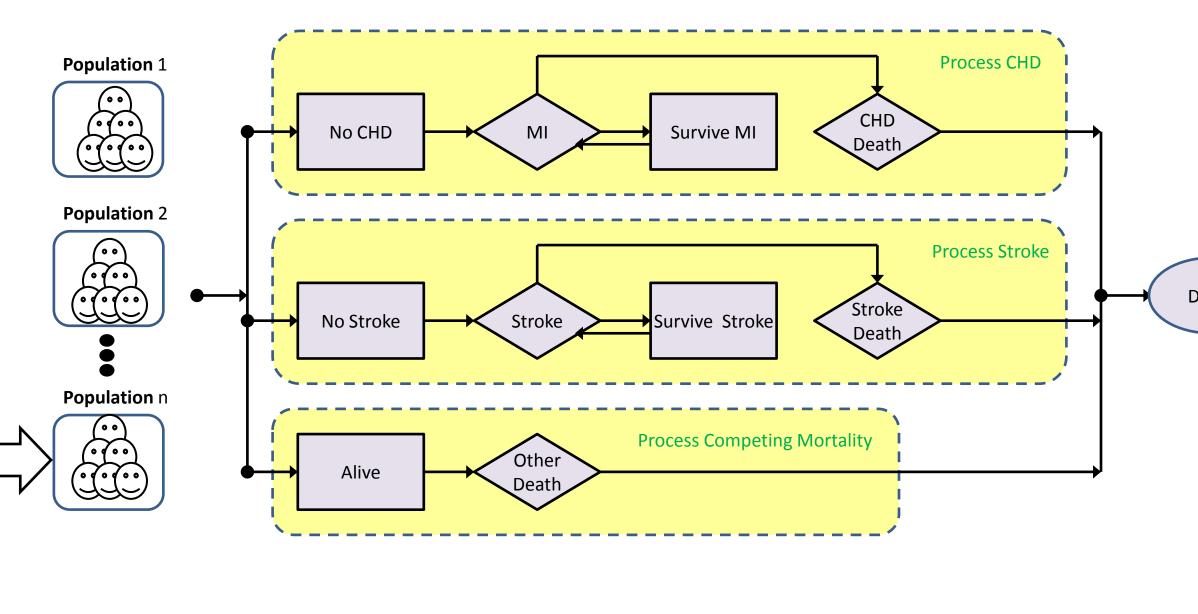
Population Generation Approach Generation Expressions: Define how to generate a single individual Test if individual fits the inclusion/exclusion criteria Define ties and correlations between characteristics INSPYRED = **Bio Inspired Computation MIST = MIcro Simulation Tool** by Aaron Garrett by Jacob Barhak Monte **Evolutionary Expression** Result Selection Computation Objectives: Define aggregate targets for the entire population **Population** Converges to Reduce random generation error Objectives Handle skewed distributions to fit target

Validation & Optimization Using an Assumption Engine

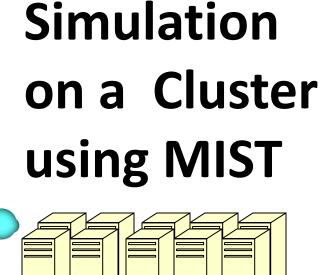
- The Assumption Engine allows us to "throw" assumptions at it
 - A model is an assumption!
- The Assumption engine figures out which assumptions work well together to fit observed outcomes data
 - Points to significant modelsRejects incompatible models
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- Optimizes components in parallel using Gradient Descent
 - Components can cooperate
 - Components can compete = multiple initial guesses
- Define constraints such as:
 - Equations contribute partial information
 - Non negative contribution

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The Reference Model



MIST Runs
Over the Cloud!



Final result:

- 1. The model mixture that best fits:
 - The outcomes
 - The query
 - Modeling assumption
- 2. The fitness/error of each cohort

Acknowledgments:

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