

**Public Response Letter to the Authors of:**  
**Modeling good research practices: a report of the ISPOR-SMDM**  
**Modeling Good Research Practices Task Force**

17 April 2013

Jacob Barhak  
Unaffiliated  
Austin, Texas  
Jacob.barhak@gmail.com  
<http://sites.google.com/site/jacobbarhak/>

H. Stephen Leff  
Harvard Medical School  
Cambridge, Massachusetts  
sleff@hsri.org  
<http://www.hsri.org/about/leadership/>

Respected modeling task force committee members,

The seven part manuscript [1-7] contains important guidelines for modeling. The guidelines are quite extensive and well summarized in the first part. Nevertheless, some important issues, especially ones related to the way new computing technologies can be used to aid disease modeling, receive no direct reference or limited attention. We have decided to write about these issues to raise awareness of the modeling community to these issues.

Here are relevant points:

**USE OF COMPUTING POWER FOR MODELING:**

There has been an exponential increase in computing power predicted by Moore's law [8] that still continues. This increase in computing power is characterized by more computing cores in a computer and overall cheaper computing power and memory. This leads to affordability of computer clusters and cloud computing. This allows affordable access to more computing units for modelers, and is particularly suitable for embarrassingly parallel solutions such as Micro-simulation. Even other modeling techniques such as Markov Models that are not complicated to program can benefit from the increased computing power trying many more scenarios in parallel leading to much more extensive sensitivity analysis. The use of computing power was briefly addressed in the Quandaries in the first paper [1], yet it belongs in the guidelines since this new computing power makes it possible to use free software tools with Graphic User Interfaces that can support such simulations [9-11]. This technology is now accessible and therefore the use of more advanced tools should no longer be a "quandary," instead there should be specific guidelines for use of such technology in modeling.

**COMPETING AND INTERACTING DISEASE PROCESSES:**

Disease processes compete and interact. The Discrete Event Simulation (DES) paper [4] and the State Transition paper [2] have touched these points. Nevertheless, the discussion should be expanded further since the interaction among different disease processes impacts more than mortality. For example mental health has an effect on physical Health and vice versa. Mental health services without physical health services can lead to early mortality. Physical health services without mental health services can frustrate early intervention and lead to lack of adherence to medical regimens [12,13,14]. It is important to model the interactions of these two types of disease and care to better plan and manage services.

While DES systems are well suited to handle competition and interaction between events from parallel disease processes, there are ways today to model parallel state transition processes in a synchronous way [9]. These methods can reduce the number of states and helps prevent the state explosion phenomenon. Beyond interaction between disease processes, competition among models is a method that should be encouraged for modeling as it is done in the Mount Hood challenge [15] by employing human ingenuity or in a systematic computerized way as demonstrated in [10-11].

### MODEL VERSIONING:

This is an important topic that was not explicit in the published guidelines. Assigning a version to any software and improving it in subsequent versions are essential elements in software development and easier given the use of web-implemented models. Model versioning is important because the modeling process is also an exploration process. With each model version the aim is to better explain observed phenomena. New observations may falsify an older version and expose its limitations requiring a new version that incorporates corrections and enhancements [16]. Versioning is also important from a documentation point of view to keep record of what elements have been introduced and to support traceability back to original data. It is possible to practice versioning without special tools. However, newer version control tools help streamline the work process and online tools open the door to collaborative modeling. Model developers should be encouraged to use similar version control tools, to further collaborative sharing of knowledge that may improve our understanding.

### SYMBOLIC MATH TOOLS:

These tools allow manipulating equations the way humans do on paper while automating operations using computing power. This is highly useful in disease modeling. For example, an entire Markov chain for several time steps can be represented using polynomial representation.

The code below describes a two state Markov chain implemented using freely available tools python [17] and sympy [18]:

```
>>> import sympy          # use the sympy library after it was installed
>>> p12 = sympy.Symbol('p12') # define the symbol p12
>>> p21 = sympy.Symbol('p21') # define the symbol p21
>>> P = sympy.matrices.Matrix([[1-p12, p12], [p21, 1-p21]]) # make Markov
matrix
>>> P # Show Markov matrix
[-p12 + 1,      p12]
[      p21, -p21 + 1]
```

Now the probability of reaching state 2 from state 1 after 4 steps can be calculated by:

```
>>> P_4steps = P*P*P*P # multiply the Markov matrix 4 times
>>> P_4steps[0,1]      # Extract the 1,2 element in the 4 year matrix
p12*(p21*(p12*(-p12 + 1) + p12*(-p21 + 1)) + (-p12 + 1)*(p12*p21 + (-p12 +
1)**2)) + (-p21 + 1)*(p12*(p12*p21 + (-p12 + 1)**2) + (-p21 + 1)*(p12*(-p12 +
1) + p12*(-p21 + 1)))
```

This formula can now be derived, substituted with values, and otherwise manipulated automatically. This opens new opportunities for modelers for estimation [19,20], and can be useful in sensitivity analysis. With contemporary computing power a model can be represented as a function using exact mathematical formulation. The exact formulation reduces the uncertainty associated with modeling since functional analysis can now be used to replace stochastic tools.

## SUMMARY

The technology to support the above topics has matured and there are freely available tools to support it as well as vibrant user communities for exchange of ideas and mutual support. Neglecting such topics in guidelines misses the opportunity of supporting further technological development. Disease modeling is still an emerging field in the sense that there is a lot to explore and explain. The above tools and methodologies should be added to the arsenal of disease modeling tools to help cope with future challenges.

We are in hope that the modeling task force will find these comments helpful and use them to supplement their recommendations.

## REFERENCES:

- [1] J. Jaime Caro, Andrew H. Briggs, Uwe Siebert, Karen M. Kuntz, ISPOR-SMDM Modeling Good Research Practices Task Force. Modeling Good Research Practices—Overview: A Report of the ISPOR-SMDM Modeling Good Research Practices Task Force-1. *Value in Health* - September 2012 (Vol. 15, Issue 6, Pages 796-803, DOI: 10.1016/j.jval.2012.06.012)
- [2] Roberts M , Russel L , Paltiel AD , et al. Conceptualizing a model: a report of the ISPOR-SMDM modeling good research practices task force-2 . *Value in Health* - September 2012 (Vol. 15, Issue 6, Pages 804-811, DOI: 10.1016/j.jval.2012.06.016)
- [3] Siebert U , Alagoz O , Bayoumi AM , et al. State-transition modeling: a report of the ISPOR-SMDM modeling good research practices task force-3 . *Value in Health* - September 2012 (Vol. 15, Issue 6, Pages 812-820, DOI: 10.1016/j.jval.2012.06.014)
- [4] Karnon J , Stahl J , Brennan A , et al. Modeling using discrete event simulation: a report of the ISPOR-SMDM modeling good research practices task force-4 . *Value in Health* - September 2012 (Vol. 15, Issue 6, Pages 821-827, DOI: 10.1016/j.jval.2012.04.013)
- [5] Pitman R , Fisman D , Zaric GS , et al. Dynamic transmission modeling: a report of the ISPOR-SMDM modeling good research practices task force-5 . *Value in Health* - September 2012 (Vol. 15, Issue 6, Pages 828-834, DOI: 10.1016/j.jval.2012.06.011)
- [6] Briggs AH , Weinstein MC , Fenwick E , et al. Model parameter estimation and uncertainty: a report of the ISPOR-SMDM modeling good research practices task force-6 . *Value in Health* - September 2012 (Vol. 15, Issue 6, Pages 835-842, DOI: 10.1016/j.jval.2012.04.014)
- [7] Eddy DM , Hollingworth W , Caro JJ , et al. Model transparency and validation: a report of the ISPOR-SMDM modeling good research practices task force-7 . *Value in Health* - September 2012 (Vol. 15, Issue 6, Pages 843-850, DOI: 10.1016/j.jval.2012.04.012)
- [8] G. E. Moore, Cramming more components onto integrated circuits. *Electronics*, 1965, 38(8).
- [9] J. Barhak J., D.J.M. Isaman, W. Ye, D. Lee: Chronic disease modeling and simulation software. *Journal of Biomedical Informatics*, Volume 43, Issue 5, October 2010, Pages 791-799, DOI: [10.1016/j.jbi.2010.06.003](https://doi.org/10.1016/j.jbi.2010.06.003)
- [10] J. Barhak, The Reference Model for Disease Progression. SciPy 2012, Austin Tx, 18-19 July 2012. Paper: [https://github.com/Jacob-Barhak/scipy\\_proceedings/blob/2012/papers/Jacob\\_Barhak/TheReferenceModelSciPy2012.rst](https://github.com/Jacob-Barhak/scipy_proceedings/blob/2012/papers/Jacob_Barhak/TheReferenceModelSciPy2012.rst) , Poster: [http://sites.google.com/site/jacobbarhak/home/PosterTheReferenceModel\\_SciPy2012\\_Submit\\_2012\\_07\\_14.pdf](http://sites.google.com/site/jacobbarhak/home/PosterTheReferenceModel_SciPy2012_Submit_2012_07_14.pdf)
- [11] J. Barhak, The Reference Model for Chronic Disease Progression. 2012 Multiscale Modeling (MSM) Consortium Meeting, October 22-23, 2012, Abstract:

[http://www.imagwiki.nibib.nih.gov/mediawiki/images/7/77/Reference\\_Model\\_for\\_Chronic\\_Disease\\_Progression\\_Barhak.pdf](http://www.imagwiki.nibib.nih.gov/mediawiki/images/7/77/Reference_Model_for_Chronic_Disease_Progression_Barhak.pdf) . Poster:  
[http://www.imagwiki.nibib.nih.gov/mediawiki/images/c/c4/PosterTheReferenceModel\\_IMAGE\\_MSM\\_Submit\\_2012\\_10\\_17.pdf](http://www.imagwiki.nibib.nih.gov/mediawiki/images/c/c4/PosterTheReferenceModel_IMAGE_MSM_Submit_2012_10_17.pdf)

- [12] Richard A. LaBrie, Debi A. LaPlante, Allyson J. Peller, Donald E. Christensen, Kristina L. Greenwood, John H. Straus, Michael S. Garmon, Cheryl Browne, Howard J. Shaffer, (2007). "The interdependence of behavioral and somatic health: implications for conceptualizing health and measuring treatment outcomes." *Int J Integr Care* 7: e10.
- [13] J. Unutzer, M. Schoenbaum, B.G. [Druss](#), W.J. [Katon](#) (2006). "Transforming Mental Health Care at the Interface With General Medicine: Report for the Presidents Commission." *Psychiatr Serv* 57(1): 37-47.
- [14] B. G. Druss, B. J. Mauer (2010). "Health care reform and care at the behavioral health - Primary care interface." *Psychiatric Services* 61(11): 1087-1092.
- [15] Mount Hood Challenge. Online: <http://sites.google.com/site/mounthoodchallenge/> (accessed 31-Jan-2013)
- [16] C Anthony Hunt, Glen EP Ropella, Tai ning Lam, Andrew D Gewitz, Relational grounding facilitates development of scientifically useful multiscale models. PMCID: PMC3200146. *Theor Biol Med Model.* 2011; 8: 35. Published online 2011 September 27. DOI:[10.1186/1742-4682-8-35](https://doi.org/10.1186/1742-4682-8-35)
- [17] Python Programming Language – Official Website. Online: <http://www.python.org/> (accessed 31-Jan-2013)
- [18] SymPy. Online: <http://sympy.org/> (accessed 31-Jan-2013)
- [19] W. Ye., J. Barhak, D.J.M. Isaman, Use of Secondary Data to Estimate Instantaneous Model Parameters of Diabetic Heart Disease: Lemonade Method. *Information Fusion* Volume 13, Issue 2, April 2012, Pages 137-145, <http://dx.doi.org/10.1016/j.inffus.2010.08.003>
- [20] D.J.M. Isaman, J. Barhak, W. Ye: Indirect Estimation of a Discrete-State Discrete-time model using Secondary Data Analysis of Regression Data. *Statistics in Medicine* Volume 28, Number 16, Pages 2095 - 2115, 2009. <http://dx.doi.org/10.1002/sim.3599>