**2018 IMAG Futures Meeting – Moving Forward with the MSM Consortium (March 21-22, 2018)**

*Pre-Meeting Abstract Submission Form*

*\*Please submit to the NIBIB IMAG mailbox (*NIBIBimag@mail.nih.gov*) by* ***January 8th, 2018***

*\*Save your abstract as “MSM PI Last Name \_ 2018 IMAG Futures Pre-Meeting Abstract”*

**PI(s) of MSM U01: David Kaplan, Markus Buehler**

**Institution(s): Tufts University and MIT**

**MSM U01 Grant Number: U01EB014976**

**Title of Grant:** Models to predict protein biomaterials performance

**Abstract**

Which MSM challenges are you addressing from the IMAG 2009 Report and how?

<https://www.imagwiki.nibib.nih.gov/content/2009-imag-futures-report-challenges>

(indicate which challenge (#) you’re addressing)

*You may insert images by copying and pasting below*

1) Next-generation multiscale models that integrate between different scientific fields (e.g. cardiovascular and neuroscience) and predict integrated functions – Our studies focus on the multi-scale design and modeling of protein polymers as biomaterial systems, including aspects of mechanics, mineralization, dynamic shape change, and related themes. These features relate polymer design to topics of degradability in vivo, mineralization in vivo and the filling of soft tissue defects.

5) Reproducible and reusable multiscale models that will be integrated and adopted into model-poor fields (e.g.  tissue engineering, regenerative medicine, drug and gene delivery, preventive interventions) – Our studies address the need for hierarchically-based models related to protein biomaterial designs, to meet the needs in the fields of tissue engineering, regenerative medicine and drug delivery. This includes proactive biomaterials with biological signaling (e.g., stem cell differentiation related to osteogenesis) and inhibition of mineralization related to tissues where mineralization is to be avoided due to mechanical needs.

6) Multiscale models strongly coupled with standardized protocols for model-driven data collection – Our multiscale models focus on both validation and prediction of new material behaviors, which then enables model-driven data collection. The integrated modeling-synthesis-characterization paradigm enables us to expand the reach of modeling and experiment in system design.

9) Model predictions that drive a community of experimentalists towards systematic testing and validation – Our models and experimental approaches are being widely disseminated via the consortium web site, as well as via published protocols, publications, and on line venues to try and excite and drive the field toward these needs, their use, and their continued improvement.

Are you using machine learning and or causal inference methods and how?

*You may insert images by copying and pasting below*

 We use machine learning to study protein folding. We develop amino acid text embedding and generating systems to design, build, and test proteins. Based on coherent analogy and similarity between natural language processing techniques and protein structure analysis we aim to establish a mapping table of terminologies to connect these two fields. Public datasets of known material structures, UniProt and RCSB PDB databanks, serve as “text corpuses” to develop machine learning embedding systems that can learn a continuous vector representation of amino acid sequences and preserve biological relational meaning among them, which is similar to the role of the “word2vec” embedding in Neuro Linguistic Programming (NLP).

Please briefly describe significant MSM achievements made (or expected).

*You may insert images by copying and pasting below*

 We have developed new fundamental strategies to integrate experimental and modeling approaches to address the challenges in biomaterial designs, including specific insights into the role of molecular weight, the impact of domain sizes and distributions within the polymer chains, the impact of hydrophobic/hydrophilic partitioning with the protein domains, and the role of charged termini in terms of how they impact protein polymer assembly and the resulting mechanical properties of the biomaterials that are formed. We have been able to utilize these approaches to bioengineer protein-based biomaterials (e.g., collagens, silks, elastins) with specific goals, including: To predict in vivo degradation of protein-biomaterials based on in vitro models (e.g., silk biomaterials); To predict dynamic material behavior based on specific environmental stimuli (e.g., thermal); To optimize biomaterial interfaces with respect to control (positive or negative) of mineralization; To predict the impact of mutations in collagen chains related to disease state (e.g., *Osteogenesis imperfecta*)

Please suggest any new MSM challenges that should be addressed by the MSM Consortium moving forward.

*You may insert images by copying and pasting below*

 Increased focus on process simulation/manufacturing.

What expertise are on your team (e.g. engineering, math, statistics, computer science, clinical, industry) and who?

*Please list as “Expertise – Name, email”*

Modeling – Markus Buehler (mbuehler@mit.edu) Protein Bioengineering – David Kaplan (david.kaplan@tufts.edu)

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