

White Paper #4: Reporting Finite Element Analysis Studies of Biological Structures

Ahmet Erdemir

Computational Biomodeling Core
Department of Biomedical Engineering
Lerner Research Institute
Cleveland Clinic

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Virtual Discussion

IMAG - MSM 2010

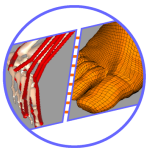
CREDITS

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Trent Guess
Jason Halloran
Srinivas Tadepalli
Ganesh Thiagarajan

Working Group 6 members
Working Group 10 members

IMAG members
Biomechanics community



Efficient Methods for Multi-Domain Biomechanical Simulations
R01EB006735



Predicting Cell Deformation from Body Level Mechanical Loads
R01EB009643



Online Access

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Online editable version of the white paper

http://www.imagwiki.org/mediawiki/index.php?title=Reporting_in_FEA

Discussion on the white paper

http://www.imagwiki.org/mediawiki/index.php?title=Talk:Reporting_in_FEA

Definitions: Model

The term model in this white paper refers to a **computational model**.

Computational representation of the biological structure for finite element analysis:

- discretized geometric representation
- constitutive relationships of substructures
- interactions between substructures
- loading and boundary conditions

The computational model relies on the

mathematical model – principles of solid mechanics

biological model – deformation of biological structures

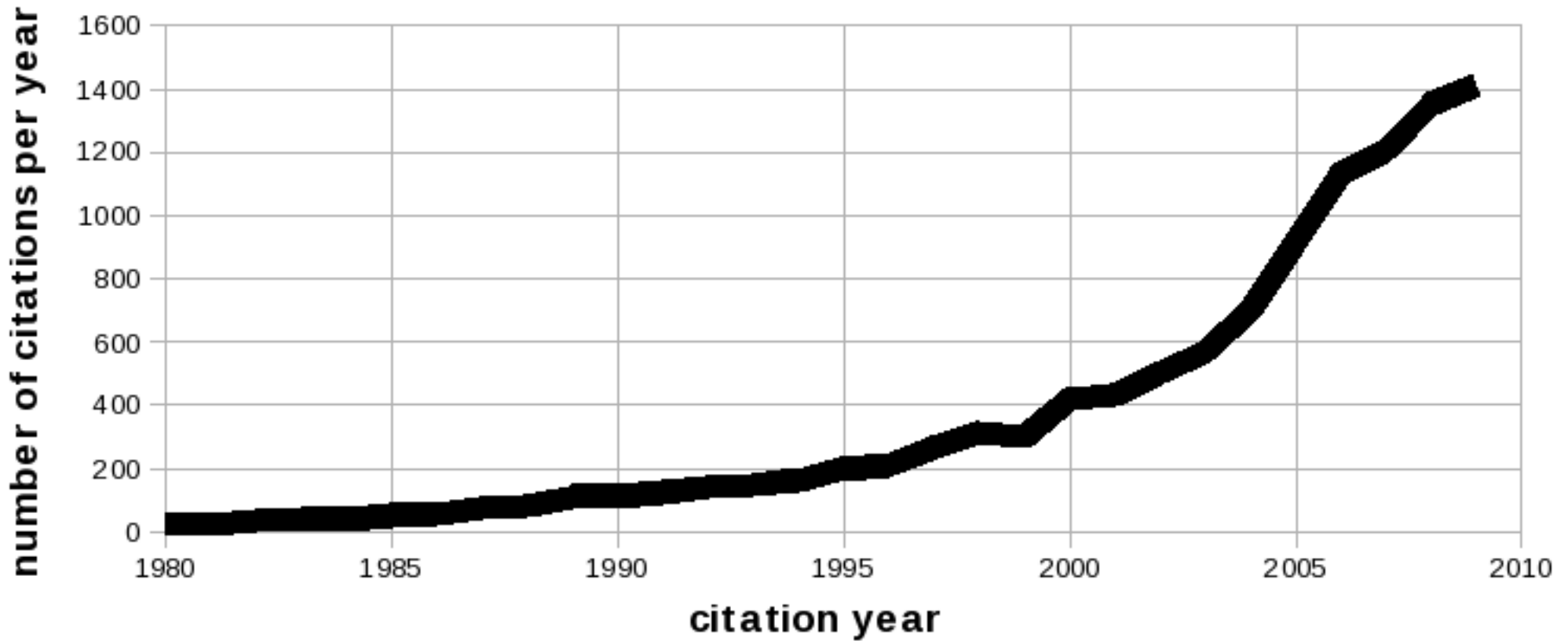
Definitions: Multiscale

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The term multiscale in this white paper refers to **interactions between higher spatial scales** of the physiome:

joint/organ biomechanics – tissue mechanics
tissue mechanics – cell biomechanics

FEA in Medicine



Search conducted on Pubmed (<http://www.pubmed.org>) with the search string "finite element".

Why Recommendations for Reporting?

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Good reporting practice:

clarifies uncertainty of **reproducibility**
promotes **reusability**
establishes **accountability**

---> **CONFIDENCE IN MODELING & SIMULATION**

Adequate reporting procedures has the potential to **delineate model and simulation process.**

PATHWAY TO SHARING AND STANDARDS

Why Recommendations for Reporting?

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Advances in complex model development and simulation **software** facilitates modeling and simulation but

Modeler's decision making process is usually **opaque**
Modeler is sometimes **uninformed**
Reader/user/reviewer is mostly **uninformed**

Codes & standards for verification & validation
are helpful but they

do not address communication
are not easy to follow

NEED FOR A CHECKLIST TO BE UTILIZED NOW

Why Recommendations for FEA?

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Common tool for simulation of models representative of body/organ/tissue/cell scales

Unfortunately, **models are tightly coupled** to the method of **simulation**

- mathematical models embedded in FEA software

- FEA software specifically designed for biological phenomena

- models sometimes accommodate solver capabilities

- too many simulation software -> too many mark-up languages

Current standards are not readily applicable to complex biomechanical models, need a solution

- to use now

- to inform future

Why Initial Focus on Single Scale?

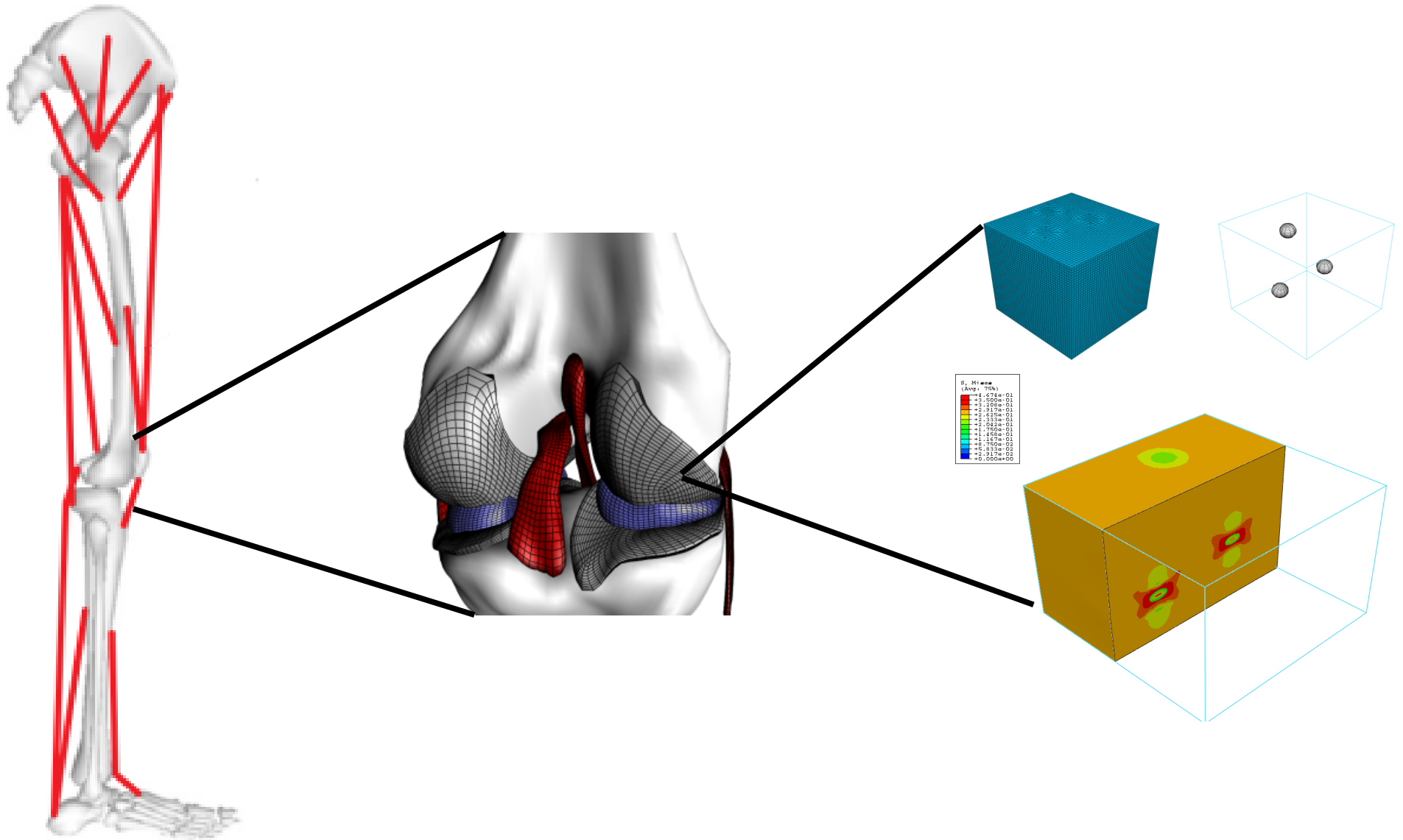
Models of a single spatial scale were and potentially will be used for

- decision making
- surgical simulation
- intervention design
- regulatory practice

Models of a single spatial scale will likely be

- reused in multiscale simulations
- dictate response at higher spatial scales

Relevance to Multiscale Analysis

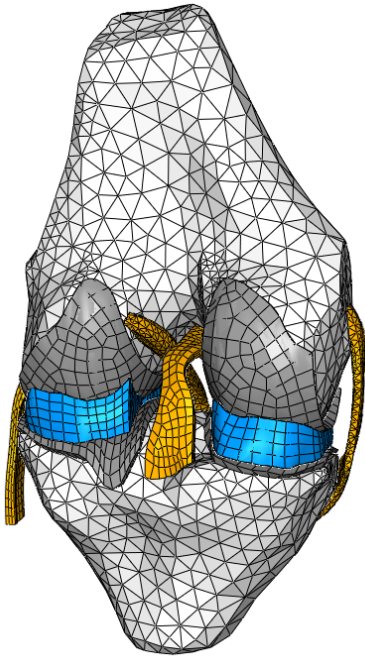


For cell scale to macro scale integration refer to MSM 2010 – White Paper #2 by Lin et al.

Relevance to Modular Modeling

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Joint Scale

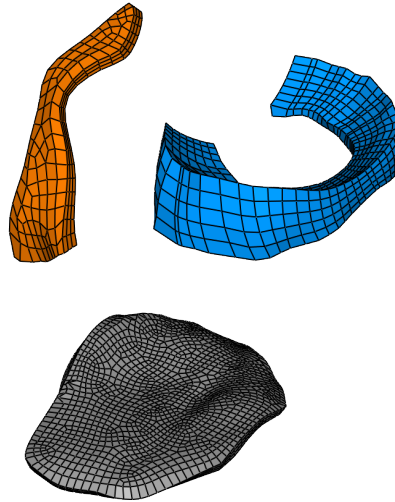


Input/Output:
kinematics/kinetics

Properties:
tissue organization

Module to:
musculoskeletal models

Tissue Scale

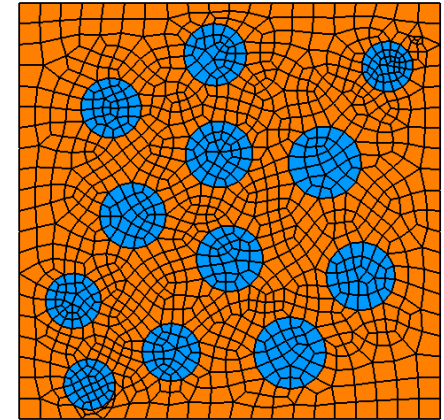


Input/Output:
loading & BCs (attachment)
tissue deformation

Properties:
constitutive relation

Module to:
joint models

Cell Scale



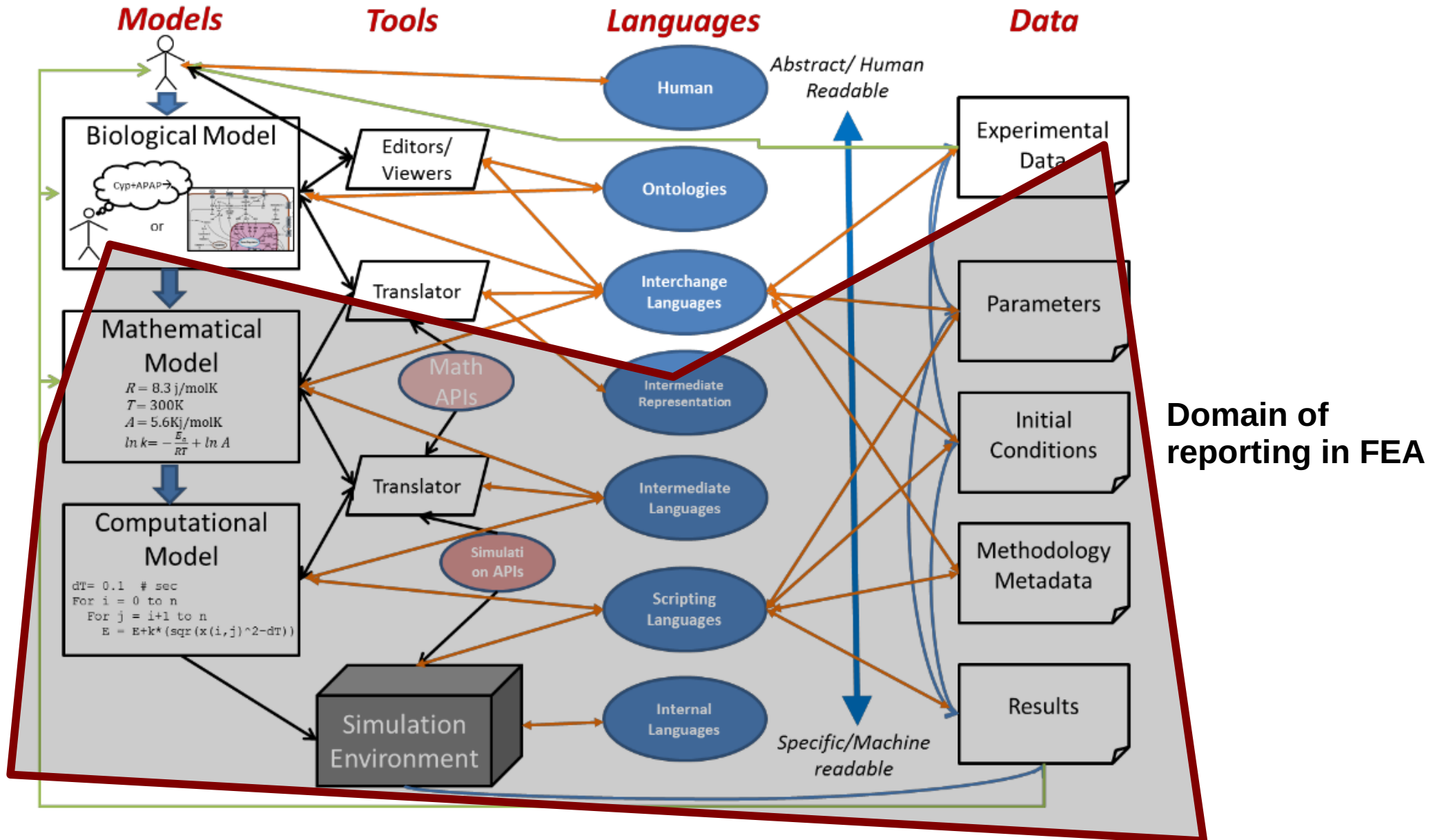
Input/Output:
constitutive relation
microstructural deformation

Properties:
microstructural organization

Module to:
tissue models

For modular modeling refer to MSM 2010 – White Paper #3 by Bassingthwaighte et al.

Relevance to Model Abstraction



For levels of model abstraction refer to MSM 2010 – White Paper #1 by Glazier et al.

Relevance to Mark-Up Languages

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Identify information to incorporate as metadata for storage of models and simulation results

Generate specifics for mark-up languages to extract key model information (automated-reporting)

Clarify model exchange parameters to translate between open mark-up languages and commercial ones used by proprietary simulation software

Implementation

For a model to be useful

the model itself does not need to be complete

the **reporting** of the model should be

complete
explicit

Adaptations of **standards for model sharing and unified simulations** should be a **long term goal** but it may not be practical

Adaptation of **reporting standards** can be implemented **at this moment** and facilitate transition to higher level modeling standards

A Spin-Off from Standards Proposal

Checklist of model standards

CHECKLIST FOR MODEL AGAINST DESIRED STANDARDS: CHECK X FOR THOSE MET			
Check YES (either manual or auto if standard met)	YES		
model author = checked by author; checked within model code by math?	model author	checked in code?	Problem? Limit? Other?.
Group 1: Identification and Description			
1. Model Name, Key words (generic and specific)			
2. Brief one or two line description			
3. Detailed description, diagrams, equations			
4. Reference to Publication describing the model			
5. Pointer to the publication or pdf			
6. Related Models, antecedents, comparables, and successors			
Group 2. Model Structure and Content			
1. Domain definition (cells, mito, tissues, organ system, organism)			
2. Main variables (chemicals, pressures, etc.), with units			
3. Parameters, with units, and with source references			
4. Descriptions and references for subsidiary models			
5. Source Code: Clear, deeply commented, explained, referenced.			
6. Inputs and outputs defined. All nodes and edges defined.			
7. Define linkage type (Chemical, electrical, mechanical, etc.)			
8. Ontology base for notation			
9. Numerical solvers used, and conditions set			
Group 3. Verification: math of model and solution methods are sound			
1. Unitary Balance: (units on all variables and parameters)			
2. Mass balance: (list constituents whose conservation is checked)			
3. Charge balance: (ion currents, membrane potential)			
4. Osmotic balance: (volume, total activities, fluxes)			
5. Thermodynamic Balance (Haldane constraints on reactions)			
6. All equations correct, units balance, with all terms defined			
7. Numerical solutions checked against analytical solutions			
8. Running code supplied in a common format			
9. Solutions show little dependence on time or space step size			
10. Methods for verification defined. Reference model solution?			
Group 4. Validation: model is physiologically realistic			
1. Initial and boundary conditions in accord with physiology			
2. Data provided, and fitted by model			
3. Model is predictive, shown to fit other data not used as basis			
4. Parameters justified (sources provided) and evaluated			
Group 5: Availability of Source Code and Forum for critiques			
1. Website source from which to download model code and data			
2. Website or email or address to accept queries			
3. Website for public commentary and responses			
4. References to subsequent publications or alternative models			

Revised 12sep09 by JBBassingthwaighte

Working Group 10

Standards for Modeling

Targeted at biophysical/biochemical models

Customized for complex biomechanical models simulated using finite element analysis

Customized for model reporting rather than model development

Single Scale

Identification & Description

Model name, keywords (generic and specific)

Version

Simulation software

Brief description

Summary of utility

Summary of highlights

Summary of limitations

Reference to publication

Pointer to publication

Related models

Single Scale

Model Structure & Content

Physics and domains

Assumptions

Loading and boundary conditions

Primary output variables

Secondary output variables

Reference configuration

Components (subsidiary models)

- Geometry

- Mesh

- Constitutive relationships

Interactions

- Interacting components

- Interaction properties

Solution strategy

Simulation settings

Single Scale

Verification

Methods of verification

Correctness of formulation

Comparisons with analytical solutions

Sensitivity to simulation settings

Mesh convergence

Assessment of repeatability

Single Scale

Validation

Physiological relevance of loading and BCs

Justification of parameters

Data used for model development

Data used for model comparison

Validation procedures (direct, indirect)

Sensitivity analysis

Predictive capacity

Single Scale

Availability

Website for downloads

Website (or contact) for queries

Website for public commentary, responses, and rating

Licensing

Follow-up

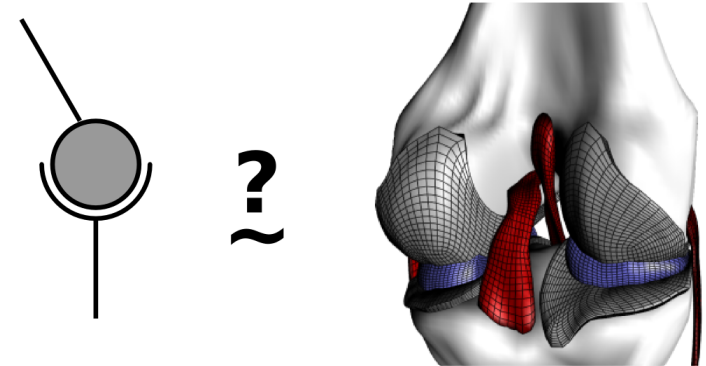
Multiscale Issues

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Mechanical Consistency

Post-processing problem

Equivalence between higher and lower scale representations

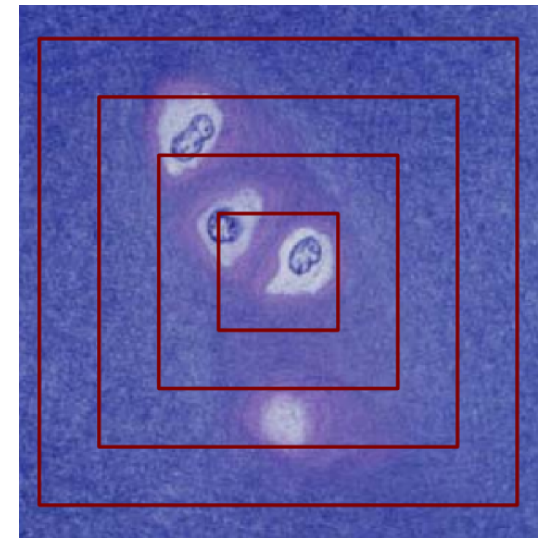


Representative Volume Element Convergence

Underlying geometry

Constitutive response

Variable of interest

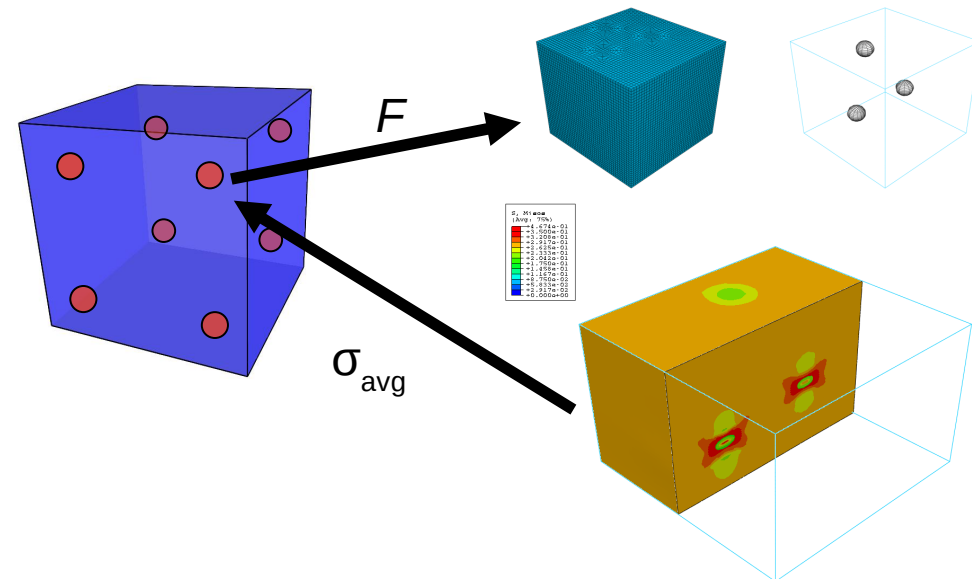


Multiscale Issues

Scale Separation

Assumptions of computational homogenization

Assumptions of post-processing



Modularity

Assumptions for hierarchical coupling

Case Study

Fill-in form to illustrate and understand boundaries of a given model

Yao J, Snibbe J, Maloney M, Lerner AL. Stresses and strains in the medial meniscus of an ACL deficient knee under anterior loading: a finite element analysis with image-based experimental validation. J Biomech Eng. 2006 Feb;128(1):135-41.

Short-Term Directions

Collaborative evolution and adoption by

investigators
journals
funding agencies
societies

to

document
review

with the ultimate goal of establishing

confidence
reproducibility
reusability

Long-Term Directions

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Customization to other discipline specific modeling modalities, for example

- movement analysis
- multiphysics investigations

Collaborative evolution to move from reporting standards to

- model exchange & sharing standards
- implementation in mark-up languages
- incorporation in multiscale modeling frameworks
- storage with models as metadata

Contact



Ahmet Erdemir
erdemira@ccf.org
+1 (216) 445 9523

<http://www.lerner.ccf.org/bme/cobi>

<http://www.lerner.ccf.org/bme/erdemir>