

Quantitative Electrocardiography: Two Steps Forward and One Step Back

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Northeastern University

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The Credits



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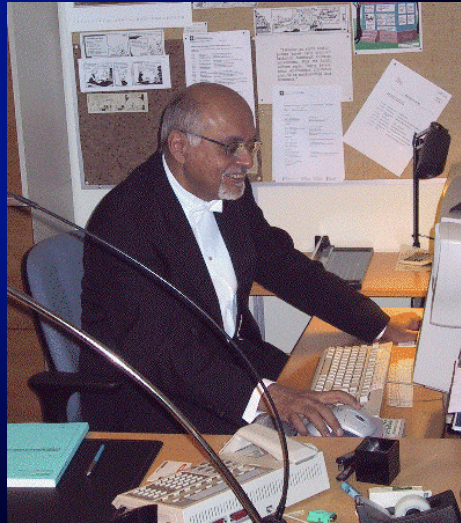


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Ramesh M. Gulrajani

12.12.1944 -

18.3.2004

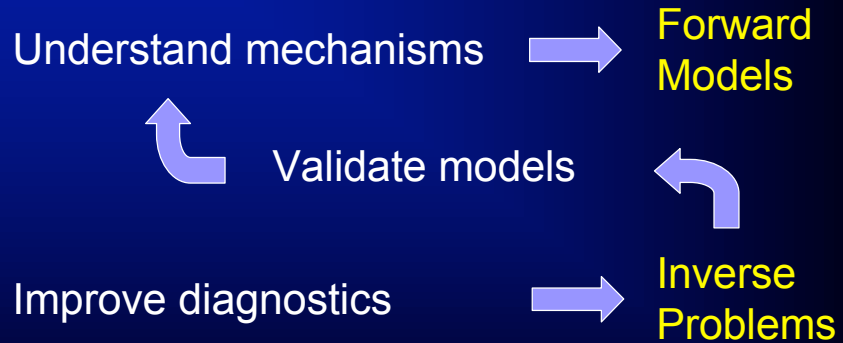


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Goals of Quantitative Electrocardiography

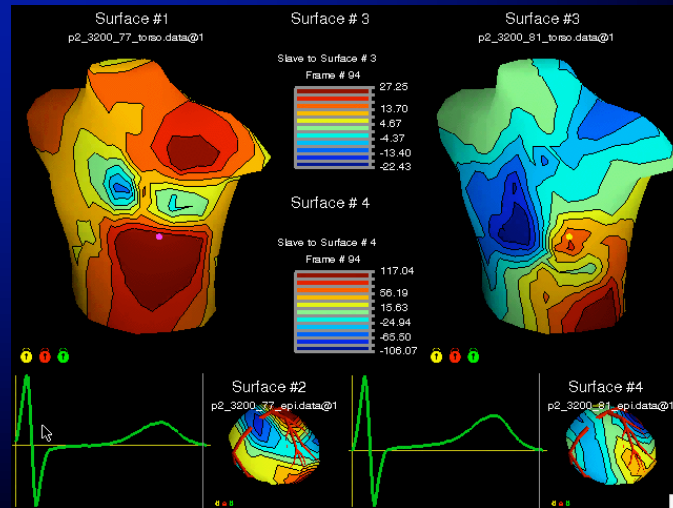


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The Motivation



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Driving Themes

Technical

- Forward models:
 - myocardial tissue to whole heart
- Signal processing:
 - catheter based cardiac mapping
- Inverse solutions:
 - multiconstrained approaches
- Software:
 - making it all work

Biomedical

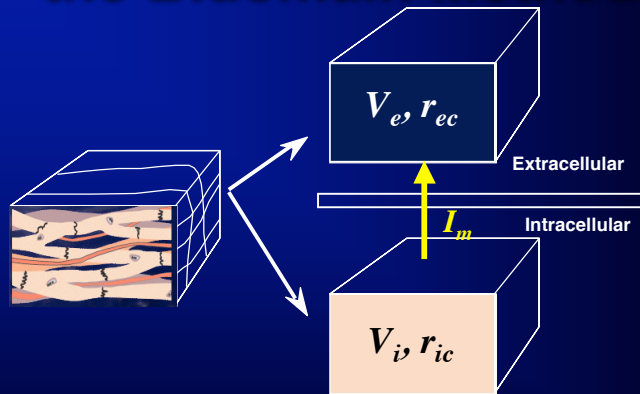
- Tissue function
 - coupling and anisotropy
- Organ Pathology
 - ischemia
 - arrhythmias
- Molecular biology
 - mutations/transgenics

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Forward Models: the Bidomain Method



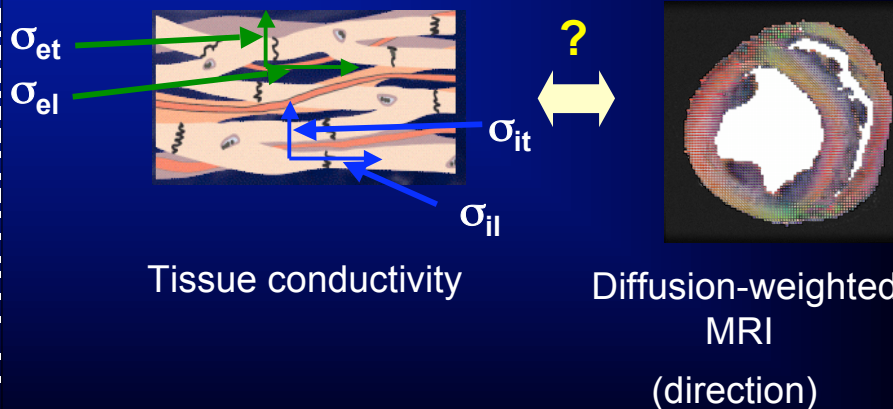
- 2 domains share the same space
- Membrane separates the domains
- All properties (e.g. V_e, r_{ec}) are macroscopic averages

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Bidomain Parameters

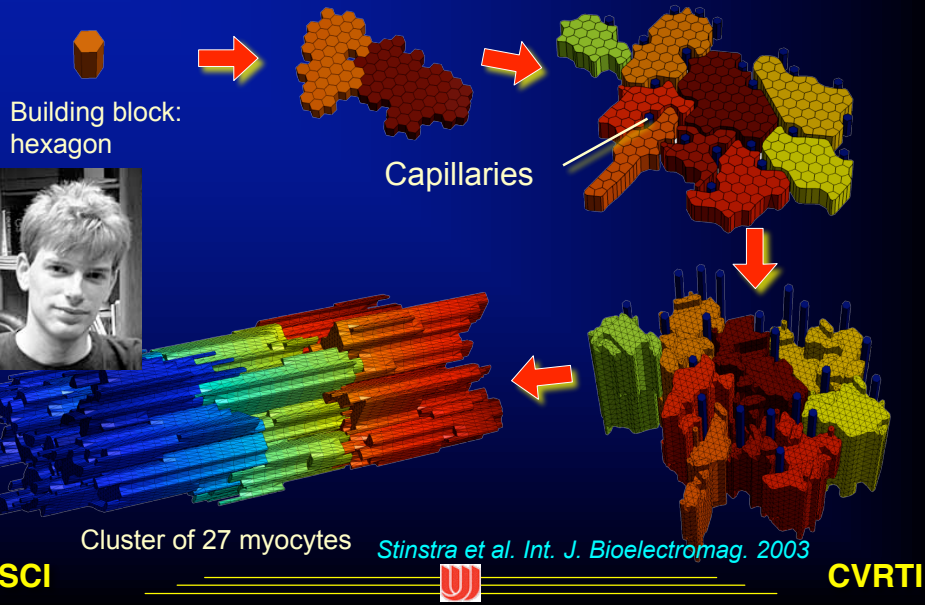


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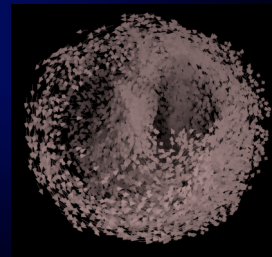
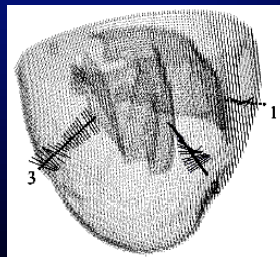
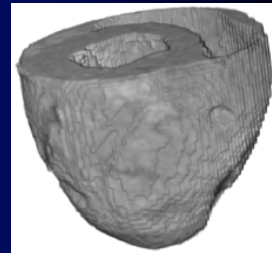
Modeling Conductivity



Mouse Heart Models

- MRI input data
- Segmented ventricles
- 225,236 hex elements

*Craig Henriquez,
Duke University*



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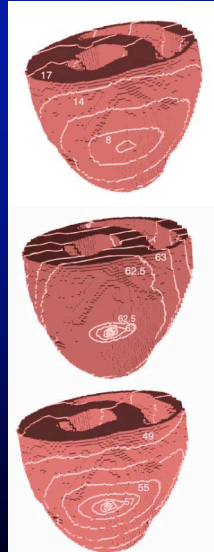
Mouse Activation Sequence

Activation

Recovery
(-60 mV)

APD

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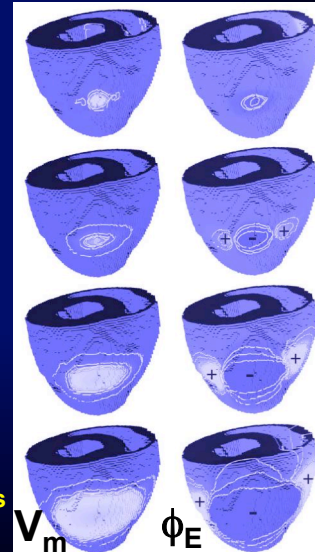


0.5 ms

6.5 ms

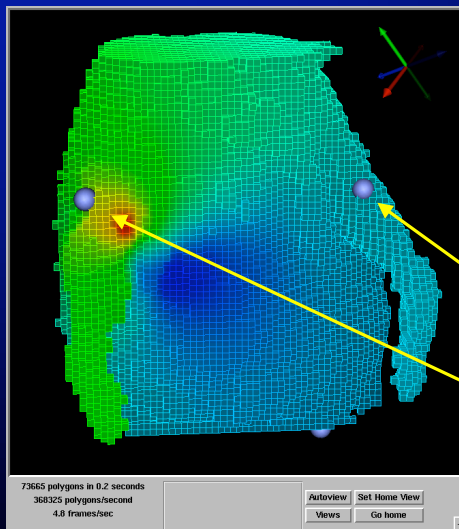
8.5 ms

10.5 ms



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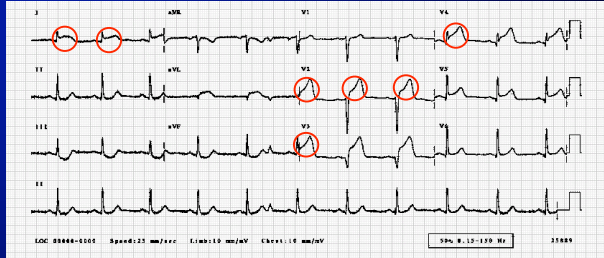
Forward Computation of ECG



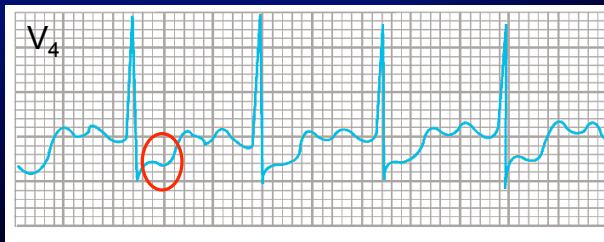
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Modeling Ischemia



ST-segment elevation



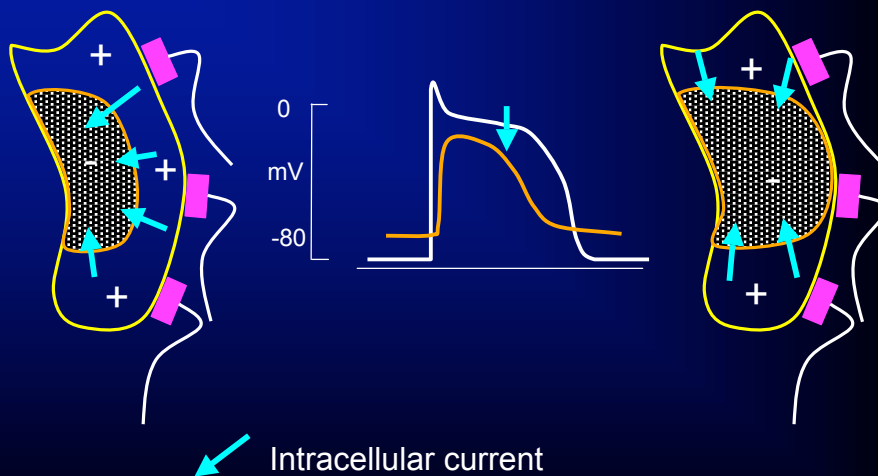
ST-segment elevation

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Biophysics of Acute Ischemia

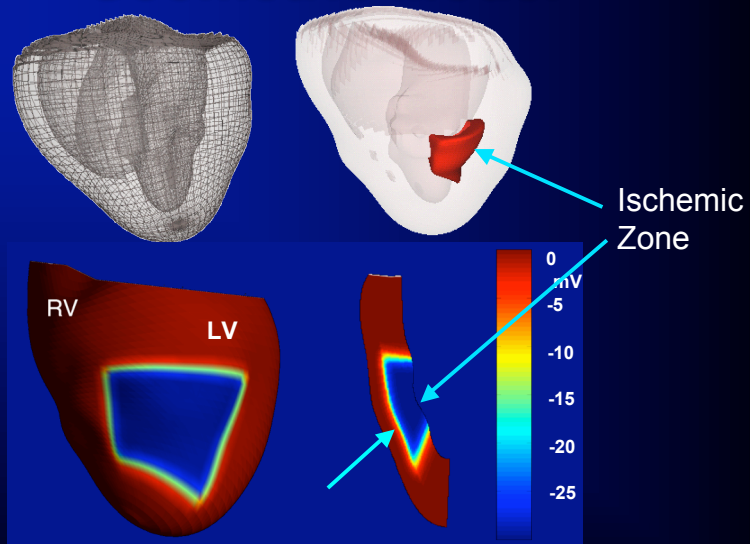


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Geometric Model



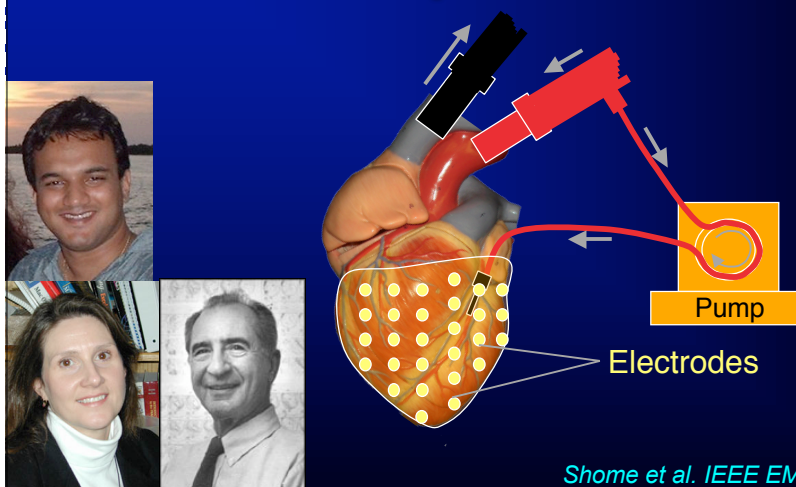
Hopenfeld et al. JCE, 15:1200, 2004

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Validation: Experimental Preparation



Shome et al. IEEE EMBS, 2004

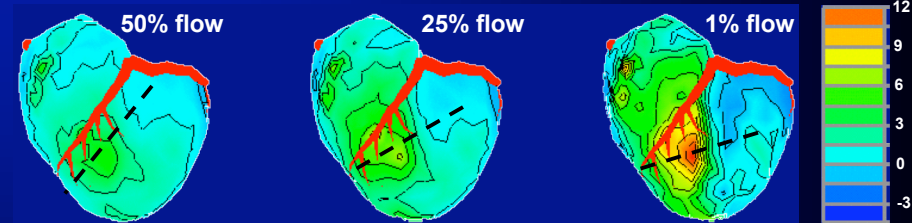
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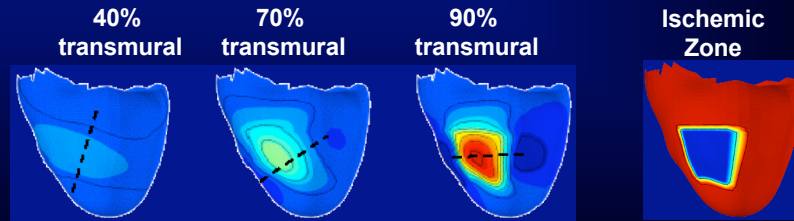
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Extent of Ischemia

Experiments



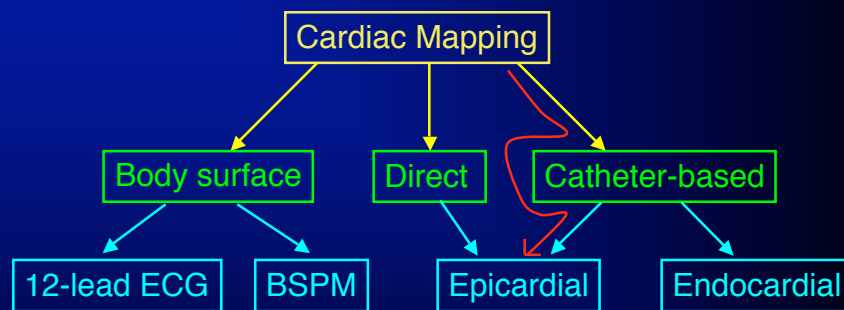
Simulations



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Signal Processing: Detection of Arrhythmias

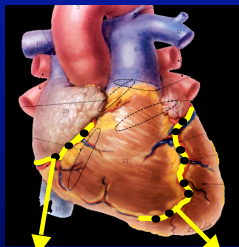


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Overcoming Limited Resolution

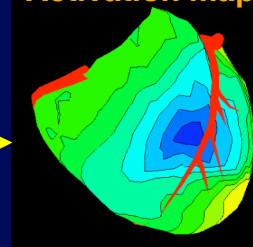
Sparse catheter measurements



Signal processing



High-resolution Activation maps



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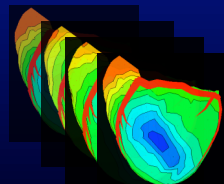


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Signal Processing



- How do we determine the relationships between known and unknown sites?
 - Interpolation
 - global pre-assumptions
 - Estimation
 - create these assumptions from a previously acquired set of data (training data)



Training Data

Learning Phase

Estimation Phase

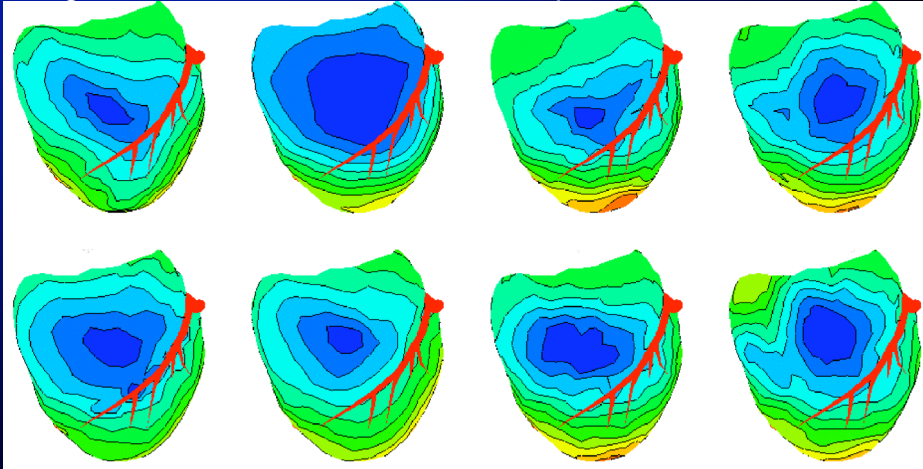
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Estimation Results

Original AME AME-Spat Act AME-Temp Act

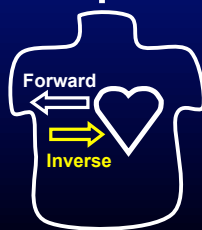
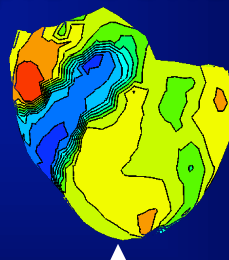
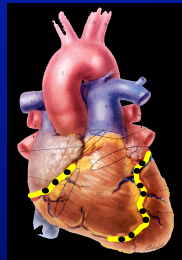


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Inverse Solutions by Multiple Constraints

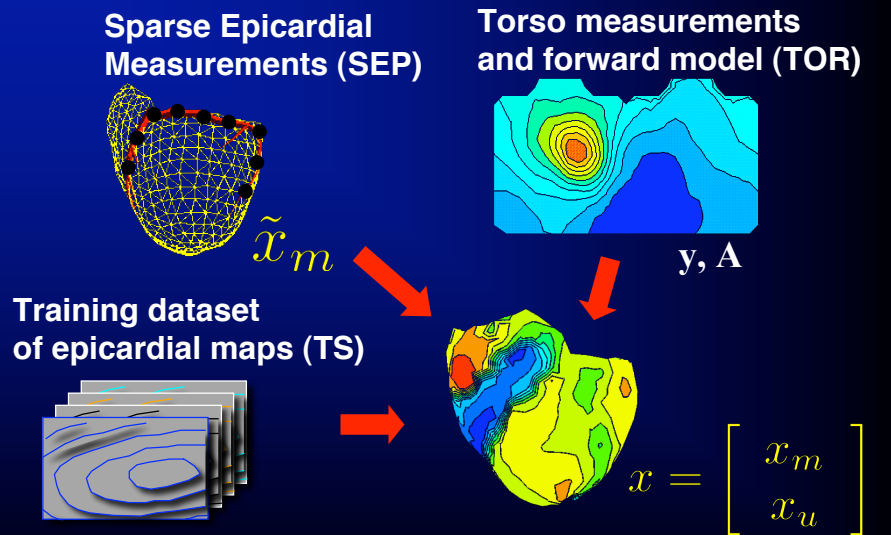


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Combing Information Sources

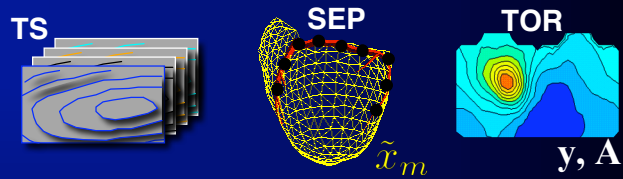


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Solution Approaches

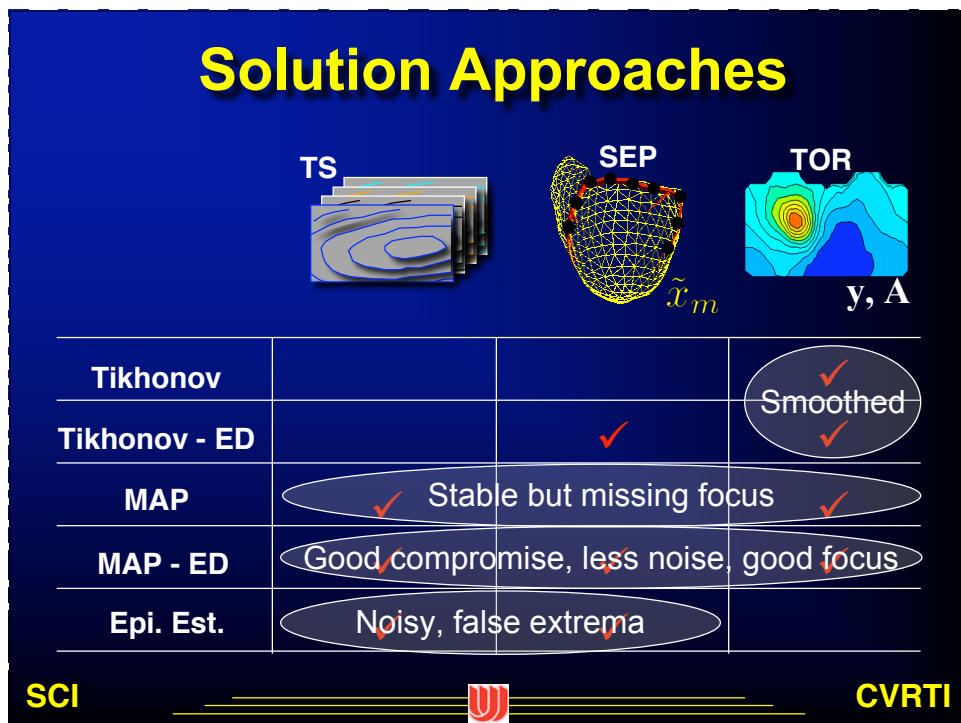
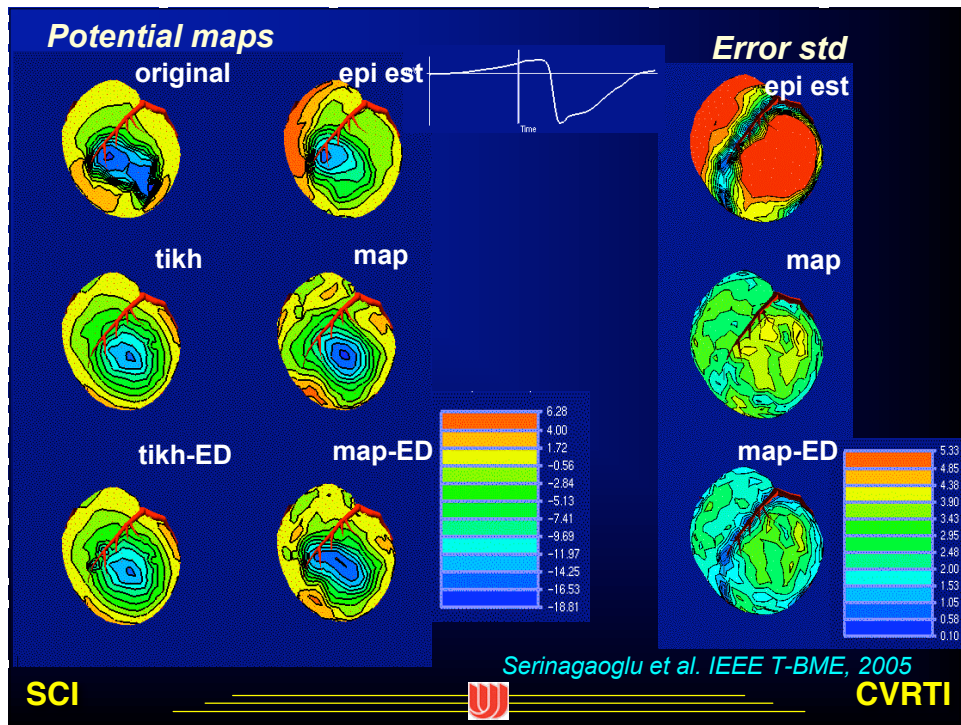


Tikhonov			✓
Tikhonov - ED		✓	✓
MAP	✓		✓
MAP - ED	✓	✓	✓
Epi. Est.	✓	✓	

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The Software: Requirements (Wish List)

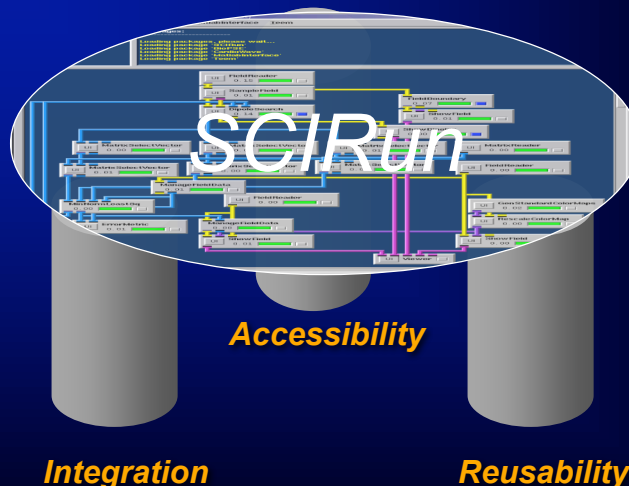
- Flexible
- Portable
- Integrated
- Extensible
- Powerful
- Efficient
- Easy to learn
- Cheap (aka free)
- MATLAB
 - Brainstorm
 - MatMap
 - utility code
- SCIRun/BioPSE
- *map3d*
- Cardiovave
- ECGSim
- NeuroFEM/Vgrid

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Pillars of SCIRun

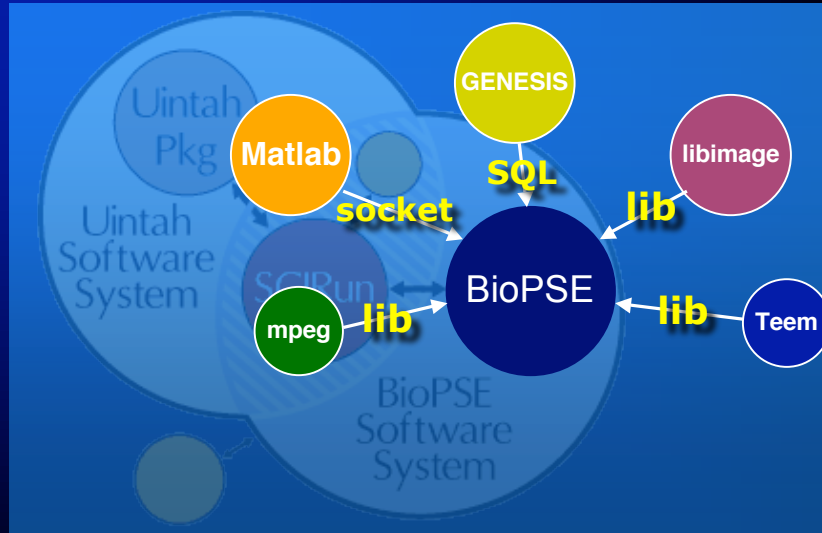


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BioPSE



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One Step Back

- What is the role of tissue structure?
 - gap junctions
 - discrete vs. continuous models
- How can we use ischemia models?
 - body surface information
 - effects on propagation
- What do cardiac maps tell us?
 - covariance matrix
 - detection of arrhythmias
- What are relevant inverse constraints?
 - identification
 - parameterization
- How do we span scales?
 - multiscale modeling
 - inclusion of molecular biology information

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