

Multilevel Schwarz and Multigrid preconditioners for the Bidomain system

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Outline

- 1. Introduction to the **Bidomain model**
- 2. Numerical methods
- 3. Parallel implementation
- 4. Numerical results

The macroscopic Bidomain model

Reaction-Diffusion system of two parabolic PDEs coupled with a system of ODEs.

DATA: $I_{app}^{i,e}$ (applied current per unite volume), v_0, w_0, c_0 (initial conditions)

UNKNOWN: u_i, u_e (intra and extracellular potentials), w (gating variables), c (ion concentrations)

$$\begin{cases} \rho C_m \frac{\partial v}{\partial t} - \operatorname{div}(D_i \nabla u_i) + \rho I_{ion}(v, w, c) = I_{app}^i & \text{in } \Omega \times (0, T) \\ -\rho C_m \frac{\partial v}{\partial t} - \operatorname{div}(D_e \nabla u_e) - \rho I_{ion}(v, w, c) = I_{app}^e & \text{in } \Omega \times (0, T) \\ \frac{\partial w}{\partial t} = R(v, w), \quad \frac{\partial c}{\partial t} = S(v, w, c) & \text{in } \Omega \times (0, T) \end{cases}$$

+ 0 Neumann b.c. for u_i, u_e and initial conditions for v, w, c .

$v = u_i - u_e =$ transmembrane potential, ρ ratio of membrane area/tissue volume, C_m surface capacitance, $I_{ion}(v, w, c)$ is the ionic current resulting from membrane model, $D_{i,e}$ are the intra and extracellular conductivity tensors

Membrane models

- System of ODEs for gating and ion concentrations variables that model the ionic exchanges through the cellular membrane
- First membrane model proposed by [Hodgkin](#) and [Huxley](#) in '50
- Membrane models for **Left Ventricle**: Beeler-Reuter(1977), Luo-Rudy I(1991), Luo-Rudy II(1994),...

Finite element discretization in space

- Portion of **Left Ventricle** is modeled with a slab
- Structured grid, trilinear finite elements

$$V_h = \{\varphi_h \text{ continuous in } \Omega \text{ and } \varphi_h|_K \in Q_1, \forall K \in \mathcal{T}_h\}$$

- **Bidomain semidiscrete system**

$$\begin{cases} \rho C_m \mathcal{M} \frac{\partial}{\partial t} \begin{pmatrix} u_{i,h} \\ u_{e,h} \end{pmatrix} + \mathcal{A} \begin{pmatrix} u_{i,h} \\ u_{e,h} \end{pmatrix} + \rho \begin{pmatrix} MI_{ion}^h \\ -MI_{ion}^h \end{pmatrix} = \begin{pmatrix} MI_{app}^{i,h} \\ -MI_{app}^{e,h} \end{pmatrix} \\ \frac{\partial w_h}{\partial t} = R(v_h, w_h), \quad \frac{\partial c_h}{\partial t} = S(v_h, w_h, c_h) \end{cases}$$

where

$$\mathcal{M} = \begin{bmatrix} M & -M \\ -M & M \end{bmatrix}, \quad \mathcal{A} = \begin{bmatrix} A_i & 0 \\ 0 & A_e \end{bmatrix}$$

Time discretization: semi-implicit method (IMEX)

- **implicit** treatment of the **gating variables** w
- **explicit** treatment of the **ionic concentrations variables** c
- **implicit** treatment of the linear **diffusion** term
- **explicit** treatment of the nonlinear **reaction** term
- **Adaptive time-step strategy** based on $\Delta v = \max(v^n - v^{n-1})$:
if $\Delta v < \Delta v_{min} = 0.05$ then $\Delta t = (\frac{\Delta v_{max}}{\Delta v})\Delta t$
if $\Delta v > \Delta v_{max} = 0.5$ then $\Delta t = (\frac{\Delta v_{min}}{\Delta v})\Delta t$
 $\Delta t_{min} = 0.005msec < \Delta t < \Delta t_{max} = 6msec$

Time discretization II

Given $\mathbf{v}^n = \mathbf{u}_i^n - \mathbf{u}_e^n$, \mathbf{w}^n , \mathbf{c}^n ,

Find \mathbf{w}^{n+1} , \mathbf{c}^{n+1} by

$$\frac{\mathbf{w}^{n+1} - \mathbf{w}^n}{\Delta t} = R(\mathbf{v}^n, \mathbf{w}^{n+1}, \mathbf{c}^n), \quad \frac{\mathbf{c}^{n+1} - \mathbf{c}^n}{\Delta t} = S(\mathbf{v}^n, \mathbf{w}^{n+1}, \mathbf{c}^n)$$

and then \mathbf{u}_i^{n+1} , \mathbf{u}_e^{n+1} solving the linear system

$$\left(\frac{\rho C_m}{\Delta t} \mathcal{M} + \mathcal{A} \right) \begin{pmatrix} \mathbf{u}_{i,h}^{n+1} \\ \mathbf{u}_{e,h}^{n+1} \end{pmatrix} =$$

$$-\rho \begin{pmatrix} MI_{ion}^h(\mathbf{v}^n, \mathbf{w}^{n+1}, \mathbf{c}^{n+1}) \\ -MI_{ion}^h(\mathbf{v}^n, \mathbf{w}^{n+1}, \mathbf{c}^{n+1}) \end{pmatrix} + \mathcal{M} \begin{pmatrix} \mathbf{u}_{i,h}^n \\ \mathbf{u}_{e,h}^n \end{pmatrix} + \begin{pmatrix} MI_{app}^{i,h} \\ -MI_{app}^{e,h} \end{pmatrix}$$

The choice of preconditioners

- At each time step we have to solve a linear system with iteration matrix

$$\left(\frac{\rho C_m}{\Delta t} \mathcal{M} + \mathcal{A}\right)$$

which is **singular** and very **ill-conditioned**

- **One level** preconditioners (Block Jacobi, One level Schwarz) are **not scalable**
- The simulation of a whole heartbeat in a portion of ventricle (4×10^6 d.o.f.) with 36 processors of a Linux cluster (2.8 GH) takes about 50 hours
- Need **multilevel** preconditioners

Multigrid preconditioner

- Firstly used by [Dos Santos](#) for Bidomain in elliptic case (IEEE Trans. Biomed. Eng. 2004)
- V-cycle multigrid method
- Block-Jacobi smoother
- For the coarsest grid we use the parallel PCG (tol=10⁻⁸) preconditioned by BJ

Symmetrized Multiplicative Multilevel Schwarz Preconditioner (SMMS)

See e.g. [Dryja](#), [Widlund](#) (Proc. Sixth GAMM-Sem. 1991) and [Zhang](#) (Num. Math. 1992).

Let be

- $\Omega^{(i)}$ $i = 0, \dots, M$ family of triangulations of Ω
- $A^{(i)}$ the matrices obtained discretizing the PDEs on $\Omega^{(i)}$
- $R^{(i)}$ the restriction operator from $\Omega^{(i+1)}$ to $\Omega^{(i)}$

Decompose $\Omega^{(i)}$ in $N^{(i)}$ overlapping subdomains and consider

- $R_k^{(i)} : \Omega^{(i)} \rightarrow \Omega_k^{(i)}$ the restriction operator for the domain $\Omega_k^{(i)}$
- $A_k^{(i)} = R_k^{(i)} A^{(i)} R_k^{(i)T}$ the subblock of $A^{(i)}$ associated with domain $\Omega_k^{(i)}$

SMMS-The algorithm I

$$u^{(M)} \leftarrow \sum_{k=1}^{N^{(M)}} R_k^{(M)T} A_k^{(M)-1} R_k^{(M)} r$$

$$r^{(M-1)} \leftarrow R^{(M-1)}(r - A^{(M)} u^{(M)})$$

$$u^{(M-1)} \leftarrow \sum_{k=1}^{N^{(M-1)}} R_k^{(M-1)T} A_k^{(M-1)-1} R_k^{(M-1)} r^{(M-1)}$$

$$r^{(M-2)} \leftarrow R^{(M-2)}(r^{(M-1)} - A^{(M-1)} u^{(M-1)})$$

...

$$u^{(0)} \leftarrow A^{(0)-1} r^{(0)}$$

SMMS-The algorithm II

$$u^{(1)} \leftarrow u^{(1)} + R^{(0)T} u^{(0)}$$

$$u^{(1)} \leftarrow u^{(1)} + \sum_{k=1}^{N^{(1)}} R_k^{(1)T} A_k^{(1)-1} R_k^{(1)} (r^{(1)} - A^{(1)} u^{(1)})$$

...

$$u^{(M)} \leftarrow u^{(M)} + R^{(M-1)T} u^{(M-1)}$$

$$u^{(M)} \leftarrow u^{(M)} + \sum_{k=1}^{N^{(M)}} R_k^{(M)T} A_k^{(M)-1} R_k^{(M)} (r^{(M)} - A^{(M)} u^{(M)})$$

$$u \leftarrow u^{(M)}$$

SMMS-Remarks

Remarks on the algorithm

- **Additive in levels:** the local problems can be solved in parallel
- **Multiplicative between levels:** sequential through the levels

Remarks on the implementation

- For local problems we use ILU(0) solver
- For the coarsest grid we use the parallel PCG (tol=10⁻⁸) preconditioned by BJ

Parallel implementation

- Code written in FORTRAN 90
- Parallel solver is based on:
parallel library PETSc from Argonne National Laboratory
preconditioned Krylov subspace methods (KSP and PC
PETSc object)
- Platforms:
IBM Linux Cluster of University of Milan (72 CPU, 2.4 GHz, 1
Gb every 2 CPU)
IBM Linux Cluster CLX of CINECA(1024 CPU, 3 GHz, 1 Gb
every 2 CPU)

Test 1: Fixed global load

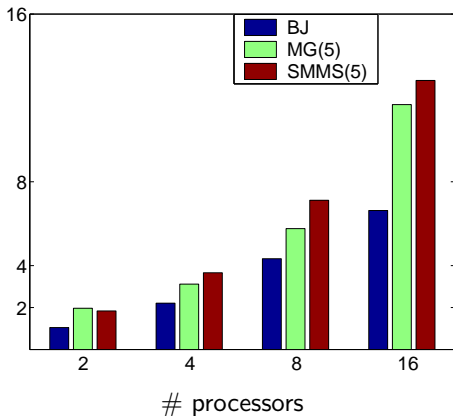
- Simulate **0.5 ms** (**10 time steps**) of ventricle excitation
- Domain is a **$2.56 \times 2.56 \times 0.01 \text{cm}^3$** slab discretized by a $256 \times 256 \times 2$ finite elements grid (**262144 d.o.f.**)
- Run on Linux cluster of University of Milan

Test 1

# SUB	BJ		MG(5)		SMMS(5)	
	IT.	TIME	IT.	TIME	IT.	TIME
1	95	23.00	3	9.11	-	-
2	108	22.27	3	4.63	3	4.95
4	109	10.40	4	2.92	3	2.49
8	111	5.31	4	1.58	3	1.28
16	114	3.47	4	0.78	3	0.71

Test 1

Speedup



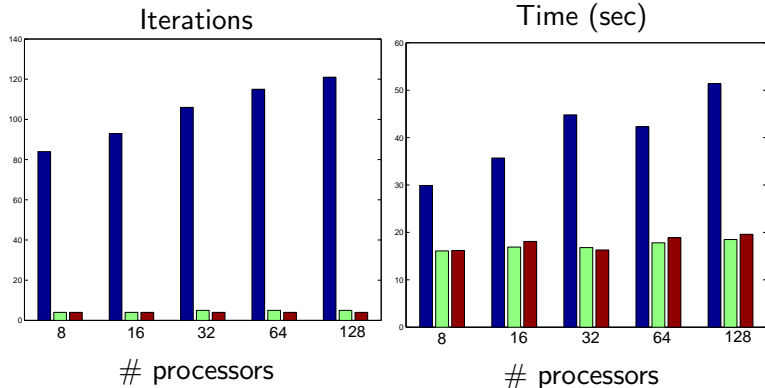
Test 2: Fixed local load

- Simulate 0.5 ms (10 time steps) of ventricle excitation
- Fixed Subdomain mesh $48 \times 48 \times 48$, i.e. 221184 d.o.f.
- Run on CLX cluster of CINECA

Test 2

# SUB	D.O.F.	BJ		MG(5)		SMMS(5)	
		IT.	TIME	IT.	TIME	IT.	TIME
8	1769472	84	29.9	4	16.1	4	16.2
16	3538944	93	35.7	4	16.9	4	18.1
32	7077888	106	44.8	5	16.8	4	16.3
64	14155776	115	42.3	5	17.8	4	18.9
128	28311552	121	51.4	5	18.5	4	19.6

Test 2



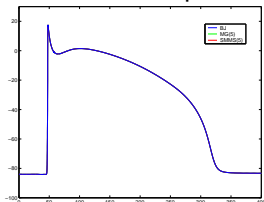
Test 3: Complete Heartbeat

- Simulate a complete heartbeat (**400 ms**, i.e. about 3000 time steps) in a portion of ventricle having dimensions $2 \times 2 \times 0.5 \text{ cm}^3$
- Mesh size = $200 \times 200 \times 50$, **4000000 d.o.f.**
- **36 subdomains**
- Run on Linux cluster of University of Milan

Test 3

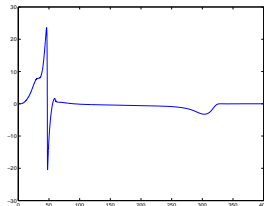
PREC	IT. (AVER.)	TIME (AVER.)	TOTAL TIME
BJ	205	46.02 sec	29 h 49 m
MG(5)	8	11.11 sec	7 h 21 m
SMMS(5)	6	9.67 sec	6 h 26 m

Transmembrane potential



time (ms)

Extracellular potential

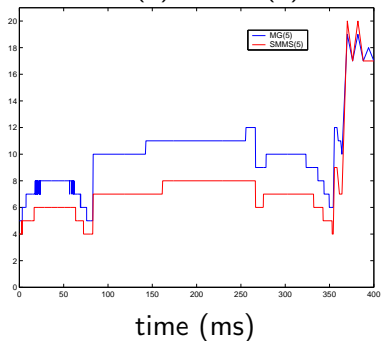


time (ms)

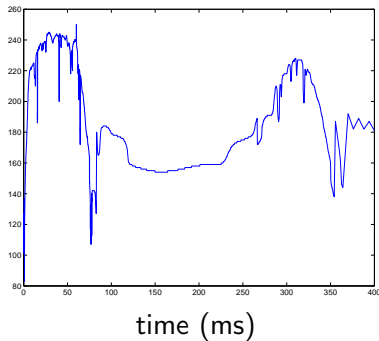
Test 3

Time evolution of the PCG iterations

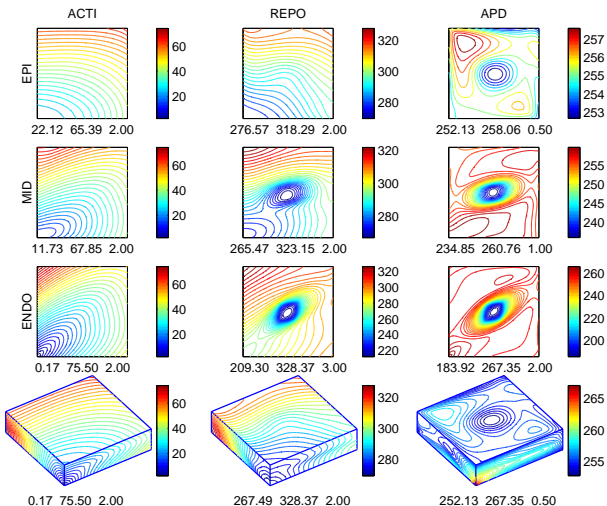
MG(5)-SMMS(5)



Block Jacobi



Test 3: Activation and Repolarization times



Conclusions and developments

- **MG** and **SMMS** preconditioners are optimal for the Bidomain system: **scalable** and **efficient**
- The complete heartbeat simulation time is reduced **four times** compared with BJ
- Extend to more **realistic domains** (ellipsoidal)
- Extend to **unstructured meshes**
- Consider the presence of **arrhythmias**