A domain decomposition strategy for a very high-order finite volumes scheme applied to cardiac electrophysiology

Y. Coudière - Rodolphe Turpault

Institut de Mathématiques de Bordeaux, Bordeaux-INP

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2 The monodomain model

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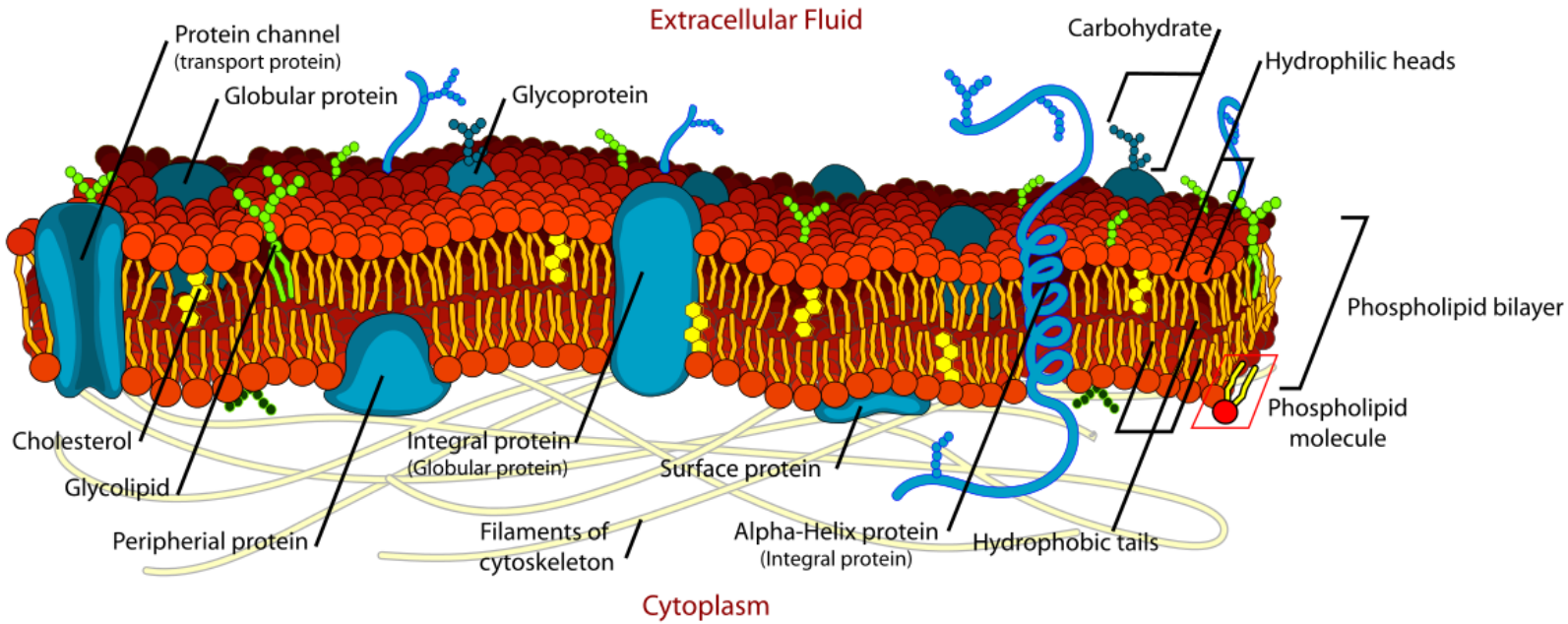
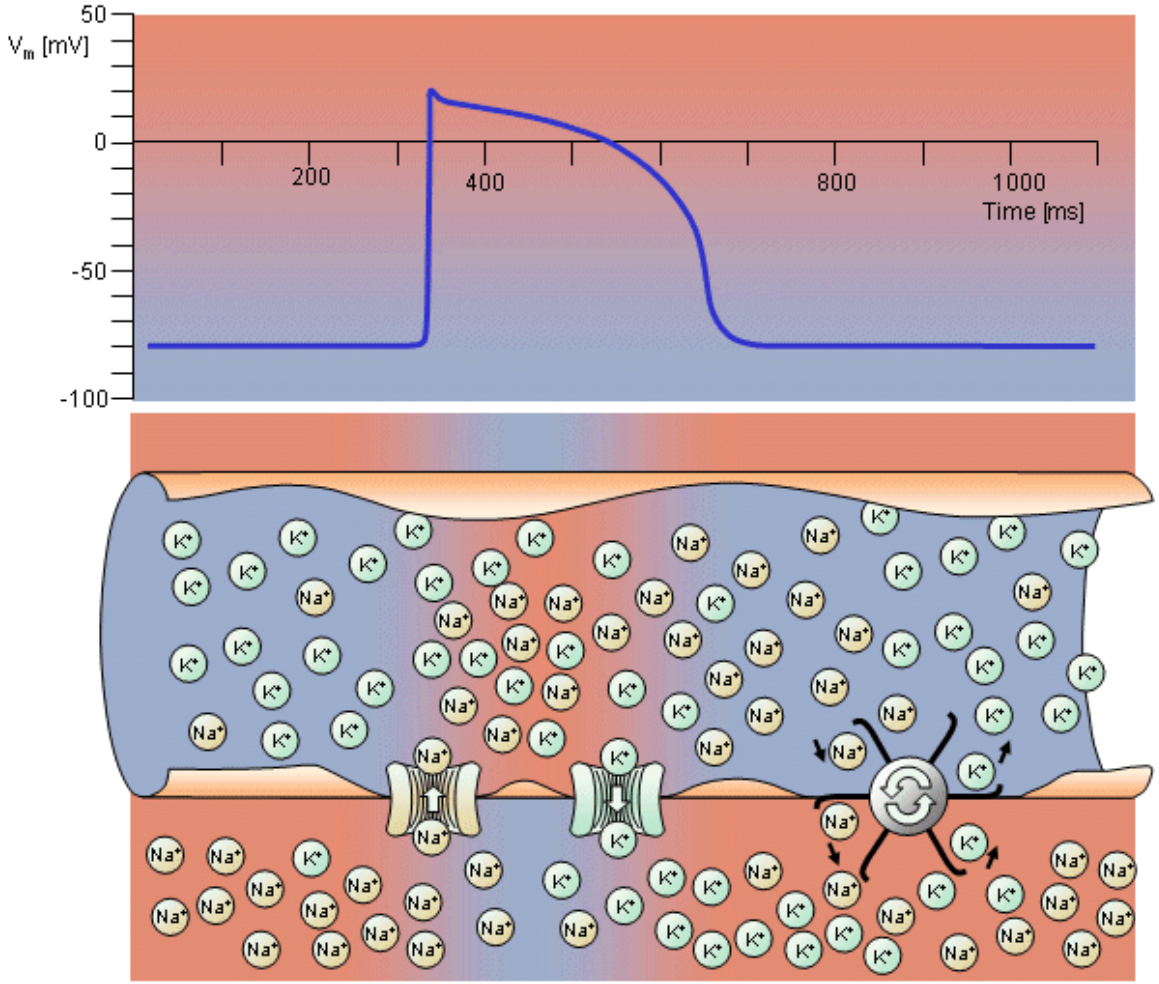
Cell level - membrane

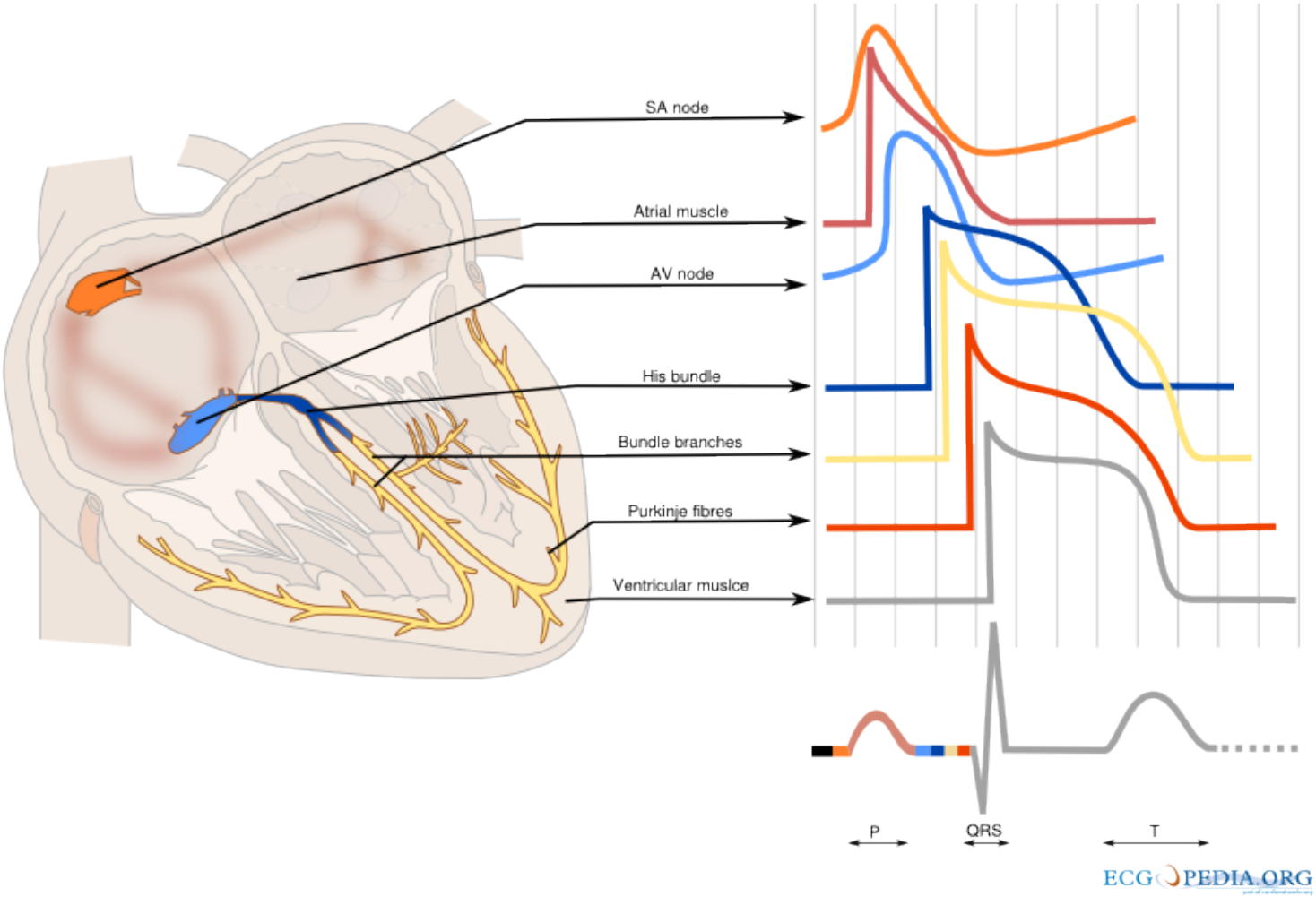


The cell membrane

Cell level - action potential



Macroscopic level



The monodomain model

$$\partial_t V + I_{ion}(V, w) = \text{div}\big(D\nabla V\big),$$
$$\partial_t w = G(V, w),$$

where :

- V $[mV]$ is the transmembrane voltage,
- $I_{ion} = I_{ion}(V, w)$ $[A.F^{-1}.cm^{-2}]$ is the normalized ioinc current par unit surface,
- $D = \dfrac{G}{A_m C_m}$ $[mS.\mu F^{-1}]$ is the normalized diffusion tensor,
- w contains all auxiliary variables.

Ionic models

The ionic current I_{ion} and G are given by a so-called *ionic model* which approximates all ionic processes in the cardiac cells :

- Phenomenological models (Fitzugh-Nagumo, Aliev-Panfilov, Mitchell-Schaeffer,...) are simple,
- Hodgkin-Huxley type models (Beeler-Reuter, Ten Tusscher et al, Luo-Rudy,..) are more complex. Markov chains variants (Iyer et al...) are nowadays widely used by biologists.

Hodgkin-Huxley formalism

Mimics the behavior of proteins in the cell membrane :
$I_{ion}(V, w) = \sum_i I_i$ where the I_is are expressed as functions of *gating variables*.
Example : $I_{Na} = g_{Na} m^3 hj(V - E_{Na})$ where :

- $E_{Na} = \frac{RT}{F} \ln\left(\frac{[Na^+]_e}{[Na^+]_i}\right)$ is Nernst's potential,
- m, h, j are gating variables $\in [0, 1]$ given by :

$$\frac{d}{dt} m = \frac{m_\infty - m}{\tau_m},$$

$w \in \mathbb{R}^N$ also contains other variables (concentrations,...) and N ranges from 8 to 100+.

Main numerical difficulties

- Stiffness
  - in time due to physiological processes (*e.g.* fast Na^+ channels),
  - in time due to ODEs,
  - in space due to depolarization fronts,
- *propagation failure*
  - No propagation when the mesh is too coarse,
  - Wrong propagation speed,
- Anisotropy

Most codes use P_1 or equivalent methods with a mesh length $\simeq 100\mu m$ (which is too coarse !) and adapt A_m.

Semi-discrete scheme

Finite volumes scheme : unknowns are mean values of V and w in each cell K :

$$\frac{d}{dt} V_K + I_K = \frac{1}{|K|} \sum_{e_i \in \mathcal{E}_K} F_i \cdot n_i,$$

$$\frac{d}{dt} w_K = G_K,$$

The scheme is determined by the choices of I_K, G_K and $F_i \cdot n_i$. Our choice : scheme based on the ideas of Clain, Machado, Nobrega and Pereira (CMAME '13).

The scheme at a glance

- Polynomial reconstruction on cell interfaces for V (diffusion),
- Polynomial reconstruction on cells for V and W (reaction),
- Both are weighted least-squares polynomials inside given stencils,
- Coefficients satisfy :

$$(X^\top \Omega X)\Gamma = X^\top \Omega \mathbb{V},$$

- Preservation of admissibility : MOOD procedure.

Time integration

- Explicit schemes : ionic model $\rightarrow$ small Δt, "reasonable" mesh, preservation of admissibility,...
- If $\Delta t = \mathcal{O}(\Delta x^2)$ then time order = (space order)/2
- Preservation of admissibility : SSP-RK.

Order of convergence

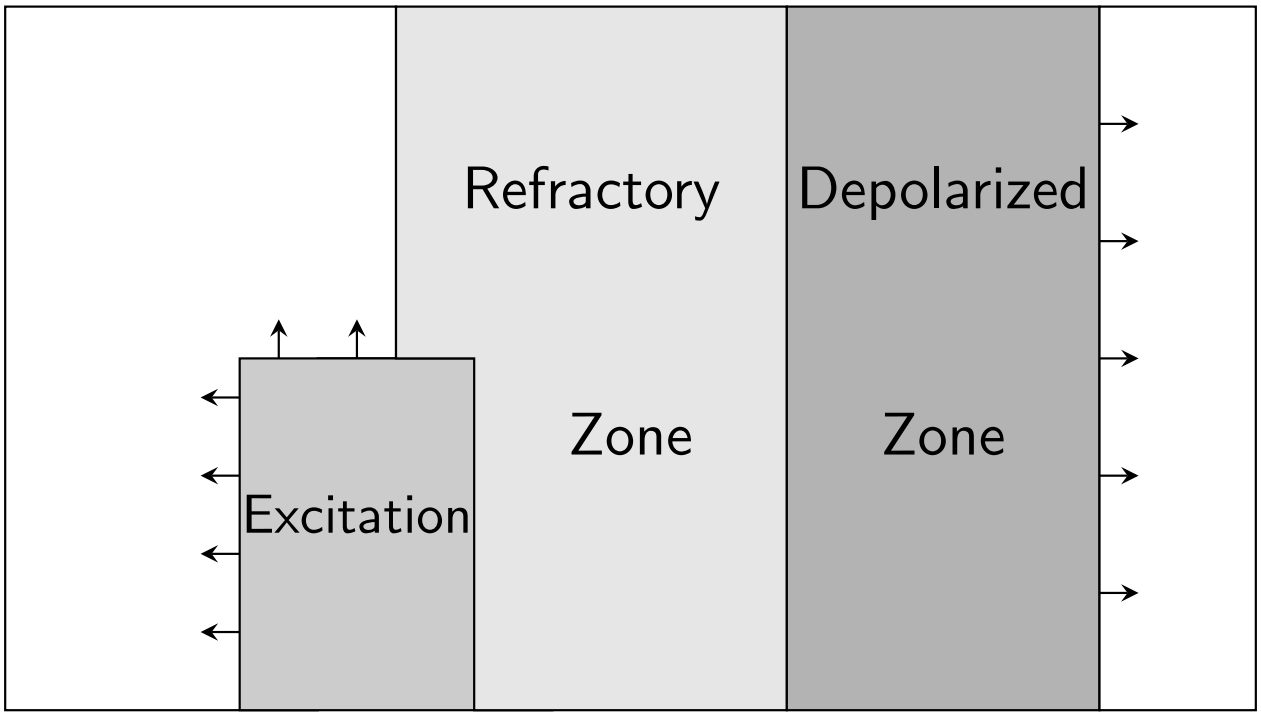
Ad hoc choice of I_{ion} in order to have an analytical solution.

h	p=2	ord.	p=3	ord.	p=4	ord.	p=5	ord.
1.2E-2	2.4E-5	n/a	6.8E-6	n/a	2.9E-6	n/a	9.5E-7	n/a
6.1E-3	5.6E-6	2.09	5.1E-7	3.75	1.3E-7	4.51	2.1E-8	5.52
3.1E-3	1.3E-6	2.09	3.2E-8	3.97	5.2E-9	4.60	3.7E-10	5.80
1.5E-3	3.2E-7	2.03	2.0E-9	4.04	2.4E-10	4.46	6.3E-11	2.57

TABLE – L^2 errors for the analytical test case

Spiral waves

Setup :



Spiral waves

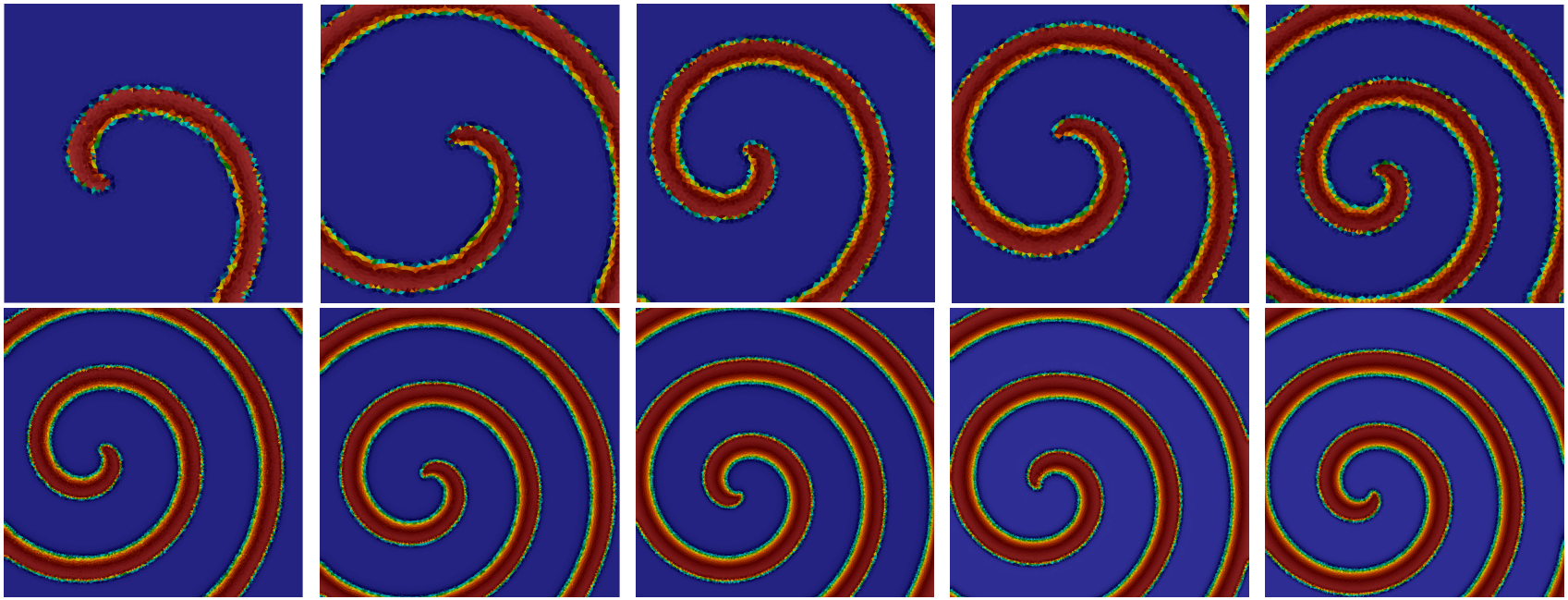


FIGURE – Spiral wave (AP model) obtained on two moderately coarse meshes with the schemes from order 2 (left) to 6 (right), $t = 150$ms.

Summary so far

- 4th and 6th order schemes allow to use reasonable meshes,
- Efficiency : 4th order is way better than 1st and 2nd order / 6th order (?),
- Efficiency : way better than implicit + P1,
- Still not fast enough for long-time realistic simulations.

Idea and questions

Basic idea : BC work fine.

Domain decomposition therefore seems a good idea.

But :

- 2 reconstructions ?
- accuracy ?
- avoid subdomains B.C. ?

Strategy

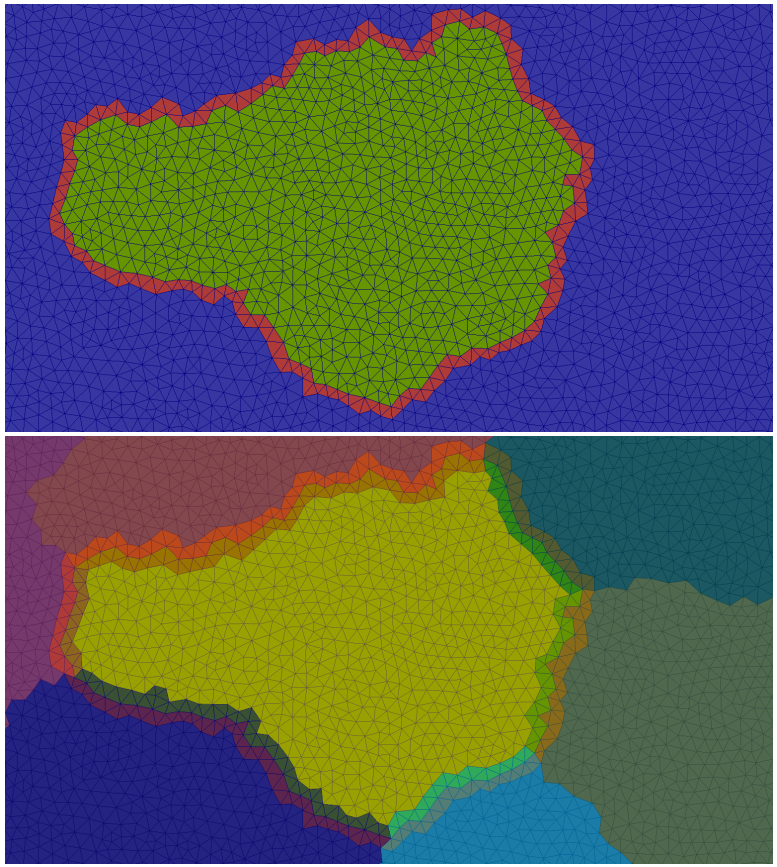


FIGURE – Domains and halos

- One thread computes one subdomain,
- Stencils are built inside extended subdomain (subdomain+halo),
- Halos = 1 layer of neighbors (1 node shared), eventually extended if necessary.

Implementation

- Domain decomposition $\rightarrow$ Scotch,
- Balance cells/interfaces,
- (Real) OpenMP,
- Renumbering,
- Vectorization $\rightarrow$ Xeon Phi,
- Reasonable modification of a (flexible) code.

Numerical results - accuracy

Ad hoc choice of I_{ion} in order to have an analytical solution.

h	p=2	ord.	p=3	ord.	p=4	ord.	p=5	ord.
1.2E-2	2.4E-5	n/a	6.8E-6	n/a	2.9E-6	n/a	9.5E-7	n/a
6.1E-3	5.6E-6	2.09	5.1E-7	3.75	1.3E-7	4.51	2.1E-8	5.52
3.1E-3	1.3E-6	2.09	3.2E-8	3.97	5.2E-9	4.60	3.7E-10	5.80
1.5E-3	3.2E-7	2.03	2.0E-9	4.04	2.4E-10	4.46	6.3E-11	2.57

TABLE – L^2 errors for the analytical test case - 24 subdomains

The relative error between 1 and 24 subdomains is less than 1%.

Numerical results - scalability

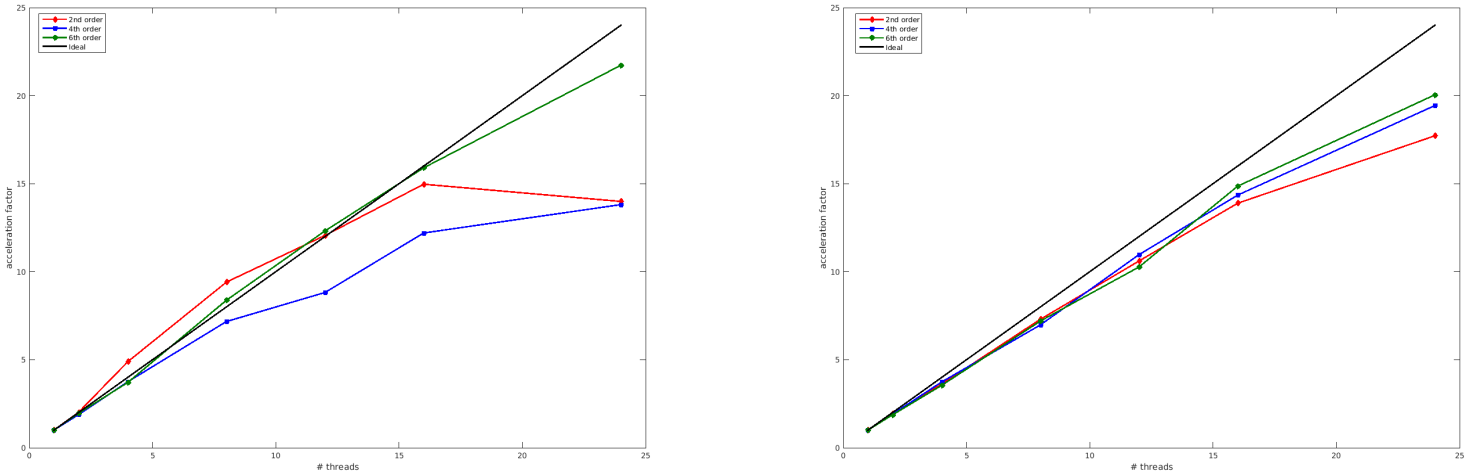
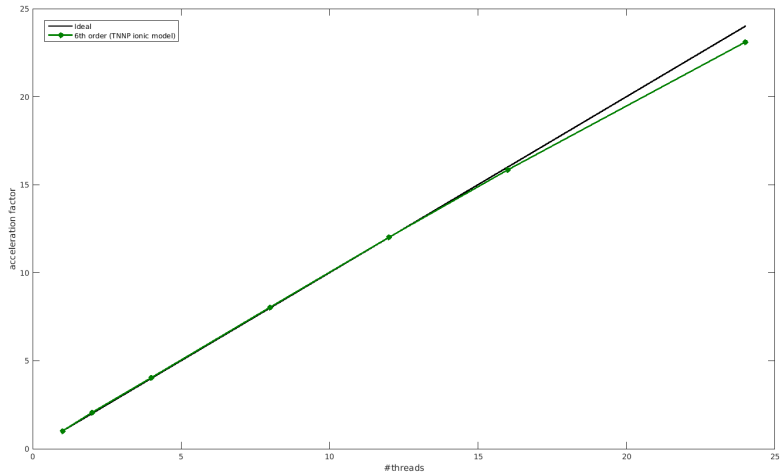
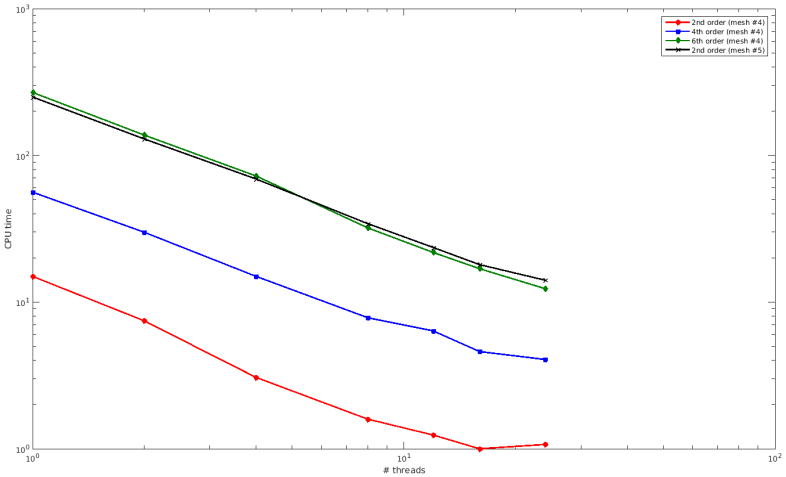


FIGURE – Scalability (AP model) - mesh #4 (l) and #5 (r)

Numerical results - scalability





- Scalability (TNNP model on mesh #4)
- CPU time (Order 2, 4 and 6 on mesh #4 and order 2 on mesh #5)

Numerical results - spiral wave

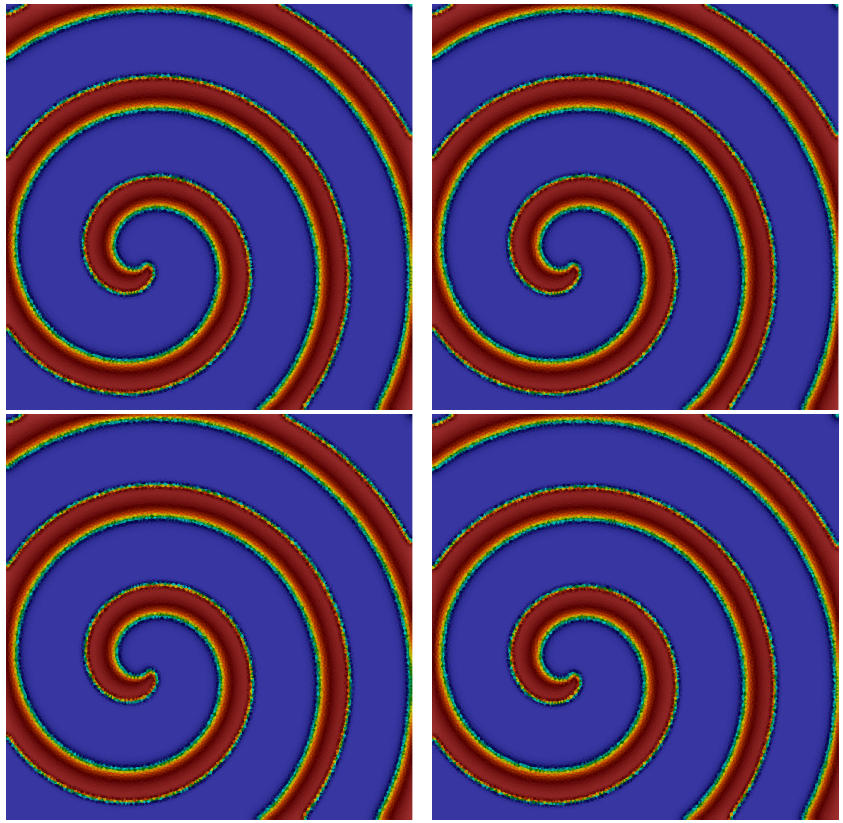


FIGURE – Spiral wave (AP model), $t = 150$ms order 6 with 1, 4, 24 and 128 subdomains.

Conclusion and perspectives

- High-order is very interesting in this context,
- The code is scalable as long as subdomains are reasonable,
- A priori extendable to MPI/hybrid/... (has to be tested),

Thanks for your attention !