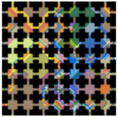


A Methodology for Multiscale-Multiscience modeling and simulations

Bastien Chopard

Computer Science Department
University of Geneva, Switzerland

Unconventional Computing, Turku, June 7, 2011

Introduction

- Modeling and simulation are central to modern science
- There is a need to develop new and better numerical approaches
- For instance the Cellular Automata (CA) and Lattice Boltzmann (LB) approaches have been successful alternatives to standard computational methods

CA and LB methods

- a discrete mathematical abstraction of reality
- The macroscopic behavior depends very little on the details of the microscopic interactions.
- Only “symmetries” or conservation laws survive. The challenge is to find them.
- Consider a fictitious world, particularly easy to simulate on a (parallel) computer with the desired macroscopic behavior.

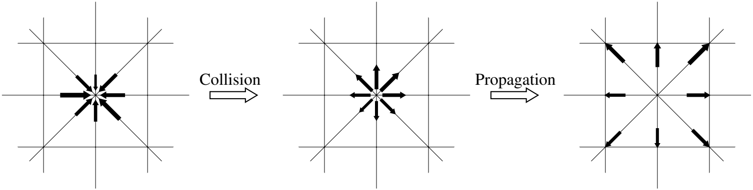
From hydrodynamics PDE

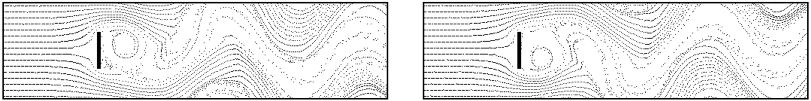
$$\partial_t \mathbf{u} + (\mathbf{u} \cdot \nabla)\mathbf{u} = -\frac{1}{\rho}\nabla p + \nu \nabla^2 \mathbf{u}$$

phenomena → PDE→ discretization → computer solution

...to virtual fluids

phenomena $\rightarrow$ computer model



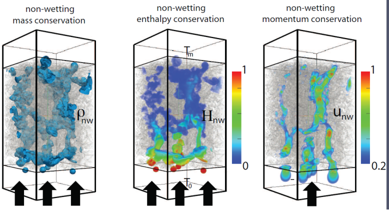


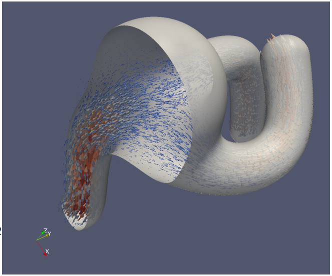
LB simulations

- Simple, flexible, intuitive, efficient
- Palabos software[1] (Jonas Latt)
  - Free, Open source software (`http://www.lbmethod.org/palabos`)
  - Python interface or full C++
  - complex multi-physics, complex data-structures
  - Offer a wide range of models, boundary conditions, dynamics
  - Can handle large scale parallel simulations
  - Automatic high performance parallelization. Scales well up to thousands of cores

1. `http://www.lbmethods.org/palabos`

Examples of LB simulations





Multiscale systems

- Most natural systems are multi-scale and multi-sciences

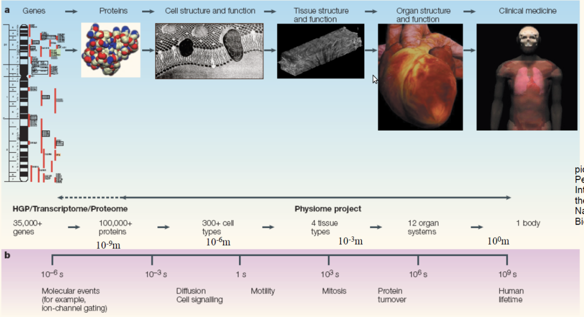


Figure 2 | **Linking molecular and cellular events with physiological function must deal with wide ranges of length scales and timescales. a** | Levels of biological organization from genes to proteins, cells, tissues, organs and finally the whole organism. The range of spatial scales — from ~1 nm for proteins to ~1 m for the whole body — requires a hierarchy of models. Different types of model are appropriate to each level, and relationships must be established between models at one level and the more detailed, but spatially or temporally limited, models at the level below. The organ-level and whole-body-level models shown are the Auckland heart and torso models, respectively[32,38]. The tissue figure is a reconstructed three-dimensional confocal image of a transmural section of rat myocardium, which is also from the Auckland Bioengineering Institute, New Zealand[28]. **b** | The range of temporal scales as shown here is even more daunting and again calls for a hierarchy of models. HGP, human genome project. Modified with permission from REF. 39 © Springer-Verlag (2002).

picture taken from:
Peter J. Hunter and Thomas K. Borg,
Integration from Proteins to Organs,
the Physiome Project,
Nature Reviews Molecular Cell
Biology, 4, 237-243, 2003

Integration versus specialization

- A computational challenge is "integration" instead of "specialization"
- But each scale and each subsystems may require its own modeling approach
- How to glue them together ?

Multiscale, multiscience modeling framework

- Propose a modeling and simulation framework for multiscale, multisciences complex systems

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  - Validation application : In-stent restenosis
  - A Multiscale Modeling Language : MML
- The follow up : the MAPPER EU project

The COAST Project

- A. Hoekstra, A. Caiazzo, E. Lorenz, U. Amsterdam (Netherlands)
- R. Hose, P. Lawford, D. Evans, J. Gunn, U. Sheffield (UK)
- B. Chopard, J-L. Falcone, B. Stahl, U. Geneva (Switzerland)
- M. Krafczyk, Y. Hegwald, TU Brauschweig (Germany)
- J. Bernsdorf, D. Wang, NEC (Germany)

- Joris Borgdorf, U. Amsterdam (Netherlands)

Motivations

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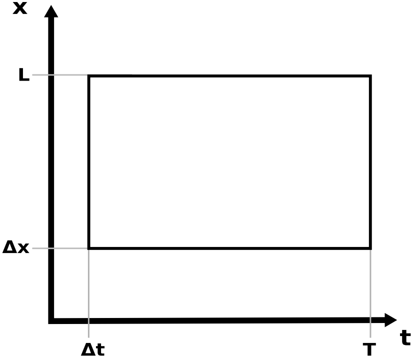
- Very few methodological papers in the literature.
- Multiscale strategies are usually entangled with applications.
- Can we develop a framework that help the design and deployment of complex multiscale-multiscience applications ?

From a multiscale systems to many single-scale systems :

Let us consider a system of size L evolving over a time T.
Computation with space and time discretization Δx and Δt

Resolved spatial scales : $\Delta x < \xi < L$ and
Resolved temporal scales : $\Delta t < \tau < T$

Scale Map



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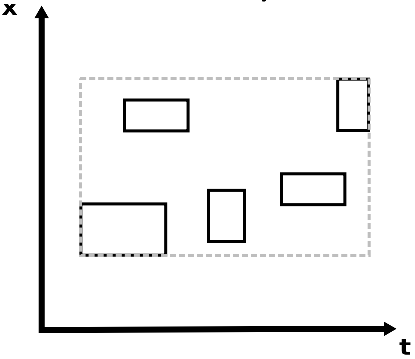

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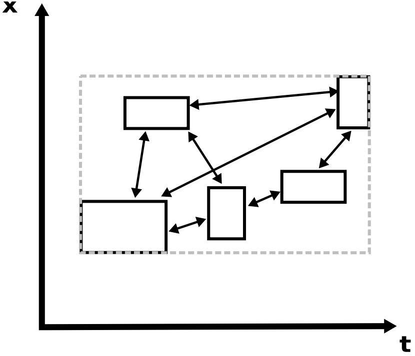
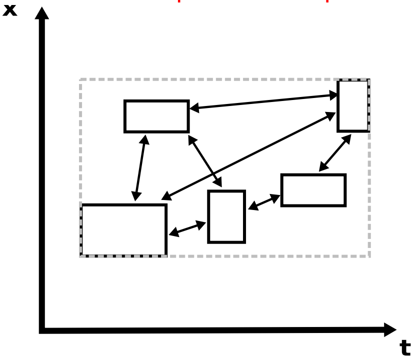


From a multiscale systems to many single-scale systems :

Scale Separation Map



- Submodels
- Smart Conduits

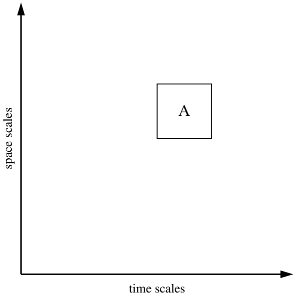
Complex Automata (CxA)

- A CxA is a set of coupled (single-scale) submodels
- **Lattice Boltzmann (LB)**, **cellular automata (CA)** models and **Finite Difference (FD)** schemes, and also **particle models**, ...
- They can be decribed with the same generic **execution loop**
- Submodels should not know about the rest of the system : they are autonomous components
- Only the **smart conduits** know about the properties of the submodels they connect.

A. G. Hoekstra, A. Caiazzo, E. Lorenz, J.-L. Falcone, and B. Chopard. *Complex Automata : multi-scale Modeling with coupled Cellular Automata*, in **Modelling Complex Systems by Cellular Automata**, chapter 3, Springer Verlag, 2010.

I. Relation between the scales

- The Scale Separation Map (SSM) specifies the relation between the sub-models in five regions :.



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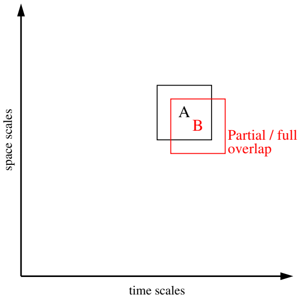

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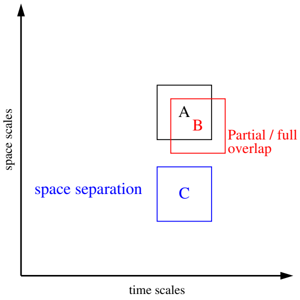

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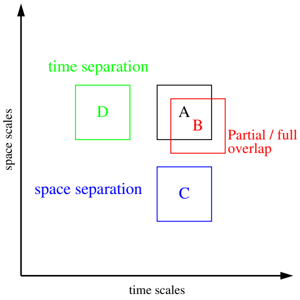

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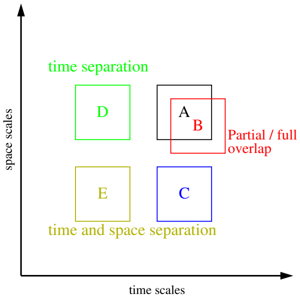
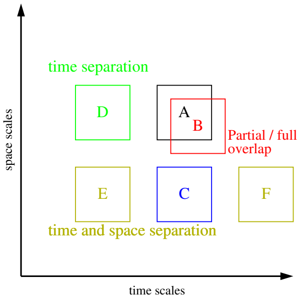


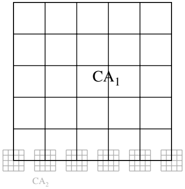
I. Relation between the scales

- The Scale Separation Map (SSM) specifies the relation between the sub-models in five regions :.
- There is more than the standard micro-macro relation and more than than the "bi-scale" modeling



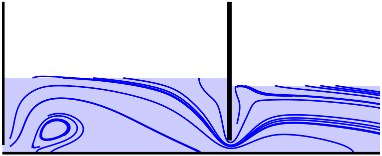
II. Relation between computational domains

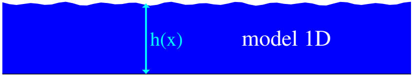
single-Domain (sD)



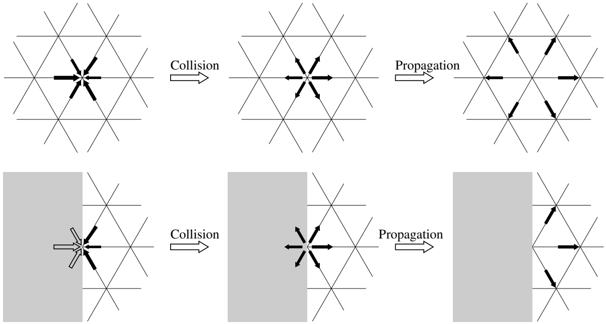
(Example : advection-diffusion, suspension flows)

multi-Domain (mD)



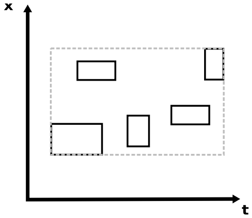


III. Update loop



- 1. Boundary (B)
- 2. Collision (C)
- 3. Propagation (P)

Generic "Submodel Execution Loop"



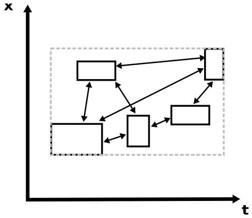
- f_{init} is for initialization
- S is for one iteration of the Solver
- B is to specify the Boundaries
- O_i is for Intermediate Observation
- O_f is for Final Observation

submodel

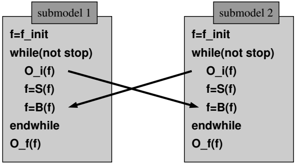
```
f=f_init
while(not stop)
    O_i(f)
    f=S(f)
    f=B(f)
endwhile
O_f(f)
```

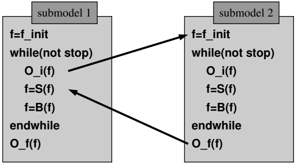
For LB and CA models, $S = PC$ (collision followed by propagation)

IV. Coupling Templates



- One has several operators in the submodel execution loop
- O_i, O_f as origin
- f_{init}, B and S as possible destinations





Example : Coral growth

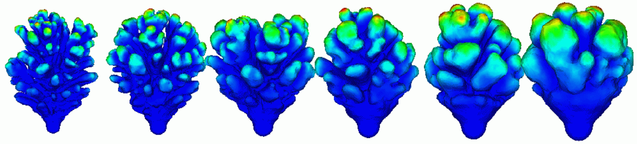
FLOW

```
D := D_init
f := f_init
while not EndCondition
  D := U(D)
  f := B(f)
  f := C(f)
  f := P(f)
  O_i[f]
end
O_f[f]
```

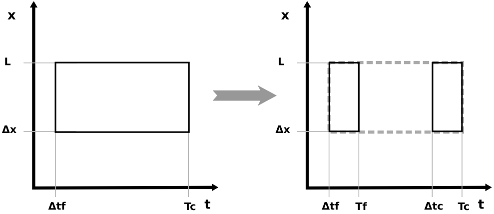
CORAL

```
D := D_init
f := f_init
while not EndCondition
  D := U(D)
  f := B(f)
  f := C(f)
  f := P(f)
  O_i[f]
end
O_f[f]
```

Coral grows due to nutrient brought by water flow



Coupling Speedup : Coral growth



Fluid is computed for

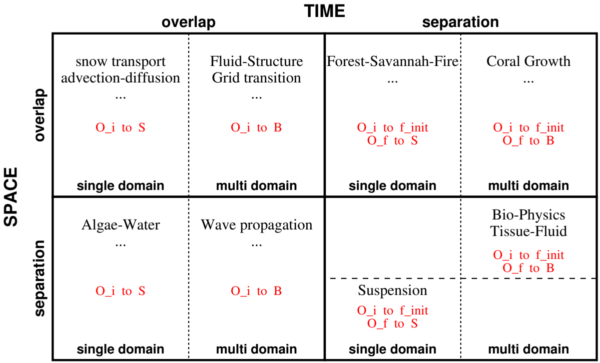
$$\frac{T_f}{\Delta t_f}\frac{T_c}{\Delta t_c} \quad \text{iterations instead of} \quad \frac{T_c}{\Delta t_f}$$

Speedup :

$$S = \frac{\Delta t_c}{T_f} >> 1$$

Classification of problems

- relation in the Scale Separation Map
- single-Domain (sD) or multi-Domain (mD) relation
- coupling templates



Relation between the scales separation and the coupling templates

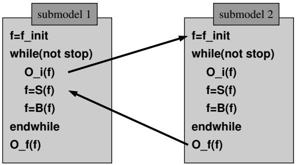
We consider two submodels, X and Y with **single-domain** (sD) relation

name	coupling	temporal scale relation
interact	$O_i^X \rightarrow S^Y$	overlap
call	$O_i^X \rightarrow f_{init}^Y$	X larger than Y
realease	$O_f^Y \rightarrow S^X$	Y smaller than X
dispatch	$O_f^X \rightarrow f_{init}^Y$	any

When the relation between computational domains is **multi-domain**, change $S \rightarrow B$

Thus, the relation in the SSM determines the workflow

CxA Execution Model



- Submodels are autonomous processes
- Asynchronous communication through the conduits :
  - Data is written to the conduit as soon as ready.
  - Submodels read the data they need from the conduits (wait if needed).
- Only local interactions are necessary : parallelization is possible and natural
- Propagation of the termination condition

Send-Receive through the conduits

Example of the Coral submodel :

```
  while not EndConditions
     DomainConduit.send(D)
     f := B(f)
     velocityMap := VelocityConduit.receive()
     f :=  C(f,velocityMap)
     f :=  P(f)
  end
DomainConduit.stop())
myStop()
```

The COAST software environment : MUSCLE

- Jade (Java Agent based lightweight middleware) as a platform to build the coupling software.
- Allows us to couple submodels (and legacy codes in C, Fortran).
- A "Jade coordinator" is used to setup the system then goes away,
- Low overhead.
- Predefined parametrized conduits
- Public release in Jan. 2009 [2]

2. http ://muscle.berlios.de

Can we do math with this approach ?

Mathematical formulation of couplings

CxA operators P and C can be used to express coupling strategies

- Time splitting
- Coarse graining
- Amplification
- ...

and estimate errors

Time splitting

Assume we have a sD problem with the following SEL

$$P_{\Delta t} C_{\Delta t} = P_{\Delta t} C^{(1)}_{\Delta t} C^{(2)}_{\Delta t}$$

Then if $C^{(1)}_{\Delta t}$ acts at a longer time scale than $C^{(2)}_{\Delta t}$ we may want to approximate

$$[P_{\Delta t} C_{\Delta t}]^M \approx P_{M\Delta t} C^{(1)}_{M\Delta t} [C^{(2)}_{\Delta t}]^M$$

Coarse graining

This strategy consists in expressing a sD problem as

$$[P_{\Delta x} C_{\Delta x}]^n \approx \Gamma^{-1} [P_{2\Delta x} C_{2\Delta x}]^{n/2} \Gamma$$

where Γ is a projection operator (implemented in the smart conduit)

Amplification

We consider a process acting at low intensity but for a long time, in a time periodic environment. For instance a growth process in a pulsatile flow.

We have two coupled (mD) processes which are iterated $n >> 1$ times

$$[P^{(1)} C^{(1)}]^n \qquad \text{and} \qquad [P^{(2)} C^{(2)}(k)]^n$$

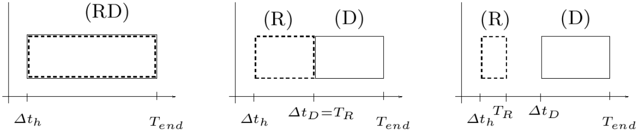
where k expresses the intensity of process $C^{(2)}$.

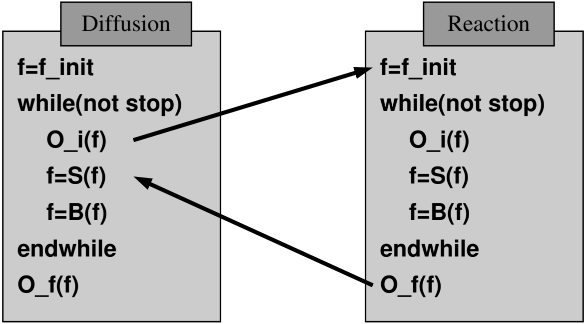
If the period of process $C^{(1)}$ is $m << n$, we can approximate the above evolution as

$$[P^{(1)} C^{(1)}]^m \qquad \text{and} \qquad [P^{(2)} C^{(2)}(k')]^m$$

with $k' = (n/m)k$, for a linear process.

Reaction-Diffusion with time splitting





$$\partial_t \rho = d \partial_{xx} \rho + \kappa(\rho_\lambda - \rho), \tag{1}$$

We assume a fast reaction i.e. $\|\kappa\| \gg \|d\|$ (in some units).

The LB model in CxA language

$$f(t + \Delta t_R) = P[I + D(\tau_R) + R(\kappa)]f(t) \qquad (2)$$

$D(\tau_R)$ the diffusion collision operator at scale Δt_R, $R(\kappa)$ the reaction collision operator, I, the identity and P the propagation. It can be time-split as

$$f(t + \Delta t_D) = P[I + D(\tau_D)][I + R(\kappa)]^{\Delta t_D/\Delta t_R} f(t) \qquad (3)$$

The error E of this time splitting can be computed analytically

A. Caiazzo, J-L. Falcone, B. Chopard and A. G. Hoekstra, *Asymptotic analysis of Complex Automata models for reaction-diffusion systems*, Applied Numerical Mathematics 59 pp. 2023–2034 (2009)

Temporal scales

The time scales are such that

$$\Delta t_R < \tau_R = 1/\kappa << \Delta t_D < \tau_D = 1/(\lambda^2 d)$$

thus, the actual scale separation is

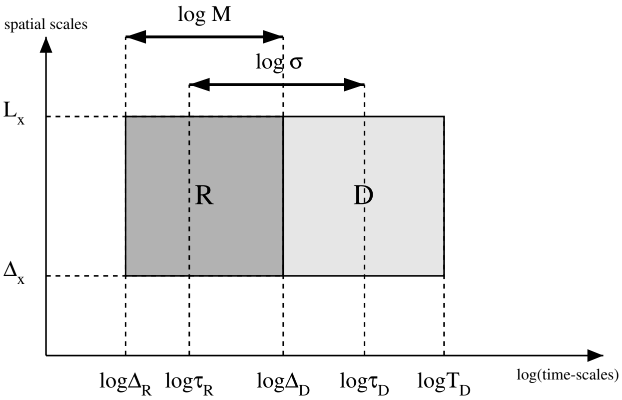
$$\sigma = \frac{\tau_D}{\tau_R} = \frac{\kappa}{\lambda^2 d}$$

whereas, the enforced scale separation is

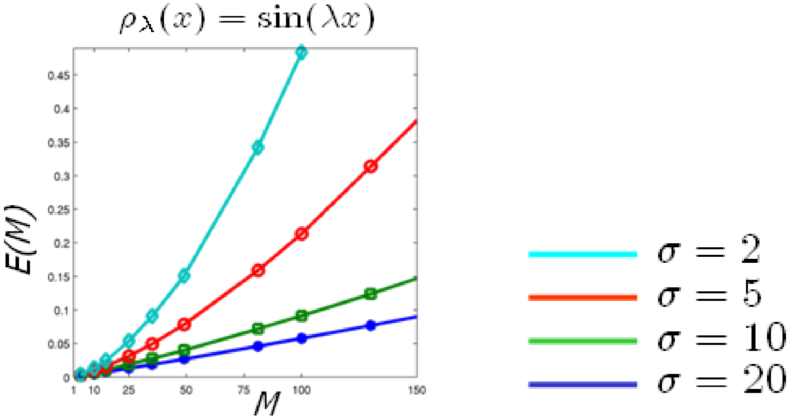
$$M = \frac{\Delta t_D}{\Delta t_R}$$

Scales separation

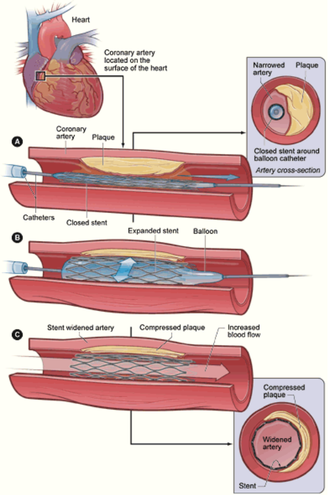
$$\log M = \log \Delta t_D - \log \Delta t_R \qquad \log \sigma = \log \tau_D - \log \tau_r$$



Time-splitting error versus scale separation



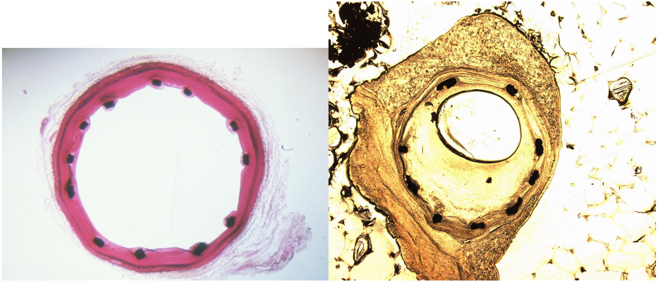
Target application : in-stent restenosis



- Coronary heart disease (CHD) remains the most common cause of death in the UK, being responsible for approximately 105,000 deaths in 2004 (BHF Stats, 2006).
- In 2005, 94% of 70,142 UK procedures involved the deployment of a stent (BCIS Stats, 2006).

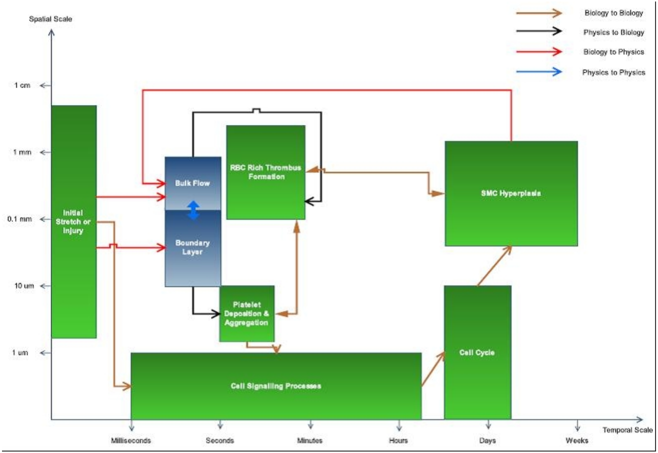
Restenosis

- After inserting the stent in the vessel, injuries cause the incontrolled growth of neo-intimal cells (hyperplasia).
- Restenosis occurs in 5-10% of patients following procedures involving stent deployment.



- Blood flow (wall shear stress) affects the growth rate
- Drug eluting stents can help !

Restenosis : the full Scale Separation Map



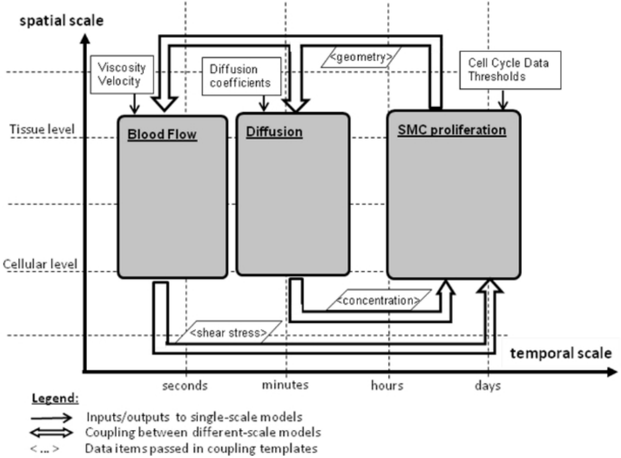
Restenosis : Single-scale submodels

- Injury score : initial conditions of the vessel wall
- Blood flow (BF) : lattice Boltzmann model
- Smooth muscle cells (SMC) : continuous particle model
- Drug diffusion (DD) : finite difference scheme

D Evans, PV Lawford, J Gunn, D Walker, DR Hose, RH Smallwood, B Chopard, M Krafczyk, J Bernsdorf, A Hoekstra. *The Application of Multi-Scale Modelling to the Process of Development and Prevention of Stenosis in a Stented Coronary Artery.* **Phil. Trans. R. Soc. A** 366, pp. 3343–3360, 2008

Restenosis : Scale Separation Map

- A 3-submodel simplification (time separation is achieved)



Wrapping things together in the software environement

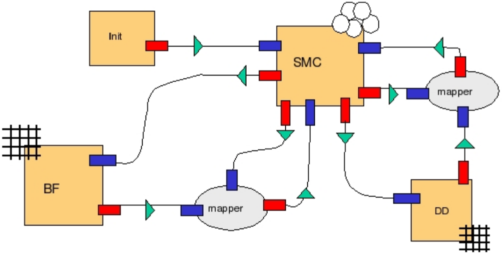
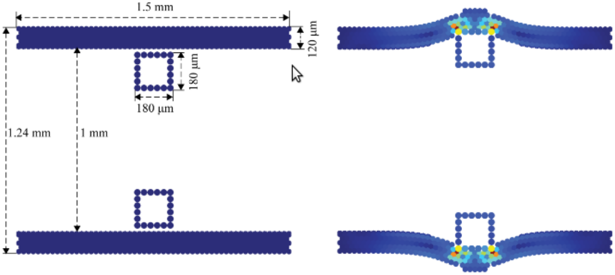


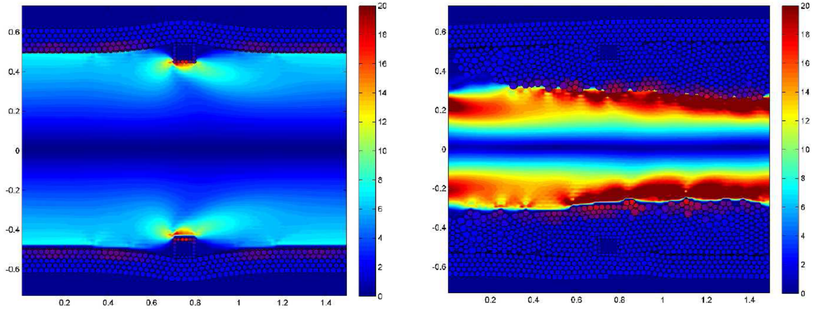
Figure 16: Example of Connection Scheme for a CxA coupling BF, SMC and DD (see technical deliverable 3.2). For each single scale model, it is indicated whether it is based on a lattice or on agent. Mappers are used to map different inputs onto the time dependent domain of cells.

Note : mappers are a way to define conduits with more than one input or more than one output.

Stent deployment and injury

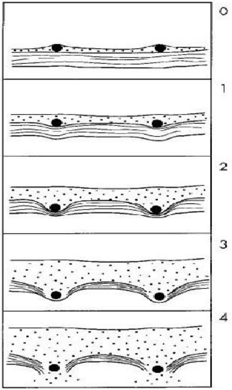


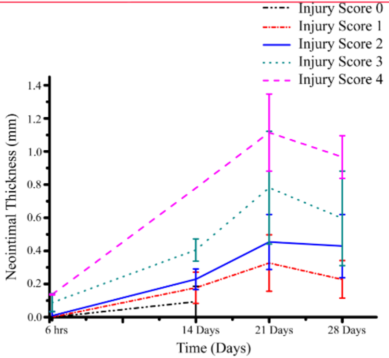
Resulting Growth of SMC from the stent



The CxA approach has been able to couple three different bio-physical processes.

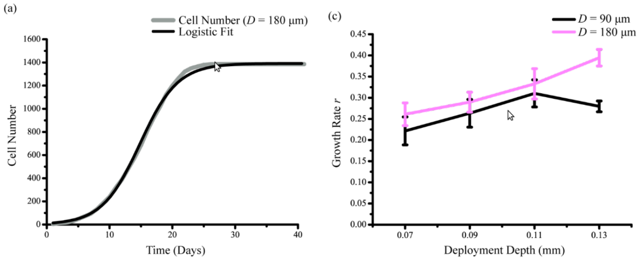
Validation : Gunn's injury score





1. No impression of metal upon media
2. Small deformation of the elastic lamina.
3. Big deformation of the elastic lamina.
4. Rupture of the internal elastic lamina
5. Rupture of the external elastic lamina

Measurements of the growth in the simulation



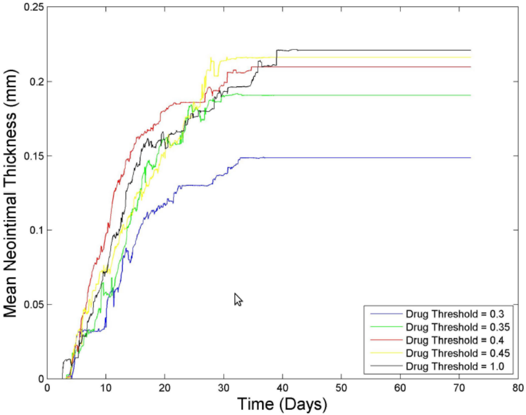
$$\frac{dN}{dt} = rN\left(1 - \frac{N}{N_{max}}\right)$$

where $N(t)$ is the no of smooth muscle cells in the artery

Multiscale simulations of the dynamics of in-stent restenosis : impact of stent deployment and design, Hannan Tahir, Alfons G. Hoekstra, Eric Lorenz, Patricia V Lawford, D. Rodney Hose, Julian Gunn, David JW. Evans, submitted to J. R. Soc. Interface, 2011

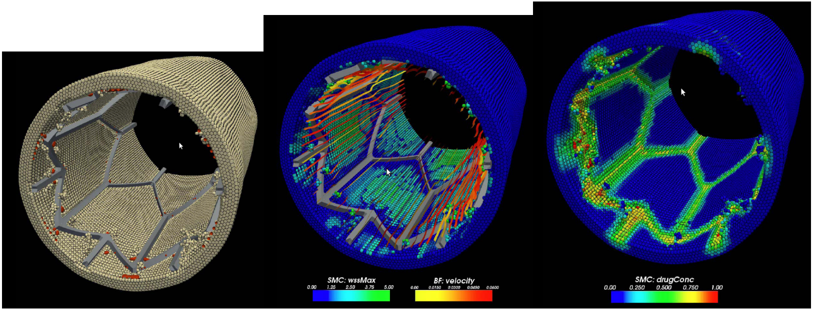
(MeDDica project)

Effect of drug eluting stents (2D)



A. Caiazzo, D. Evans, J.-L. Falcone, J. Hegewald, E. Lorenz, B. Stahl, D. Wang, J. Bernsdorf, B. Chopard, J. Gunn, R. Hose, M. Krafczyk, P. Lawford, R. Smallwood, D. Walker, A. Hoekstra, *A Complex Automata approach for In-stent Restenosis : two-dimensional multiscale modeling and simulations*, J. of Comp. Sciences, in press, 2010.

3D model


SMC: wssMax
0.00 1.25 2.50 3.75 5.00
BF: velocity
SMC: drugConc
0.00 0.250 0.500 0.750 1.00

MML : a Multiscale Modeling Language

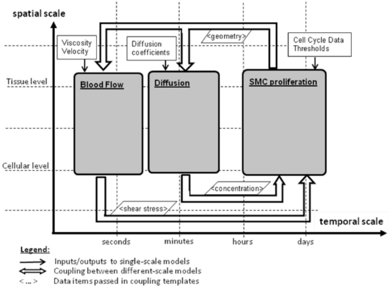
- the SSM turned out to be very powerful to design applications
- Formalize the CxA ideas into a language : high level representation of a complex multiscale application
- Allows scientists with different backgrounds and geographical locations to better co-develop a multiscale application
- Provide blueprints of a complex multiscale application that can be further augmented by other groups
- Standard for publication

J-L Falcone, B. Chopard and A. Hoekstra, MML : towards a Multiscale Modeling Language,

Procedia Computer Science 1 :11, 819-826, 2010

Main ingredients

- Sub-models
- Spatial and temporal scales
- Computational domain relation
- Coupling templates
- Conduits



We want to represent these features on a **descriptive language**

xMML

- XML-like language
- Easy grammar for the user
- Full description language
- From application description to "glue-code" production and scheduling

xMML example

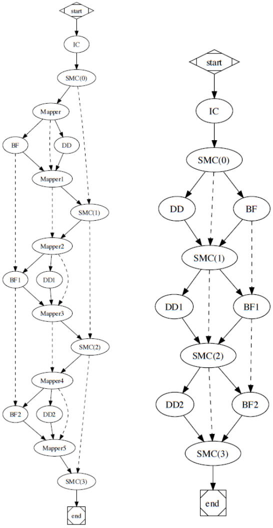
```
<model id="suspensionFlow">
  <description>
    Flow with a suspension of particles. The conentration
    of particles affect locally the flow viscosity and the
    particles are advected by the flow.
  </description>
  <submodel id="flow">
    <spacescale dimension="2" dx="1 mm" lx="10 cm" ly="30 cm" />
    <spacescale dt="1 ms" t="1 min" />
    <ports>
      <in id="concentration" operator="C" dt="1 ms" dx="1 mm" />
      <out id="velocity" operator="Oi" dt="10 ms" dx="1 mm" />
    </ports>
  </submodel>
```

xMML example continued

```
  <submodel id="advectionDiffusion">
    <spacescale dimension="2" dx="1 mm" lx="10 cm" ly="30 cm" />
    <spacescale dt="10 ms" t="1 min" />
    <ports>
      <in id="velocity" operator="C" dt="10 ms" dx="1 mm" />
      <out id="concentration" operator="Oi" dt="10 ms" dx="1 mm" />
    </ports>
  </submodel>

  <coupling from="flow.velocity" to="advectionDiffusion.velocity" />
  <coupling from="advectionDiffusion.concentration" to="flow.concentration">
    <filter kind="timeInterpolation" />
  </coupling>
</model>
```

Execution graph



(a) Complete data flow (b) Simplified data flow

Multiscale APPlications on European e-infRastructures

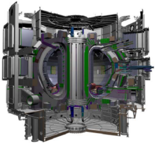
From applications → MML → computing infrastructure

- Running tightly coupled **Distributed Multiscale Applications** using several supercomputing platforms
- Deploy middleware implementing the CxA-MML-MUSCLE approach on the e-Infrastructure (EGI, PRACE, DEISA)

http ://www.mapper-project.eu

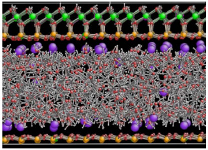
Application portfolio

virtual physiological human

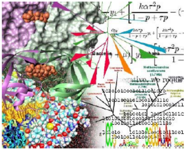


fusion

hydrology



nano material science



computational biology

- Participants : UvA NL, UCL UK, UU UK, PSNC PL, CYFRONET PL, LMU DE, UNIGE CH, CHALMERS SE, MPG DE