Modelling of metastatic growth and *in vivo* imaging

Niklas Hartung

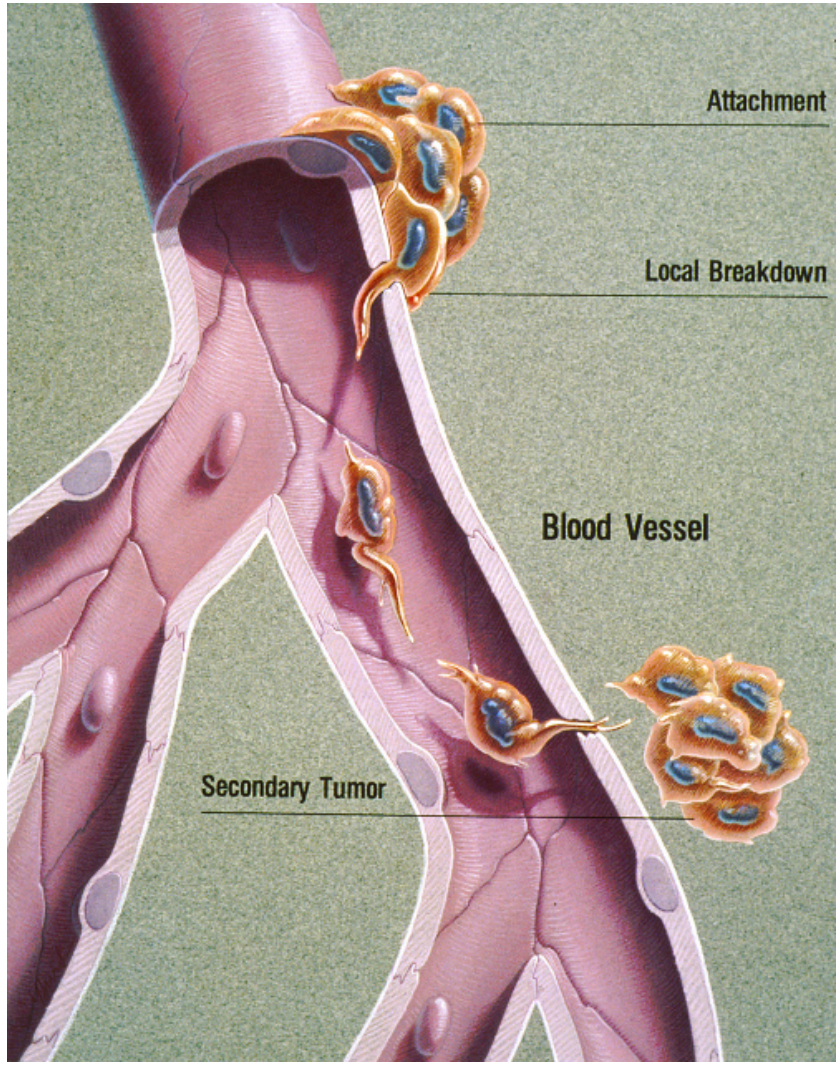
Present challenges of mathematics in oncology and biology of cancer

08/12/2015, CIRM, Marseille, France

Cancer and metastasis

Cancer

- leading cause of death in occidental countries
- major problem: **metastasis**
  - secondary tumours at different locations
  - very agressive
  - responsible for 90% of cancer-related deaths



METASTATIC PROCESS

Clinical importance of metastasis

Pivotal point in cancer history

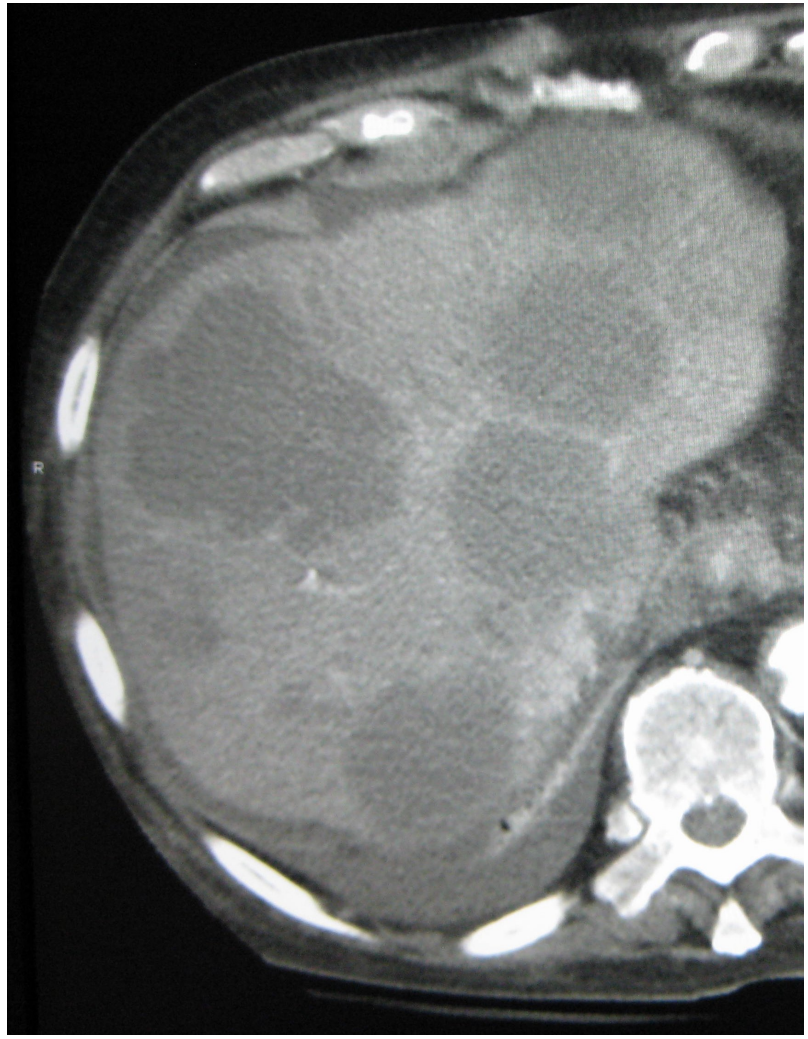
- radical change of prognosis
- treatment decisions based on metastatic state

Occult metastasis

- only metastases $> 10^7$ cells visible on imaging
- administer toxic treatment to patient without visible metastases?

Important clinical problem

Estimate the metastatic risk of patients without visible metastases



CT SCAN OF METASTATIC LIVER

Modelling of metastasis

Aim (long-term)

Develop a mathematical model usable as a **clinical tool**

- to estimate the micrometastatic state at diagnosis
- to evaluate the risk of recurrence after treatment

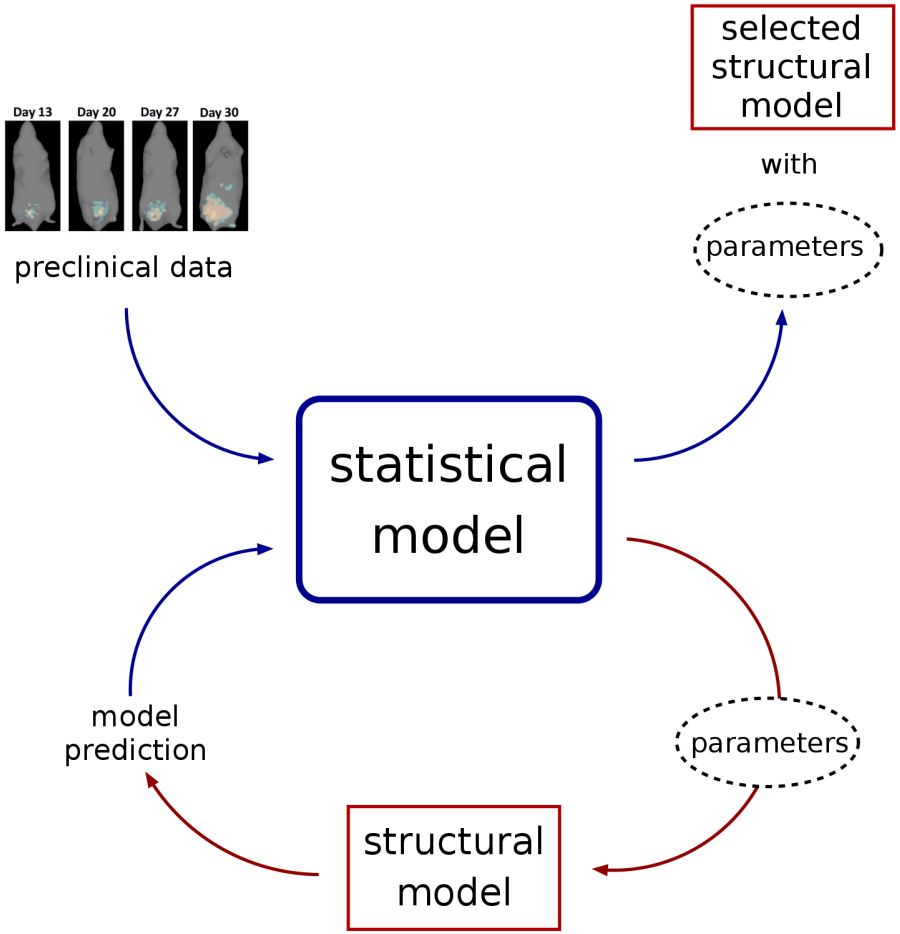
Validation step (aim of this talk)

Confront a mathematical model for metastasis to data without treatment from preclinical experiments

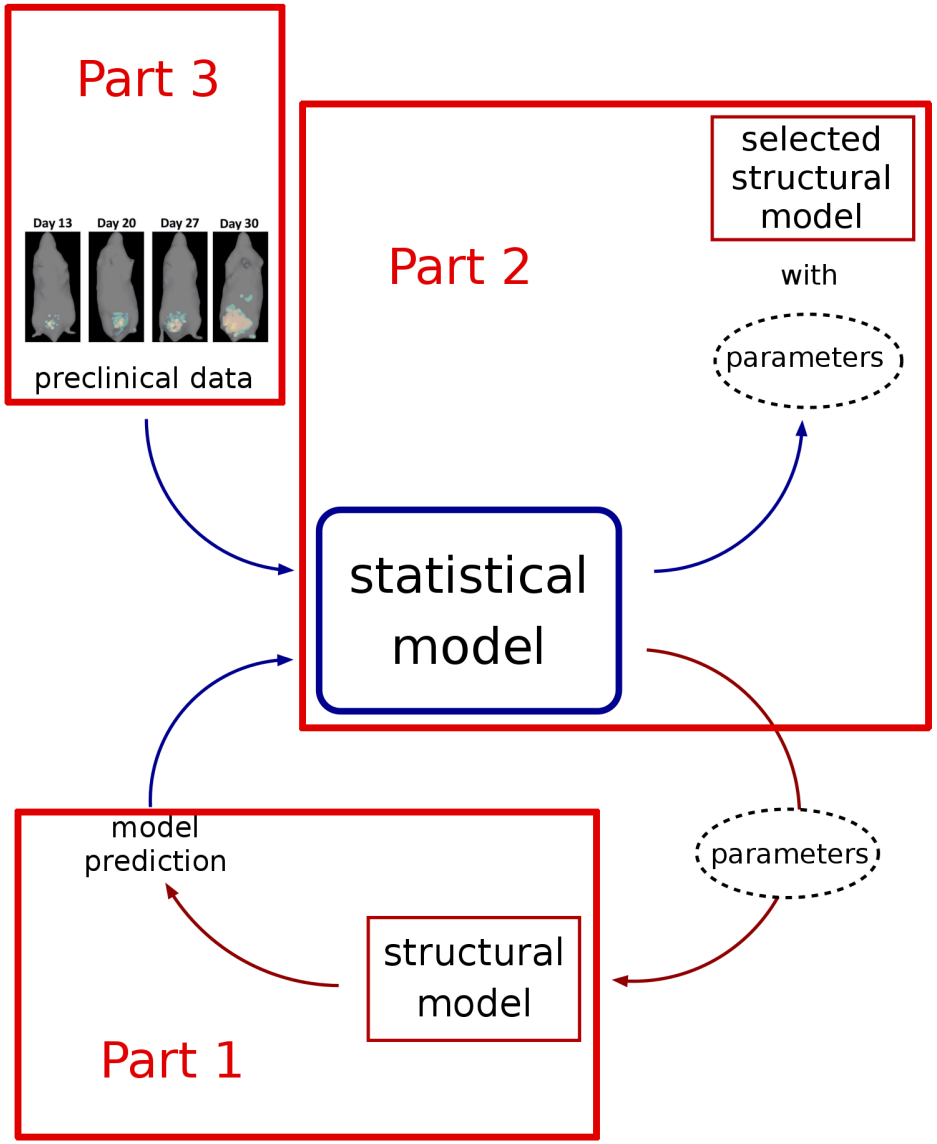
Funding:

ANR MEMOREX-PK (ANR-09-BLAN-0217-01)
INSERM (Plan Cancer no. 201107, 2011-2013)

Necessary steps



Necessary steps



Structure

Part 1:
Modelling of metastatic growth

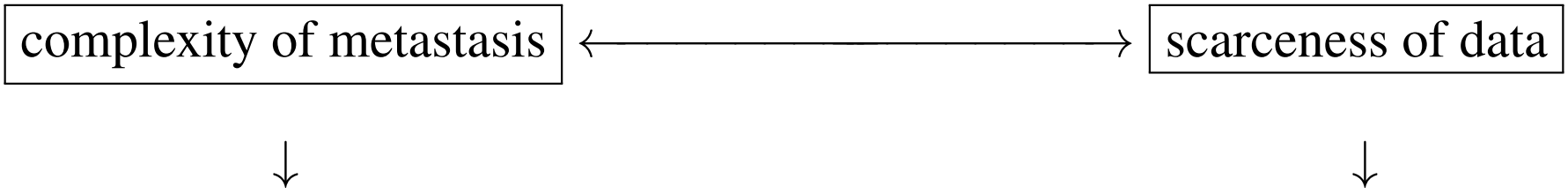
Part 2:
Confrontation to preclinical data

Part 3:
Tumour boundary reconstruction

PART 1

MODELLING OF METASTATIC GROWTH

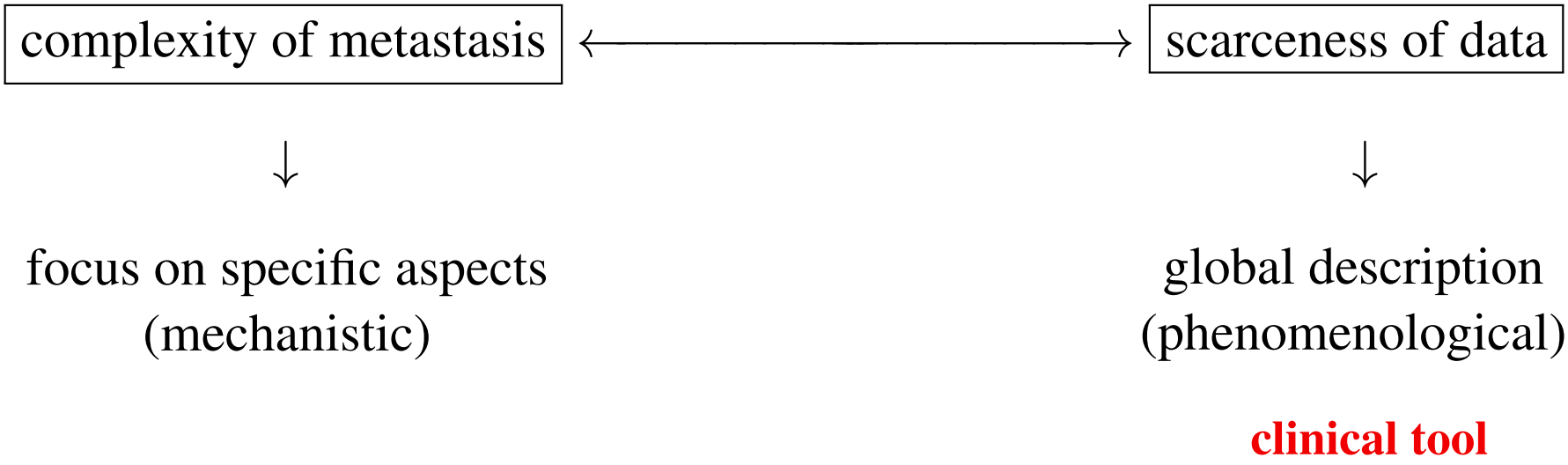
Modelling metastasis



Global description: kinetic models

- compartmental model — 🕮 **Liotta *et al.* (1970s)**
- structured population equation — 🕮 **Iwata *et al.* (2000)**
- Poisson process — 🕮 **Hanin *et al.* (2000s)**

Modelling metastasis



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Structured population equations

🕮 Metz & Diekmann (1986)

🕮 Perthame (2007)

Basic idea

- time evolution of a population of individuals
- individuals characterised by a state variable

Examples

- age pyramid
- size distribution of cells

Type of equation

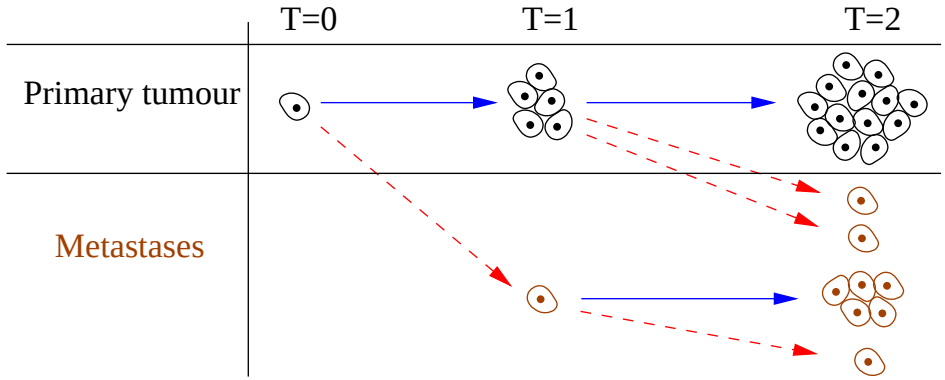
- transport in state space
- main object: density function

Size-structured metastatic model

📖 **Iwata *et al.* (2000)**

Primary tumour growth

$$x_p(t)' = g(x_p(t))$$
$$x_p(0) = 1$$



Metastatic growth

$$\partial_t \rho(x,t) + \partial_x \Big(g(x)\rho(x,t) \Big) = 0$$

Metastatic emission

$$g(1)\rho(1,t) = \beta\big(x_p(t)\big) + \int_1^b \beta(x)\rho(x,t)dx$$

No metastases at time zero

$$\rho(\cdot, 0) \equiv 0$$

Iwata parametrisation

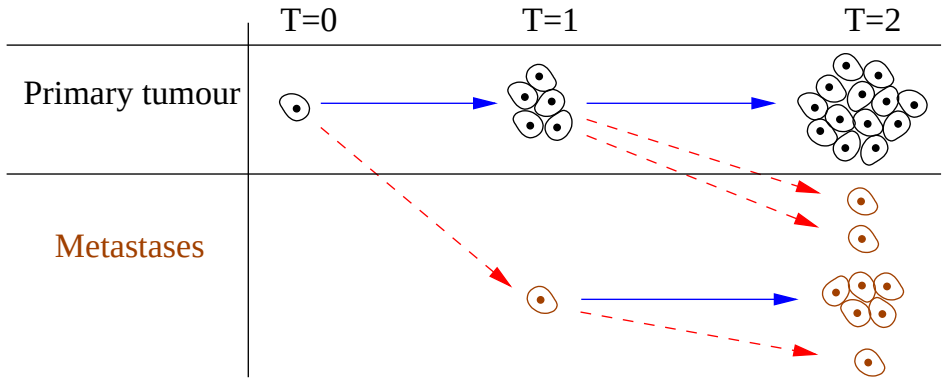
$(\longrightarrow)$ Growth: $g(x) = ax\log(b/x)$

$(\dashrightarrow)$ Emission: $\beta(x) = \mu x^{\alpha}$

Size-structured metastatic model

Primary tumour growth

$$x_p(t)' = g_p(x_p(t))$$
$$x_p(0) = x_0$$



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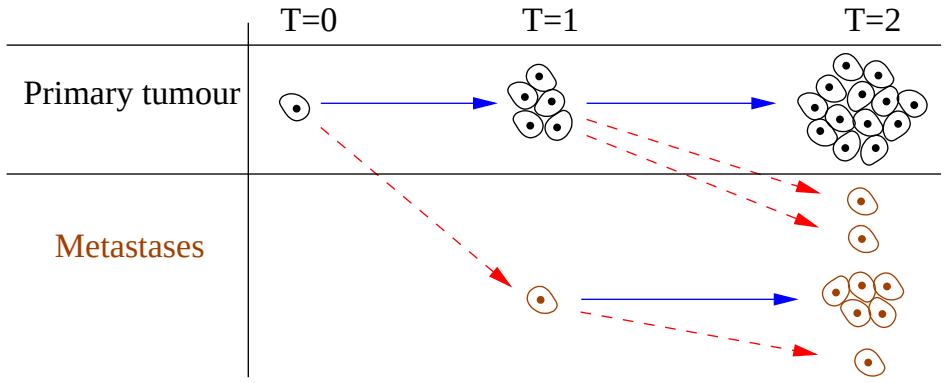
Generalisation

Growth and emission at distinct rates for primary tumour and metastases

Size-structured metastatic model



Metastatic growth

$$\partial_t \rho(x,t) + \partial_x \Big(g(x)\rho(x,t) \Big) = 0$$

Metastatic emission

$$g(1)\rho(1,t) = S(t) + \int_1^b \beta(x)\rho(x,t)dx$$

No metastases at time zero

$$\rho(\cdot,0) \equiv 0$$

Generalisation

Growth and emission at distinct rates for primary tumour and metastases

Model observables

$$\partial_t \rho(x,t) + \partial_x \Big(g(x)\rho(x,t) \Big) = 0$$

$$g(1)\rho(1,t) = S(t) + \int_1^b \beta(x)\rho(x,t)dx$$

$$\rho(\cdot,0) \equiv 0$$

Metastatic density ρ
not observed

$\hookrightarrow$ instead: **weighted integrals of the density function**

- Number of metastases

$$N(t) = \int_1^b \rho(x,t)dx$$

- Metastatic burden

$$M(t) = \int_1^b x\rho(x,t)dx$$

$\Rightarrow$

Model observable:

$$F_f(t) := \int_1^b f(x)\rho(x,t)dx$$

Confrontation to data

Data from clinical cases

	🕮 Iwata *et al.* (2000)	🕮 Barbolosi *et al.* (2011) 🕮 PhD thesis Verga (2010)
cohort of patients	X	✓
distant metastases	X	✓
longitudinal data	✓	X
parameter estimation	✓	X

Missing

Parameter estimation for

- cohort with longitudinal data
- including distant metastatic sites

$\Rightarrow$ **preclinical setting**

Numerical resolution of metastatic model

Schemes for hyperbolic PDE

- Problem: large scale differences
  - New metastasis: 1 cell
  - Late metastasis: 10^9 cells
- Upwind scheme $\Rightarrow$ **bad performance**
- WENO5 scheme $\Rightarrow$ **high computational cost** 🕮 **Devys *et al.* (2009)**

Semi-Lagrangian scheme 🕮 **Angulo *et al.* (1999)**

- tailored to transport equation 🕮 **Barbolosi *et al.* (2009)**

🕮 **PhD thesis F. Verga (2010)**

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New resolution method 🕮 **NH (2014)**

- based on model reformulation
- reduced computational complexity
- improved numerical quadrature

PDE and Volterra formulations

PDE model

$$\partial_t \rho(x,t) + \partial_x \Big(g(x)\rho(x,t) \Big) = 0$$

$$g(1)\rho(1,t) = S(t) + \int_1^b \beta(x)\rho(x,t)dx$$

$$\rho(\cdot,0) \equiv 0$$

Quantity of interest

$$F_f(t) = \int_1^b f(x)\rho(x,t)dx$$

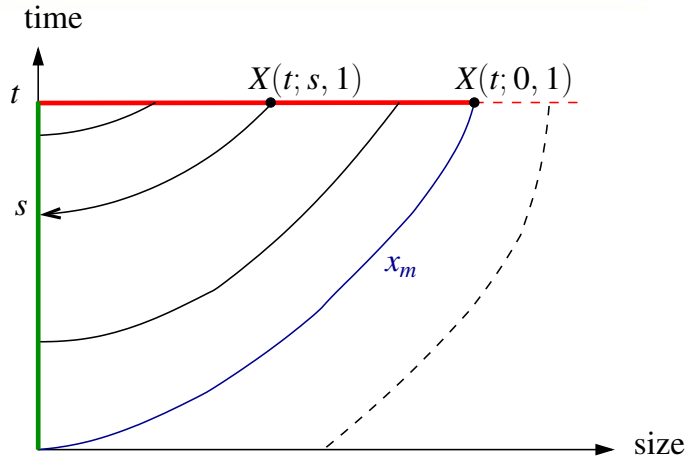
Volterra convolution equation

$$F_f(t) = \underbrace{\int_0^t f\Big(x_m(t-s)\Big)S(s)ds}_{\text{primary tumour contribution}} + \underbrace{\int_0^t \beta\Big(x_m(t-s)\Big)F_f(s)ds}_{\text{metastatic contribution}}$$

- x_m: particular characteristic curve
- convolution notation: $F_f(t) = f(x_m) * S(t) + \beta(x_m) * F_f$

Sketch of model reformulation

Start from observable $F_f(t) = \int_1^b f(x)\rho(x,t)dx$



1. straighten the characteristics

- change of variables $x = X(t; s, 1)$
- conservation relation along characteristics

$$\Rightarrow \rho(x,t)dx = g(1,s)\rho(1,s)ds \overset{BC}{=} \big(S(s) + F_\beta(s)\big)ds$$

2. key relation

$$F_f(t) = \int_0^t f\big(X(t;s,1)\big)\big(S(s) + F_\beta(s)\big)ds$$

- autonomous growth: $X(t;s,1) = x_m(t-s)$
- convolution equation for $f = \beta$: $\quad F_\beta = \beta(x_m) * \big(S + F_\beta\big)$

3. generalisation for arbitrary f

- inject convolution equation for $f = \beta$ into key relation

$$\begin{aligned} F_f &= f(x_m) * \big(S + \beta(x_m) * (S + F_\beta)\big) \\ &= f(x_m) * S + \beta(x_m) * F_f \end{aligned}$$

Comment on proof technique

Classical argument — 🕮 **Metz & Diekmann (1986)**

- Volterra equation established for *birth rate* $g(1)\rho(1,t)$
- extension by integration

} regularity of ρ needed

Alternative argument — 🕮 **NH (2014)**

- Volterra equation established for $\int \beta(x)\rho(x,t)dx$
- extension by associativity of convolution

} regularity of ρ not needed

Importance

ρ is weak solution

Numerical resolution of Volterra equations

$$y(t) = h(t) + \underbrace{\int_0^t k(t-s)y(s)ds}_{k*y(t)}$$

Rich literature

- extended Runge-Kutta schemes
- FFT-based convolution computation

Here: two strategies explored

1. resolution of full model

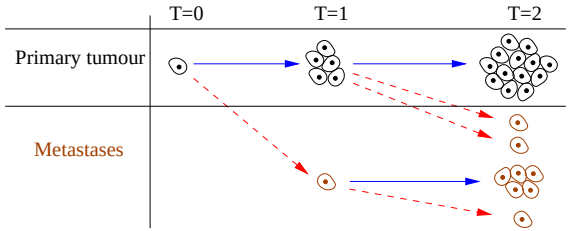
📖 **Hairer *et al.* (1985)**

$$y_n = h(t_n) + \Delta t \sum_{j=0}^{n-1} k(t_{n-j})y_j$$

- direct computation: $\mathcal{O}(n^2)$ **complexity**
- FFT-based: $\mathcal{O}(n\log(n)^2)$ **complexity**

2. generational approximation

📖 **Feller (1941)**



$$\text{PT} \xrightarrow{\text{emits}} \text{M(gen 1)} \xrightarrow{\text{emits}} \text{M(gen 2)} \longrightarrow \cdots$$

fixed number of generations: $\mathcal{O}(n\log(n))$ **complexity**

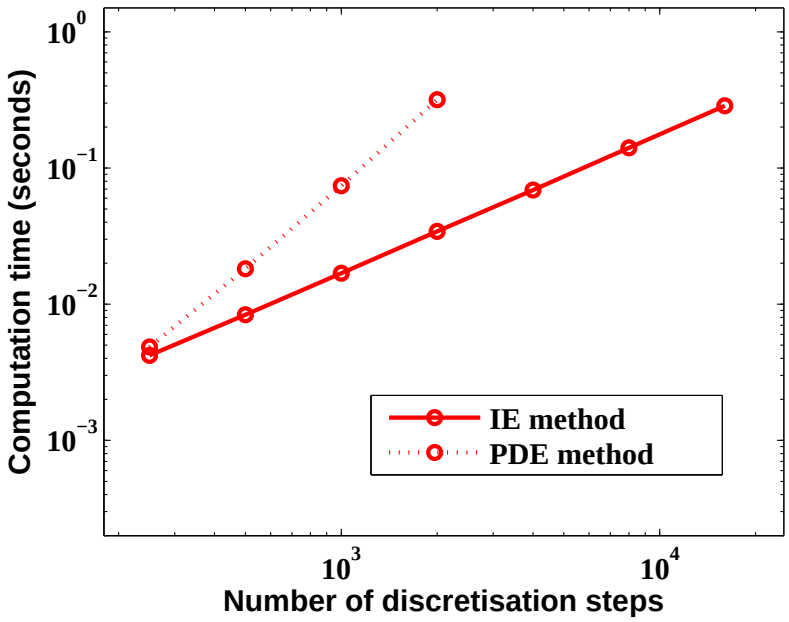
Volterra-based schemes: performance

For both Volterra-based schemes:

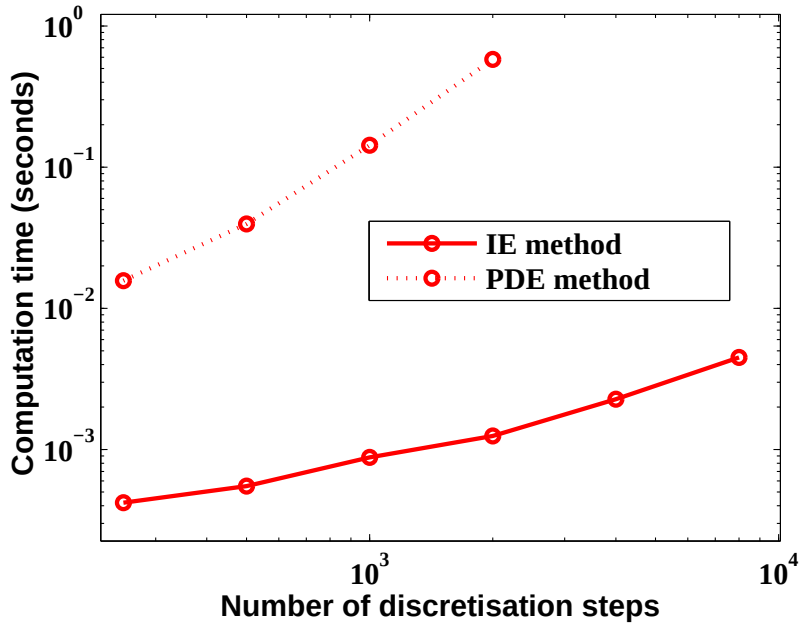
📖 **NH (2014)**

1. structural reduction through FFT

FULL MODEL



TWO GENERATIONS



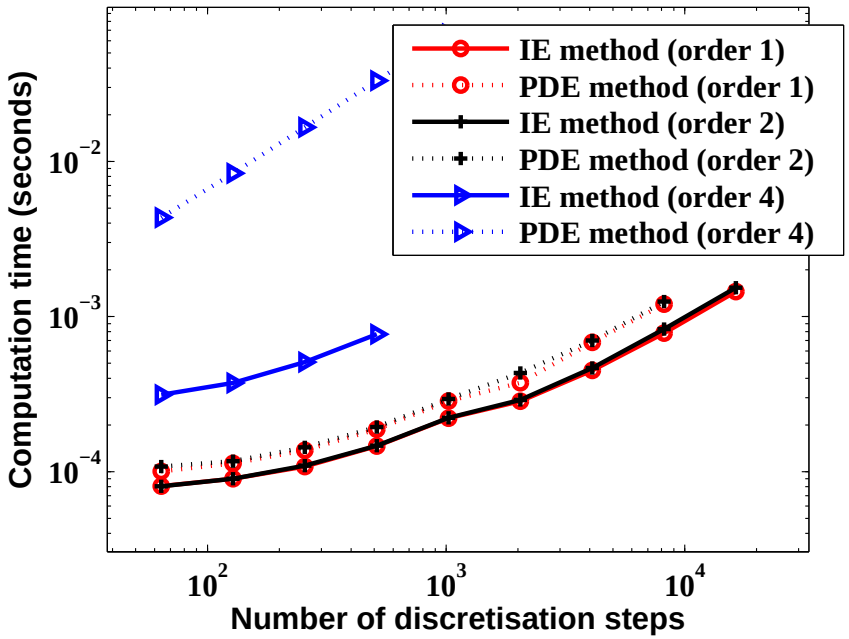
Volterra-based schemes: performance

For both Volterra-based schemes:

📖 **NH (2014)**

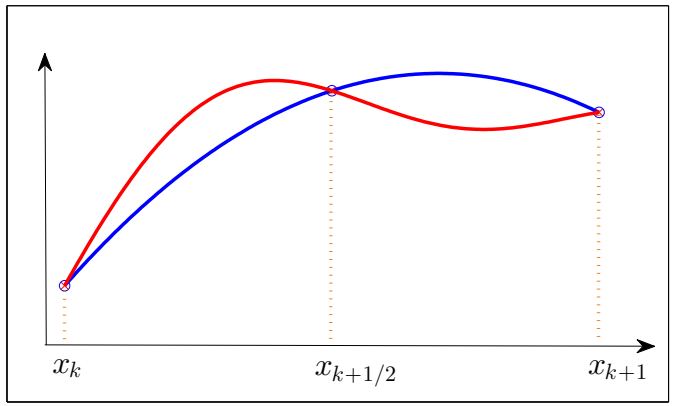
1. structural reduction through FFT
2. better high-order methods (extended RK / Newton-Cotes)

ONE GENERATION



Simpson's rule

- IE method: ✓
- PDE method: → not possible



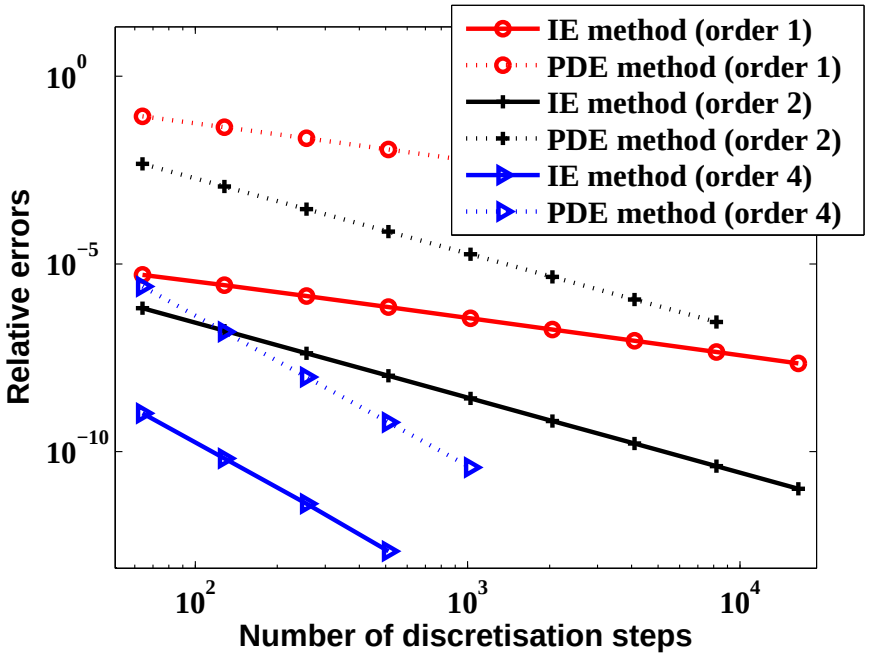
Volterra-based schemes: performance

For both Volterra-based schemes:

🕮 **NH (2014)**

1. structural reduction through FFT
2. better high-order methods (extended RK / Newton-Cotes)
3. better error constants than PDE-based scheme

ONE GENERATION



?

Explanation for improvement of error constants

First-order methods,
no secondary emission

$$M_{IE}(t_n) = \Delta t \sum_{j=1}^{n} x_j S(t_{n-1})$$

$$M_{PDE}(t_n) = \sum_{j=1}^{n} (x_j - x_{j-1}) \frac{x_j}{g(x_j)} S(t_{n-1})$$

Explanation

Semi-Lagrangian scheme

- Conservation relation continuous
- Discretisation of size space

} term $\frac{x_m(t_j) - x_m(t_{j-1})}{\Delta t} \cdot \frac{1}{x'_m(t_j)}$ left

Volterra-based scheme

- Conservation relation continuous
- Change of variables
- Discretisation of time space

} terms disappear

Conclusion of Part 1

Conclusion

- new numerical resolution method developed
- faster and more precise than methods reported in the literature

Related results

- reformulation generalised to 2D structuring variable
- structural identifiability

↪ Hartung, N. *Efficient Resolution of Metastatic Tumour Growth Models by Reformulation into Integral Equations*, **Discrete and Continuous Dynamical Systems – Series B**, 2014.

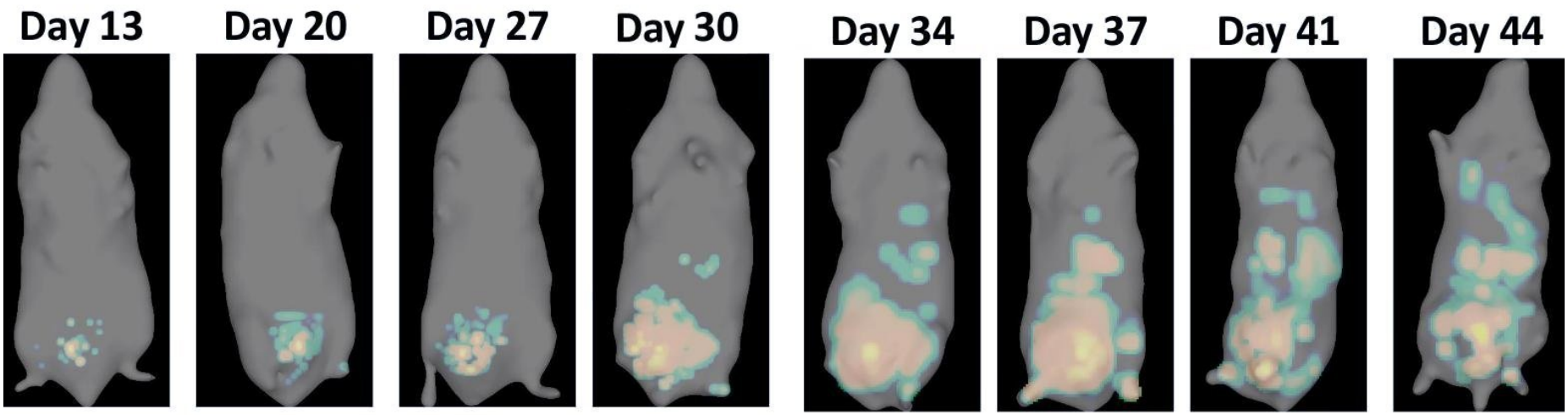
Perspective

- implementation for non-autonomous growth rate $g(t,x)$

PART 2

CONFRONTATION TO PRECLINICAL DATA

Experimental data



Population

- a cohort of 16 mice
- immunosuppressed

Tumour cells

- human breast cancer cell line
- bioluminescent

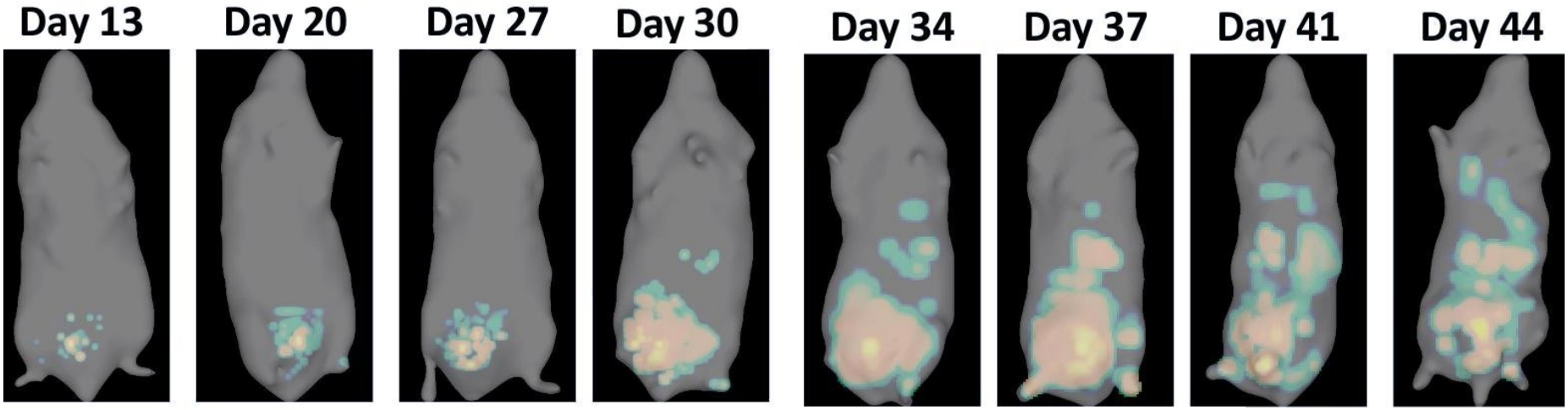
Imaging

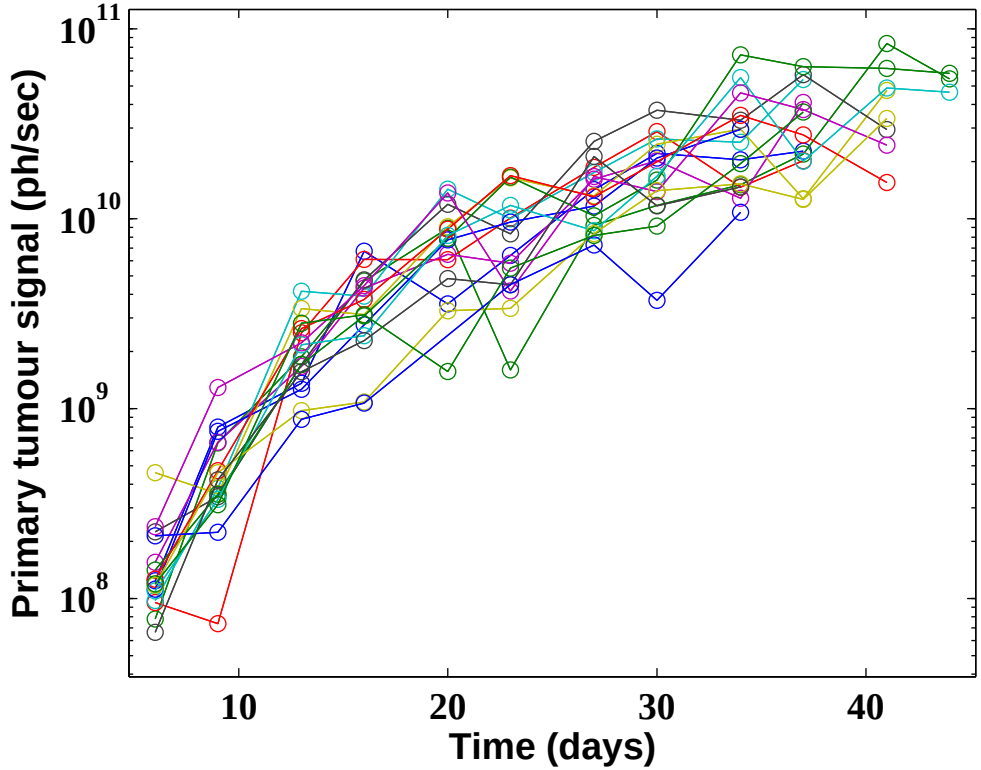
- 3D bioluminescence tomography
  $\Rightarrow$ *in vivo* following

Longitudinal data

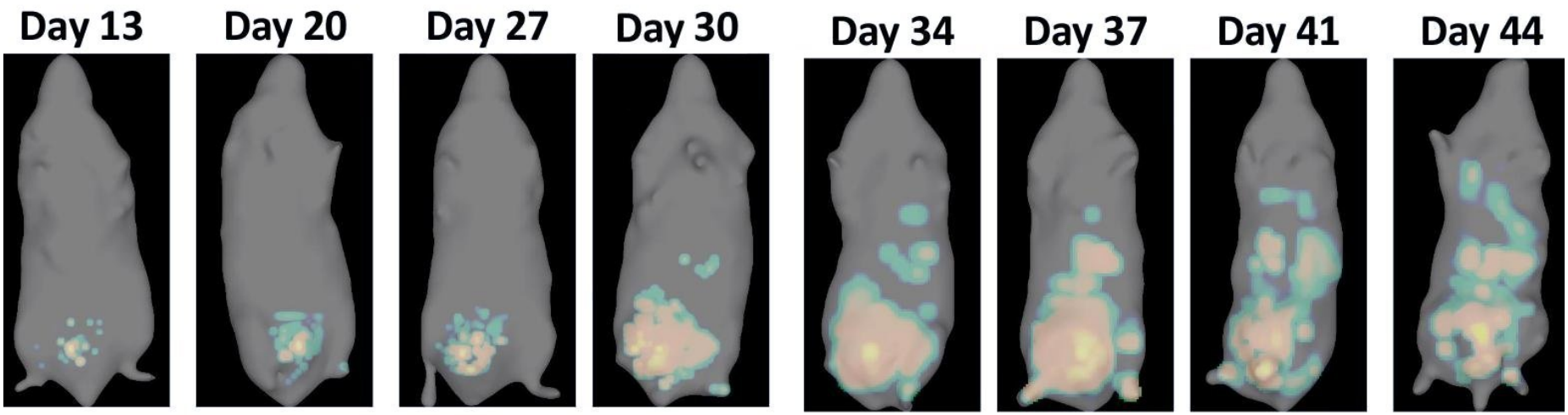
- primary tumour
- metastases

Experimental data





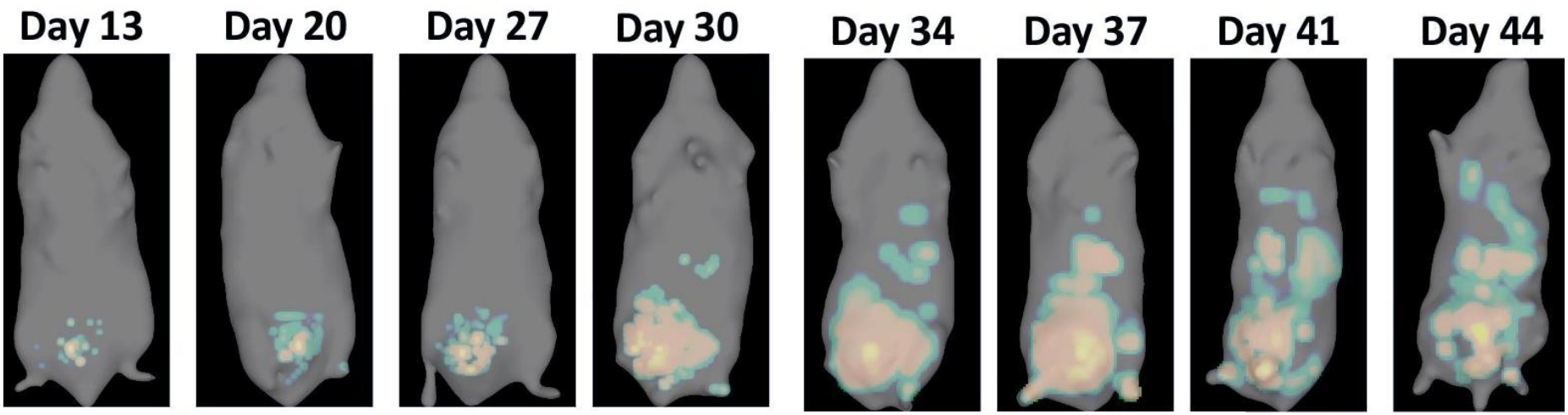
Experimental data

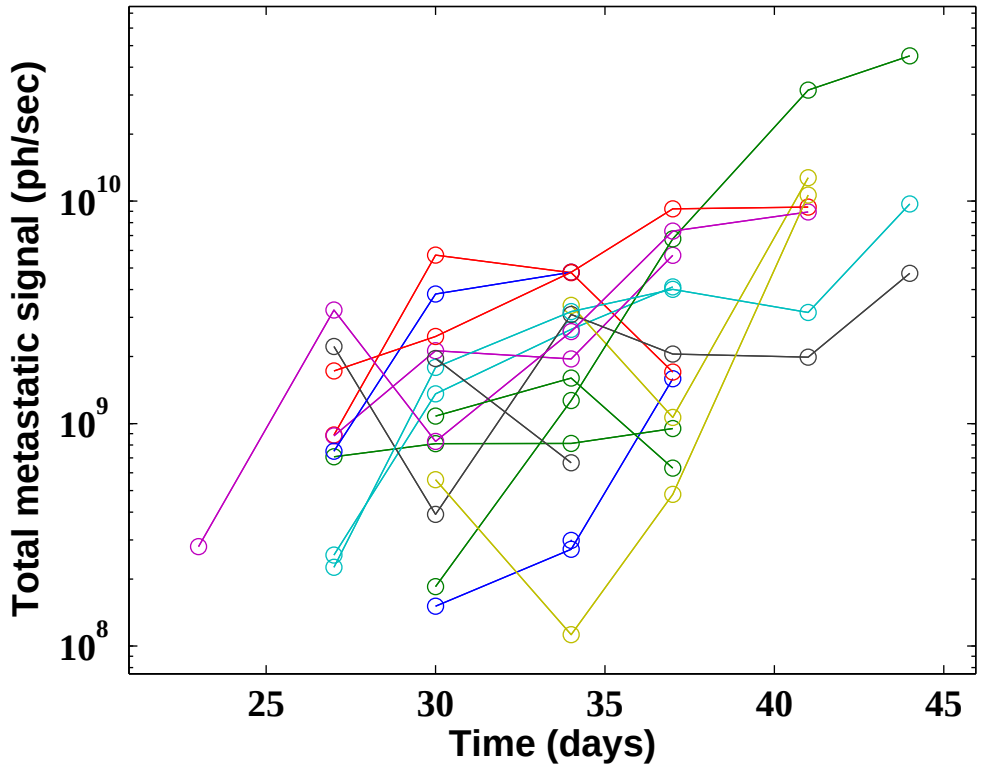


Which information on the metastases can be modelled?

- Number of metastases? $\longrightarrow$ not consistent
- Site-specific metastatic burden? $\longrightarrow$ few data for most sites
- Global metastatic burden? $\longrightarrow$ simplified, but robust

Experimental data

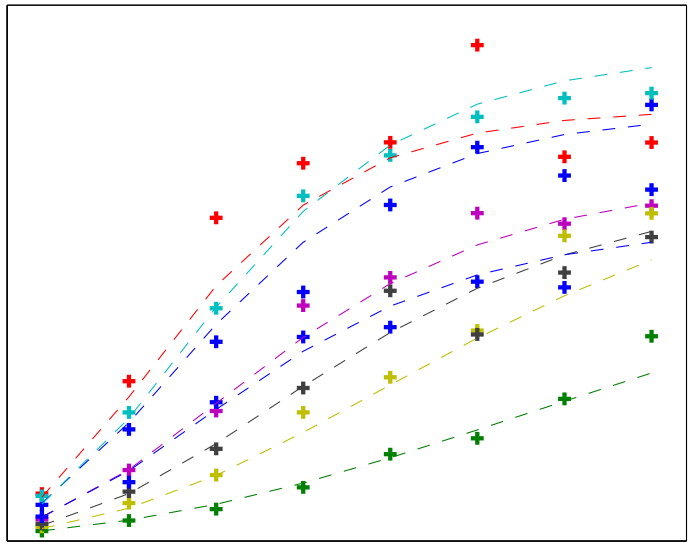


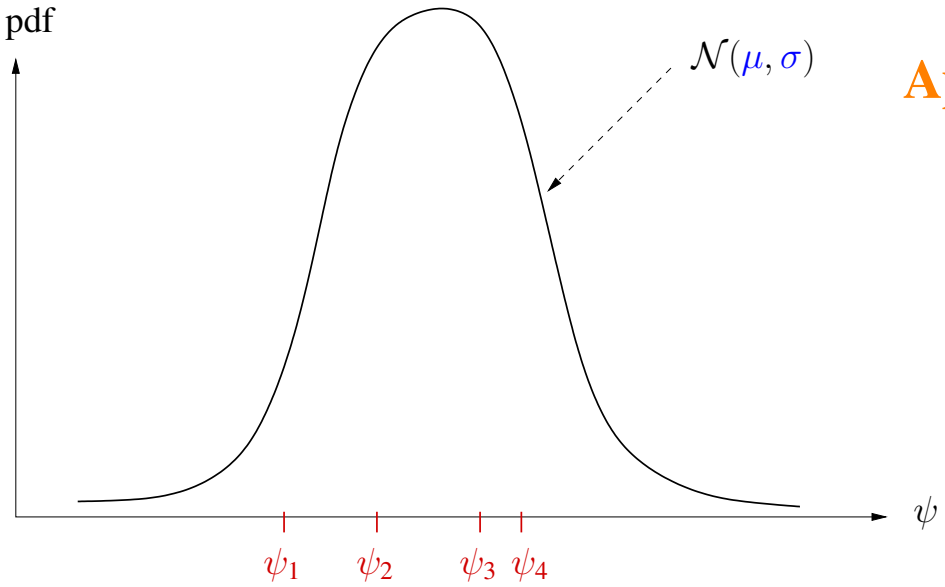


Statistical framework: mixed-effects modelling

Inter-individual variability

- common structural model $f(t, \psi)$
- different parameters ψ_i for each individual





Applicable to sparse data

- each ψ_i is a random variable with parametrised distribution $p(\psi; \theta)$
- population parameters θ: estimated
- individual parameters ψ: not estimated

Maximum likelihood estimation

Classical approach

- complete data likelihood

$$L(\psi) = p(y|\psi) \quad \Rightarrow \hat{\psi} = \arg\max L$$

Mixed-effects models

- marginalised likelihood

$$L(\theta) = \int p(y|\psi)p(\psi|\theta)d\psi \quad \Rightarrow \hat{\theta} = \arg\max L$$

- model selection criterion: $AIC = -2\log(L(\hat{\theta})) + 2K$
  - K: number of statistical parameters

- *Monolix* software

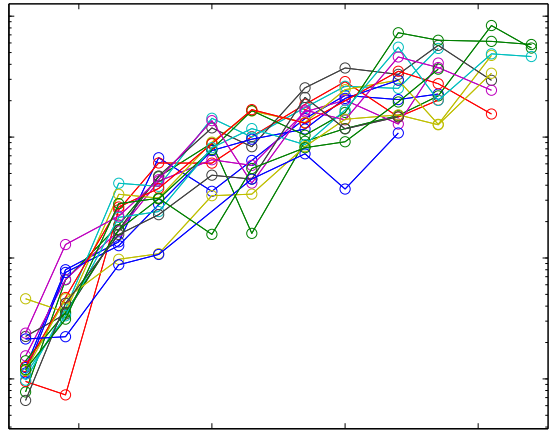
  🕮 **Lavielle *et al.* (INRIA Popix)**

  - requires many model runs
  - ok for simple models (e.g., ODE)
  - problem with complex models (e.g., PDE)

Classical tumour growth models

Phenomenologic models

- empirical laws for macroscopic growth



PRIMARY TUMOUR DATA

Models	growth law $g(x)$	AIC
Exponential	ax	387.1
Power growth	ax^{γ}	318.2
Logistic	$ax(1-x/K)$	303.1
Bertalanffy	$ax^{2/3}-bx$	263.2
Gompertz	$ax\log(K/x)$	262.0
West	$ax^{3/4}-bx$	258.8

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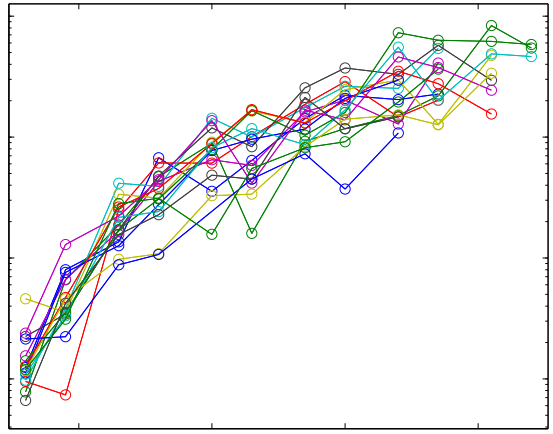

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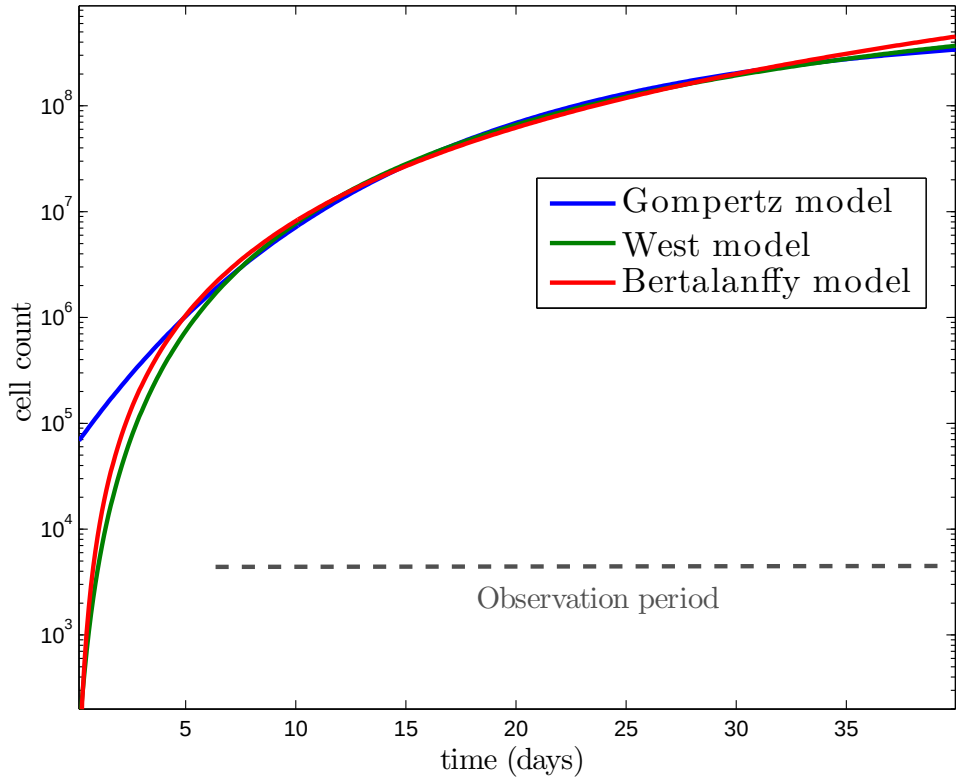
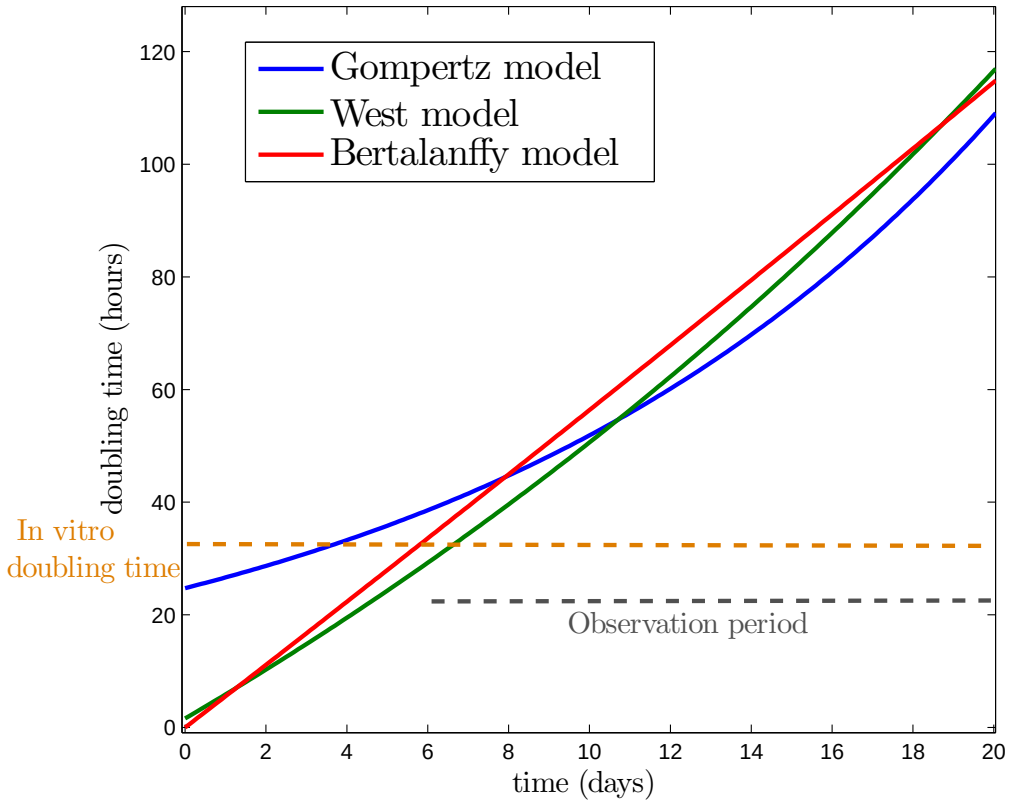
Extrapolation: initial tumour size



- Close agreement within observation period
- Different extrapolation behaviour

Extrapolation: doubling time



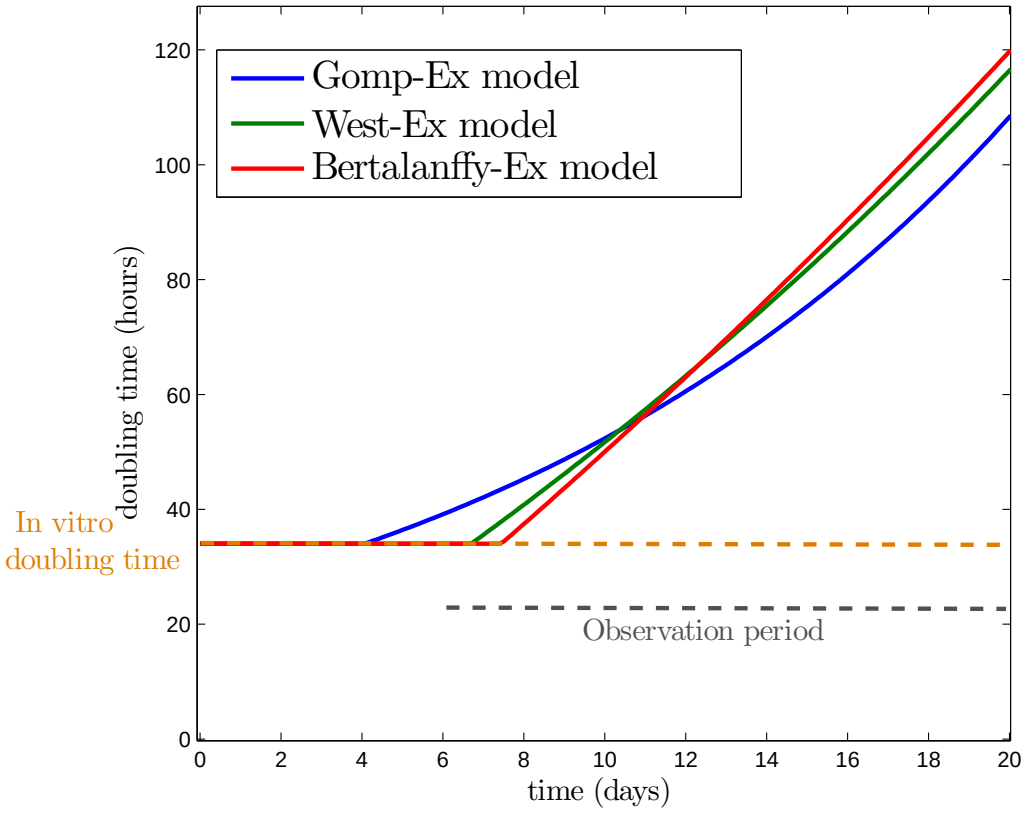
Doubling time

- time to double size with expontial growth at current speed
- given by

$$\frac{\log(2)x_p(t)}{g\left(x_p(t)\right)}$$

Hybrid models: doubling time

📖 **Wheldon (1988)**

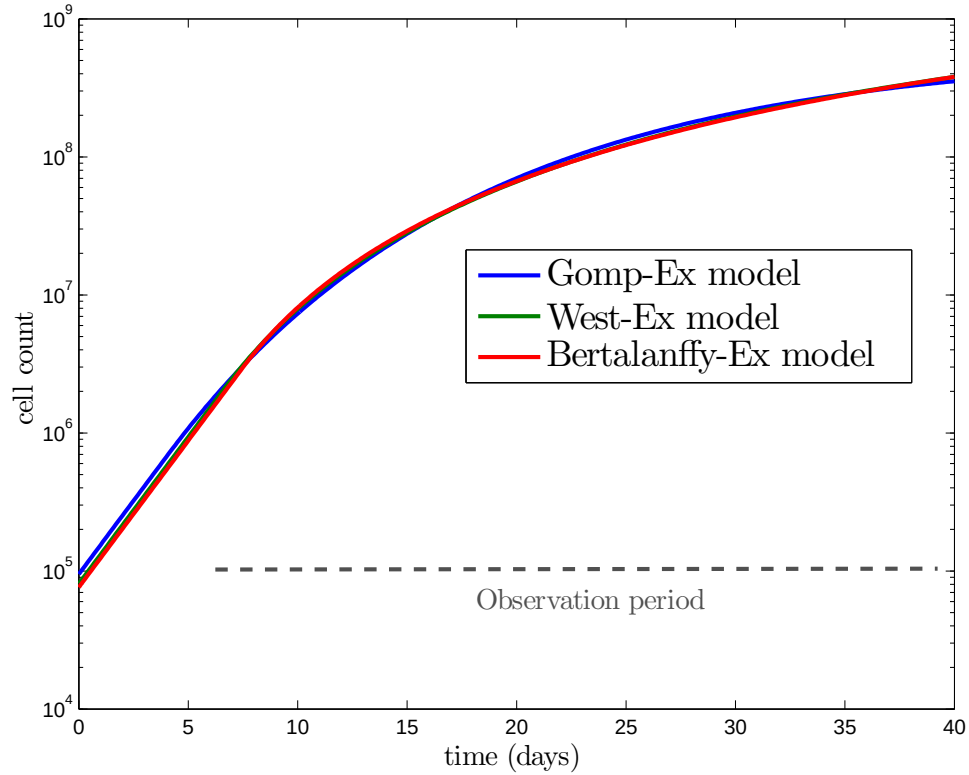


Doubling time

- limited to *in vitro* doubling time

$$g_{hybrid}(x) = \min\left(a_{vitro}x,\ g_{original}(x)\right)$$

Hybrid models: initial tumour size



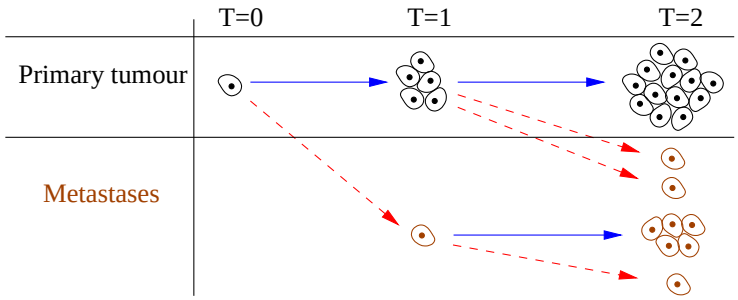
- Consistent extrapolation behaviour
- Predicted cell loss of ≈40%

$\Rightarrow$ **good description of primary tumour growth**

Metastatic emission and growth

Now: **parametrise the size-structured model**

- information from primary tumour model
- data on metastatic burden



Implementation: method based on model reformulation

$$M(t) = \int_0^t x_m(t-s)\beta_p\Big(x_p(s)\Big)ds + \int_0^t \beta\Big(x_m(t-s)\Big)M(s)ds$$

- second order method
- generational approximation

Building a metastatic model

Model selection based on AIC

- Which metastatic growth model?

  $\hookrightarrow$ **Gomp-Ex** better than West-Ex or Bertalanffy-Ex

- Parametrisation of growth and emission models?

  $\hookrightarrow$ **optimal structure:** $\left\{ \begin{array}{l} \text{1 metastatic growth parameter} \\ \text{1 metastatic emission parameter} \end{array} \right.$

Building a metastatic model

Model selection based on AIC

- Which metastatic growth model?

  $\hookrightarrow$ **Gomp-Ex** better than West-Ex or Bertalanffy-Ex

- Parametrisation of growth and emission models?

  $\hookrightarrow$ **optimal structure:** $\begin{cases} 1 \text{ metastatic growth parameter} \\ 1 \text{ metastatic emission parameter} \end{cases}$

Final metastatic model

$$M(t) = \int_0^t x_m(t-s)\beta_p\big(x_p(s)\big)ds$$

- $x_p \sim Gomp\text{-}Ex(a_p, b, x_0)$
- $x_m \sim Gomp\text{-}Ex(a_m, b, 1)$
- $\beta_p(x) = \mu x^{2/3}$

Building a metastatic model

5 structural parameters (ψ):

- (a_p, b, x_0, a_m, μ)

12 statistical parameters (θ):

- 5 typical values
- 5 inter-individual variability
- 2 residual error parameters

parameter (unit)	median	variability
a_p (day^{-1})	0.075	0.11
b (cells)	$5.4 \cdot 10^8$	0.23
x_0 (cells)	$9.0 \cdot 10^4$	0.18
μ (cells$^{-2/3}$day^{-1})	0.61	0.21
a_m (day^{-1})	$7.9 \cdot 10^{-3}$	0.11
Residual error σ_p	0.47	–
Residual error σ_m	0.90	–

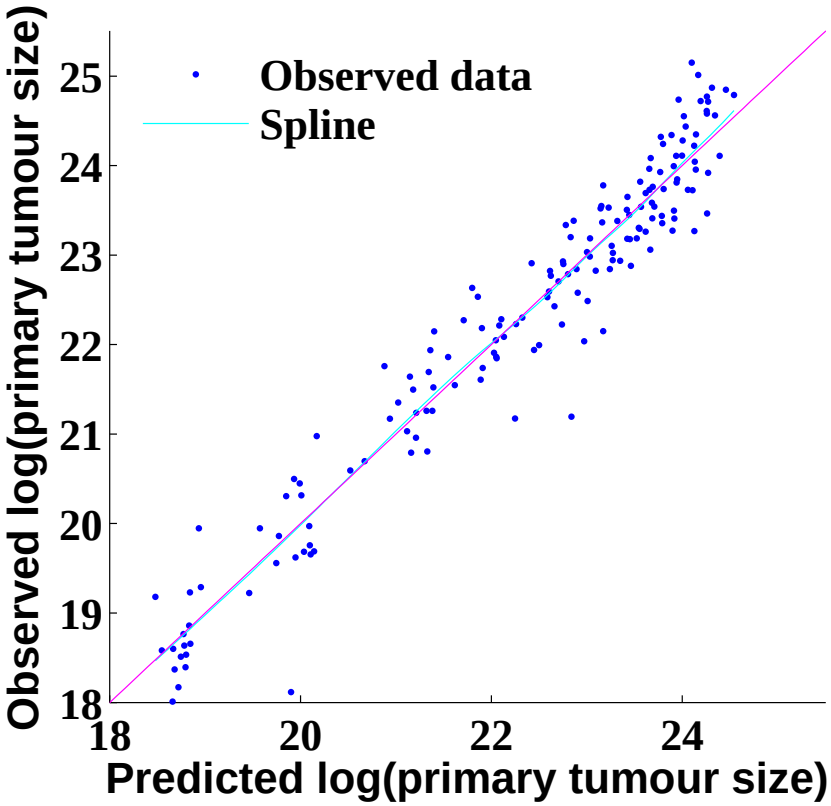
Final metastatic model

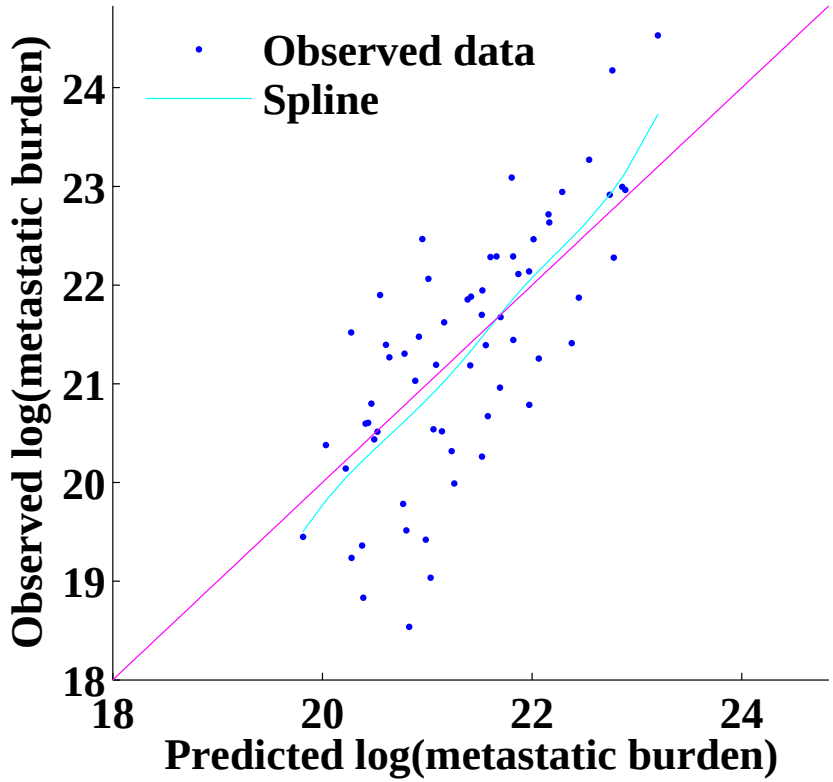
$$M(t) = \int_0^t x_m(t-s)\beta_p\big(x_p(s)\big)ds$$

- $x_p \sim Gomp\text{-}Ex(a_p, b, x_0)$
- $x_m \sim Gomp\text{-}Ex(a_m, b, 1)$
- $\beta_p(x) = \mu x^{2/3}$

Validation: diagnostic plots

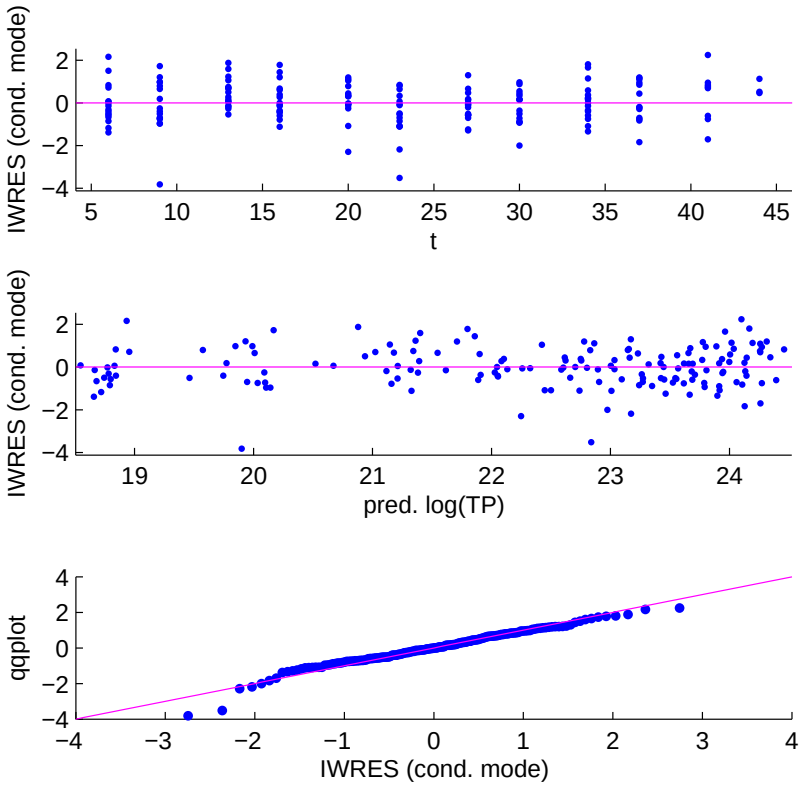
Observations vs. predictions



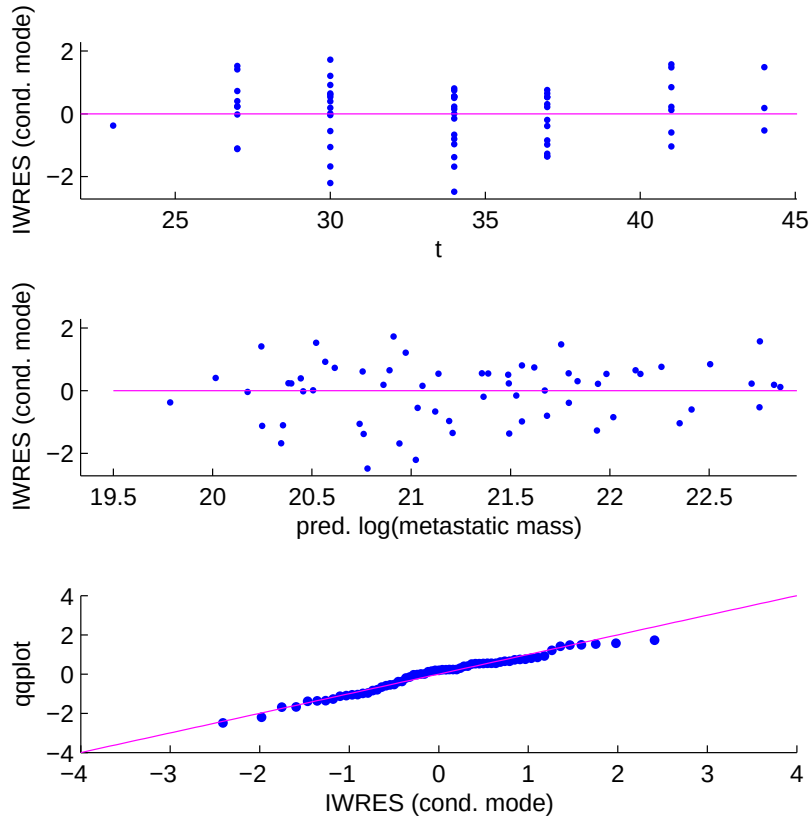


Validation: diagnostic plots

Residuals



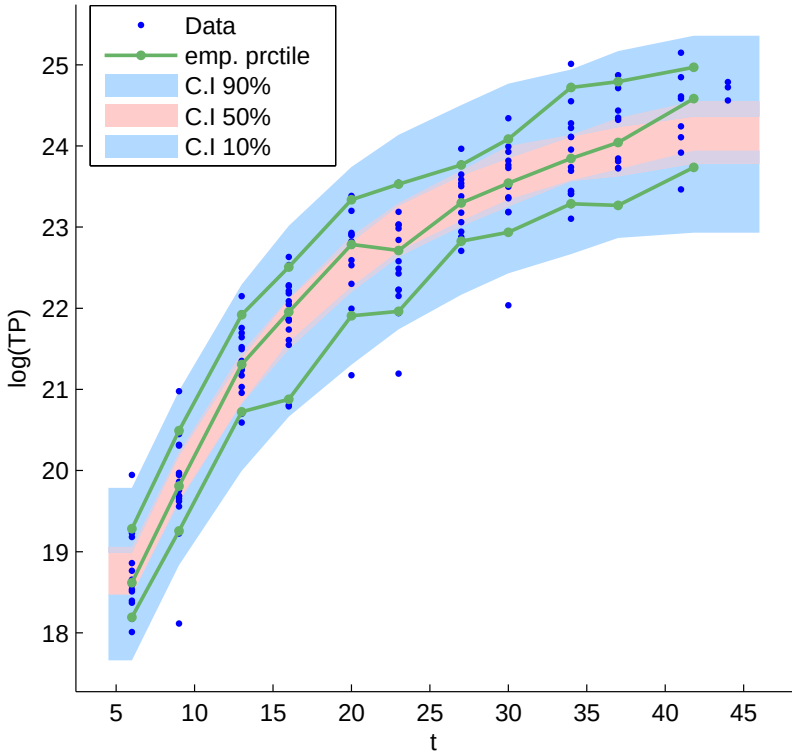
PRIMARY TUMOUR



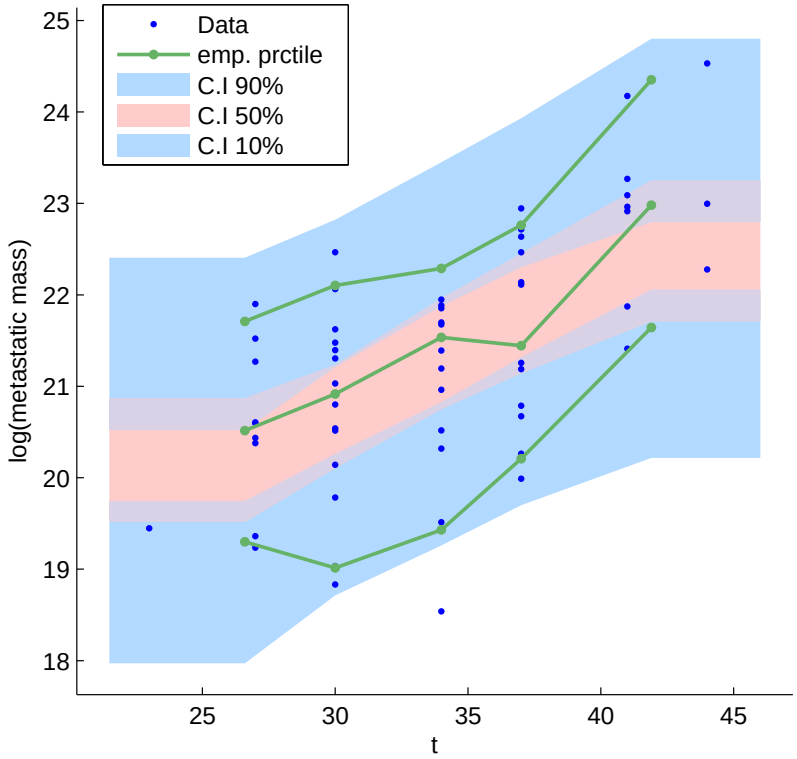
METASTASES

Validation: diagnostic plots

Visual Predictive Check



PRIMARY TUMOUR



METASTASES

Size-structured vs. ODE model

Peritoneal data

- 80% of metastatic data
- often only 1 or 2 visible metastases

$\Rightarrow$ is the size-structure necessary?

Idea: describe peritoneal burden by an ODE model

- worse fit (measured by AIC)
- inception before start of experiment
- violates *in vitro* doubling time limit

$\Rightarrow$ **Unrealistic behaviour**

Size-structure *is* necessary

Predicted number of metastases

Number of metastases

- many predicted
- few observed

$\Rightarrow$

Interpretation

Visible metastases are *multifocal*

$\Rightarrow$ **kinetic information in metastatic burden, not in number of visible metastases**

Conclusion of Part 2

Conclusion

- metastatic model built from preclinical data
- numerical method developed earlier very useful
- size-structure in metastatic model necessary
- biological predictions from calibrated model

↪ Hartung, N., Mollard, S., Barbolosi, D., Benabdallah, A., Chapuisat, G., Ciccolini, J., Faivre, C., Giacometti, S., Henry, G., Iliadis, A. and Hubert, F. *Mathematical Modeling of tumor growth and metastatic spreading: validation in tumor-bearing mice*, **Cancer Research**, 2014.

Perspectives

- identification of individual parameters via covariates
- model extension: attraction towards existing metastatic colonies

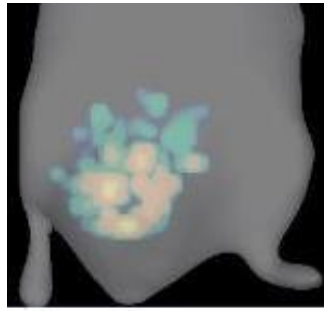
PART 3

TUMOUR BOUNDARY RECONSTRUCTION

Motivation

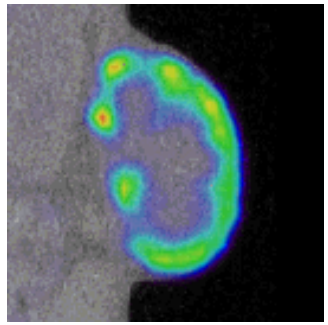
Previous section: **3D bioluminescence imaging**

- tumour size



Here: **3D SPECT imaging** 🕮 **T. Pourcher**

- functional (proliferating vs. quiescent cells)



Idea

reconstruct tumour shape from proliferating cells

Framework for boundary reconstruction

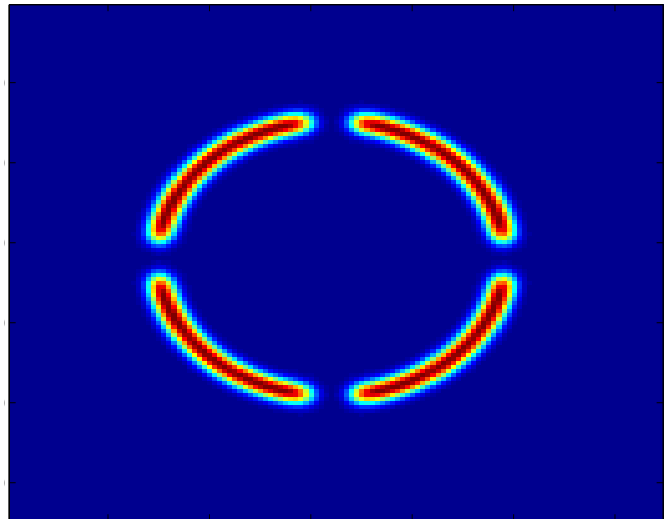
Subjective surfaces equation

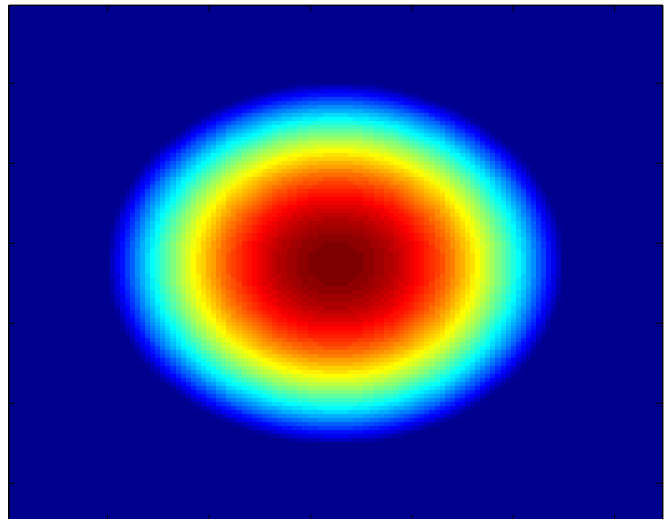
Sarti *et al.* (2000)

$$\partial_t u = |\nabla u| \operatorname{div}\left(g(|\nabla I|) \frac{\nabla u}{|\nabla u|} \right)$$

- $g(x) = \frac{1}{1+kx^2}$
- I: image

$$g(|\nabla I|)\, \underbrace{|\nabla u| \operatorname{div}\left(\frac{\nabla u}{|\nabla u|} \right)}_{\text{curvature term}} + \underbrace{\nabla u \cdot \nabla \Big(g(|\nabla I|) \Big)}_{\text{advection term}}$$





Numerical resolution

Subjective surfaces equation

$$\partial_t u = |\nabla u| \operatorname{div}\left(g(|\nabla I|)\frac{\nabla u}{|\nabla u|}\right)$$

- non-linear
- heterogeneous
- non-conservative

} **requires suitable discretisation**

Space discretisation

- literature: Finite Volume schemes

🕮 **Mikula *et al.* (2000s)**

- here: *Discrete Duality Finite Volume* schemes on Cartesian grids

Aims

- avoid additional unknowns
- efficient implementation

3D CeVeFE DDFV

Unknowns

- centers of a primary mesh $\mathcal{M}$
- vertices of $\mathcal{M}$
- faces and edges of $\mathcal{M}$

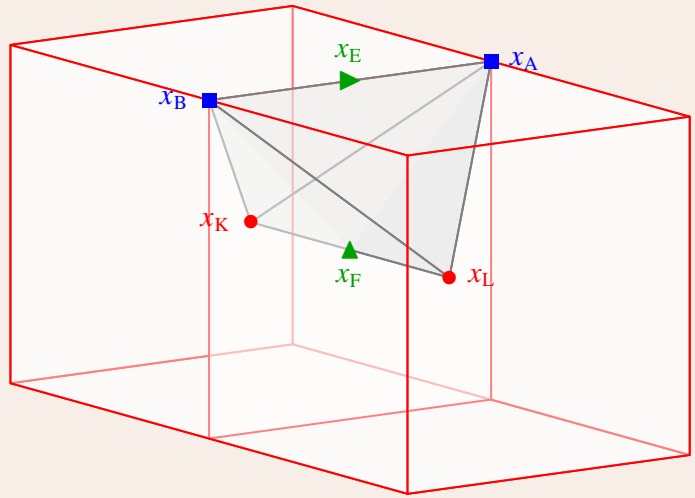
$\Rightarrow$ 3 different meshes

📖 Coudière & Hubert (2011)

Diamond cell structure

Central notion

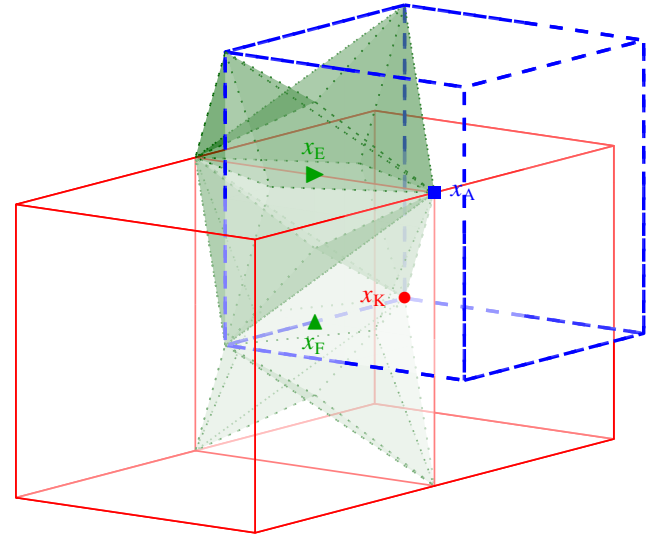
- 1:1 correspondence:
  diamond $\Leftrightarrow$ face-edge pair
- defines the cells of the three meshes
- gradients defined on diamonds

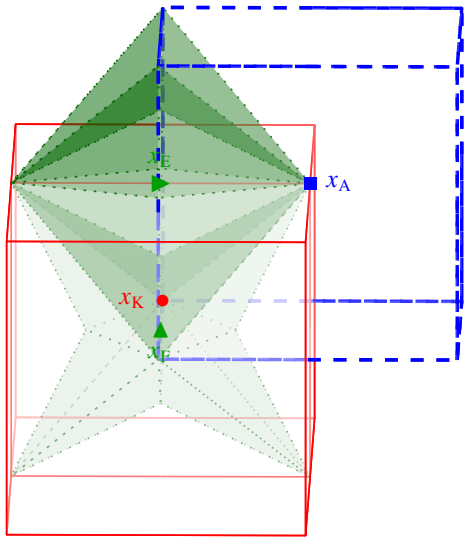


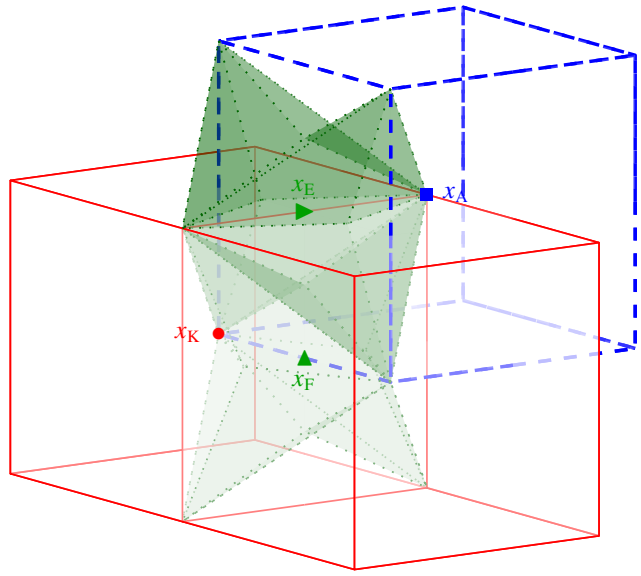
$$\left(\nabla^d(u_\mathcal{T})\right)_D = \frac{1}{3|D|}\left((u_L - u_K)\overrightarrow{N_{KL}} + (u_F - u_E)\overrightarrow{N_{EF}} + (u_B - u_A)\overrightarrow{N_{AB}}\right)$$

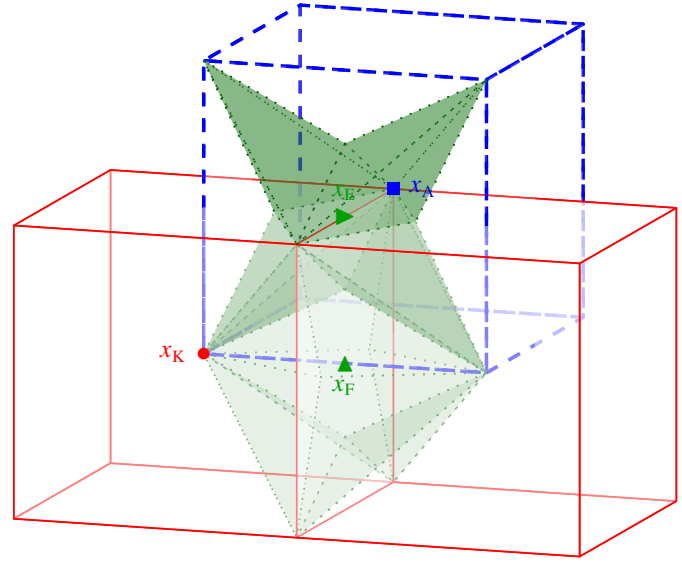
3D CeVeFE DDFV

3D DDFV meshes on a Cartesian grid





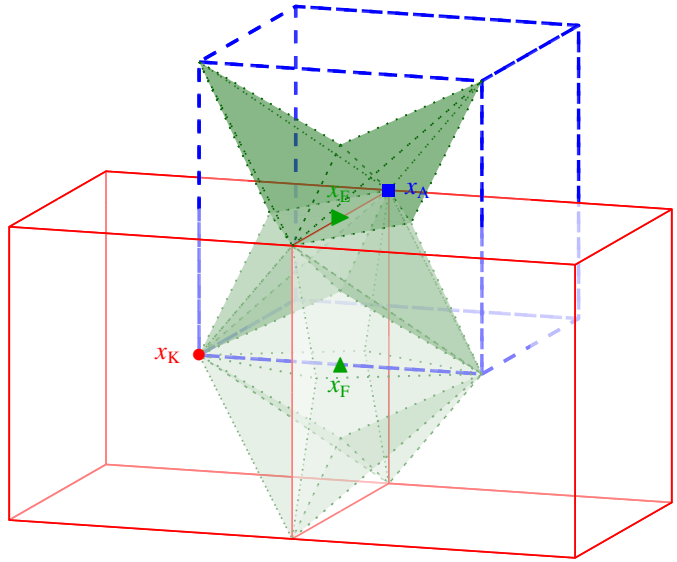




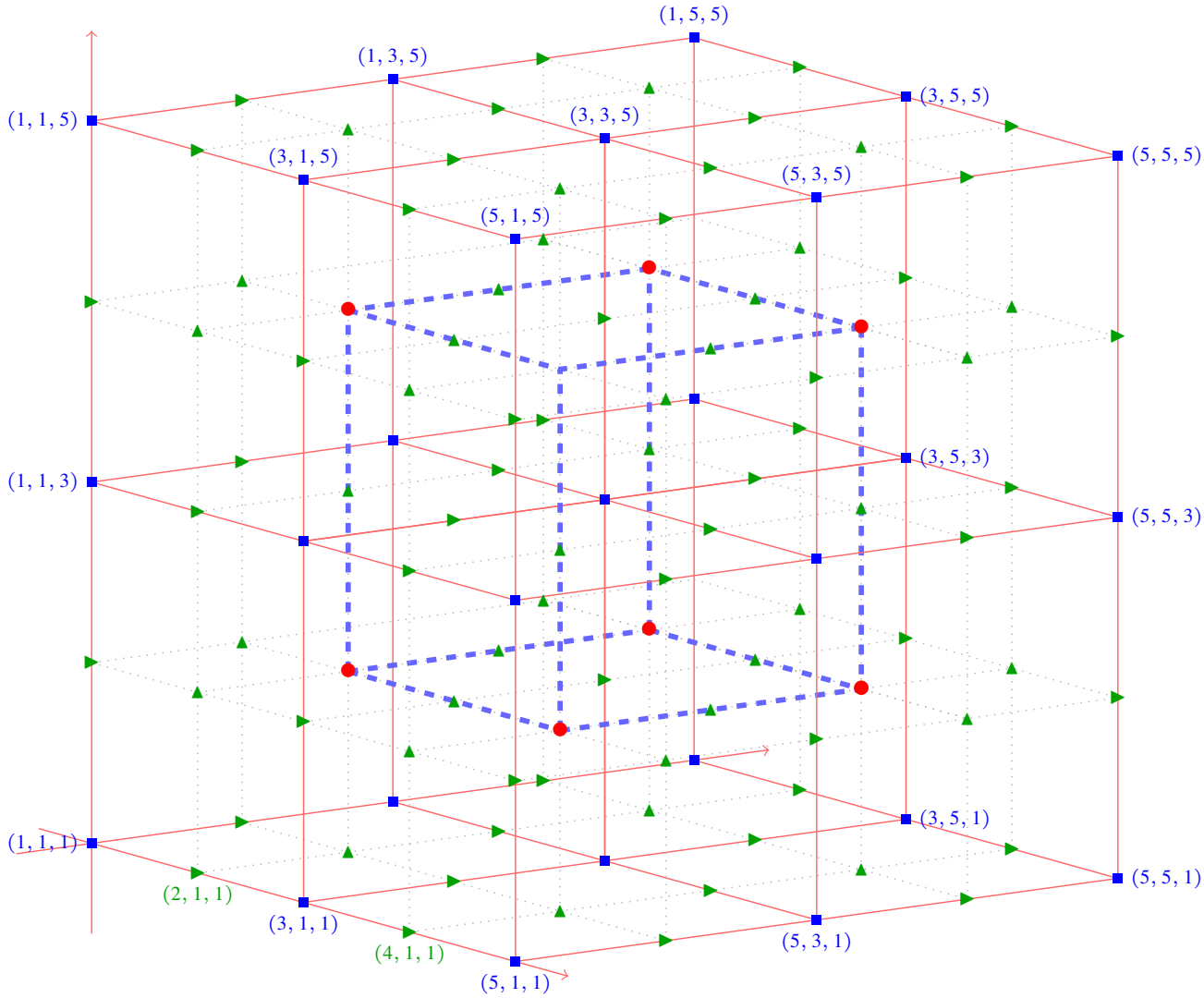
Decomposition of the Cartesian grid

Idea: colorise the Cartesian grid in three colors such that:

- ● is associated to a primary mesh
- ■ is associated to corresponding node mesh
- ▲ is associated to corresponding face/edge mesh



Decomposition of the Cartesian grid



$\hookrightarrow$ **No additional unknowns introduced**

Implementation

1. construct diamond cells

Face oriented parallel to x axis ((i,j,k) with i odd)

	Edge 1	Edge 2	Edge 3	Edge 4
x_E	$(i,j+1,k)$	$(i,j,k-1)$	$(i,j-1,k)$	$(i,j,k+1)$
x_K	$(i-1,j,k)$	$(i-1,j,k)$	$(i-1,j,k)$	$(i-1,j,k)$
x_L	$(i+1,j,k)$	$(i+1,j,k)$	$(i+1,j,k)$	$(i+1,j,k)$
x_A	$(i,j+1,k-1)$	$(i,j-1,k-1)$	$(i,j-1,k+1)$	$(i,j+1,k+1)$
x_B	$(i,j+1,k+1)$	$(i,j+1,k-1)$	$(i,j-1,k-1)$	$(i,j-1,k+1)$

Face oriented parallel to y axis ((i,j,k) with j odd)

	Edge 1	Edge 2	Edge 3	Edge 4
x_E	$(i+1,j,k)$	$(i,j,k+1)$	$(i-1,j,k)$	$(i,j,k-1)$
x_K	$(i,j-1,k)$	$(i,j-1,k)$	$(i,j-1,k)$	$(i,j-1,k)$
x_L	$(i,j+1,k)$	$(i,j+1,k)$	$(i,j+1,k)$	$(i,j+1,k)$
x_A	$(i+1,j,k+1)$	$(i-1,j,k+1)$	$(i-1,j,k-1)$	$(i+1,j,k-1)$
x_B	$(i+1,j,k-1)$	$(i+1,j,k+1)$	$(i-1,j,k+1)$	$(i-1,j,k-1)$

Face oriented parallel to z axis ((i,j,k) with k odd)

	Edge 1	Edge 2	Edge 3	Edge 4
x_E	$(i,j+1,k)$	$(i+1,j,k)$	$(i,j-1,k)$	$(i-1,j,k)$
x_K	$(i,j,k-1)$	$(i,j,k-1)$	$(i,j,k-1)$	$(i,j,k-1)$
x_L	$(i,j,k+1)$	$(i,j,k+1)$	$(i,j,k+1)$	$(i,j,k+1)$
x_A	$(i+1,j+1,k)$	$(i+1,j-1,k)$	$(i-1,j-1,k)$	$(i-1,j+1,k)$
x_B	$(i-1,j+1,k)$	$(i+1,j+1,k)$	$(i+1,j-1,k)$	$(i-1,j-1,k)$

$\Rightarrow$ **vectorisable, using 12 diamond types**

Implementation

1. **construct diamond cells**
2. **time discretisation**

$$\partial_t u = |\nabla u| \operatorname{div}\left(g(|\nabla I|) \frac{\nabla u}{|\nabla u|} \right)$$

- semi-implicit scheme:

$$\frac{u^{n+1} - u^n}{\Delta t} = |\nabla u^n| \operatorname{div}\left(g \frac{\nabla u^{n+1}}{|\nabla u^n|} \right)$$

- multiply by Λ_n with diagonal entries $\frac{|\mathrm{C}|}{|\nabla^{\mathrm{D}} u|_{\mathrm{C}} + \varepsilon}$ for the symmetric scheme

$$(\Lambda_n + \Delta t M_n) u^{n+1} = \Lambda_n u^n,$$

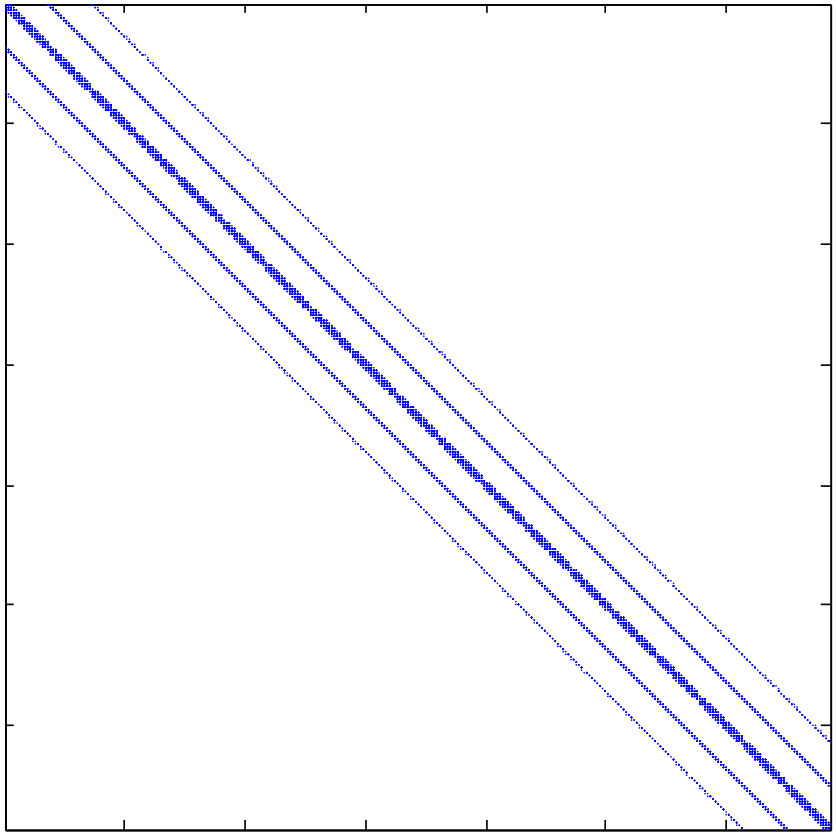
where

$$M_n u = |\mathrm{C}| \operatorname{div}^{\mathrm{D}}\left(g(|\nabla^{\mathrm{D}} I|) \frac{\nabla^{\mathrm{D}} u}{|\nabla^{\mathrm{D}} u^n| + \varepsilon} \right)$$

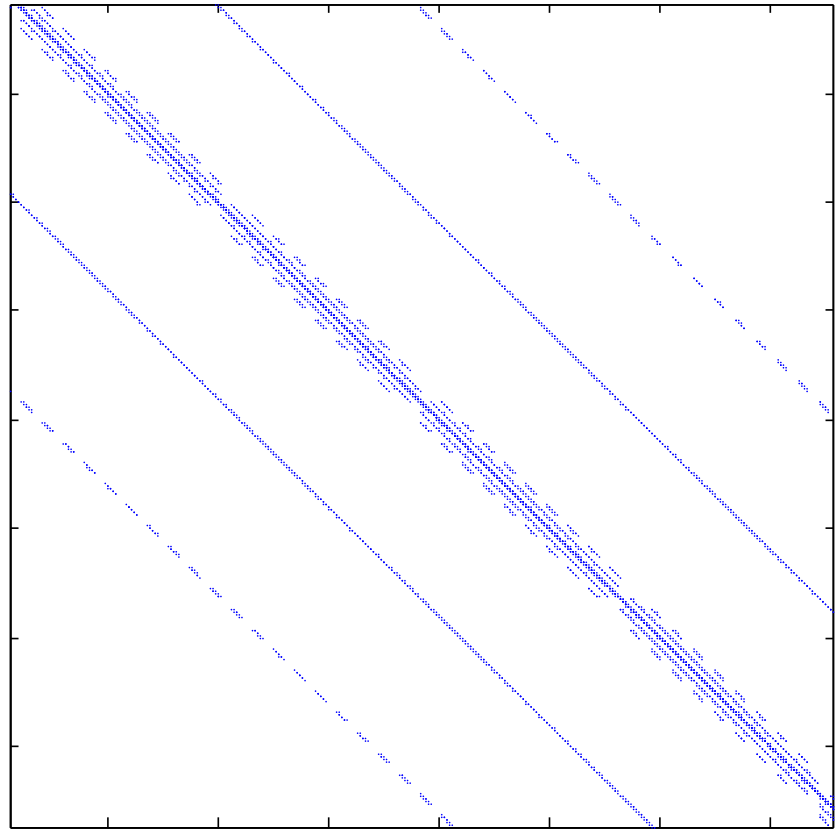
- diamondwise assembly of $M_n u$

Implementation

1. construct diamond cells
2. time discretisation
3. resolution of linear system



MATRIX PROFILE

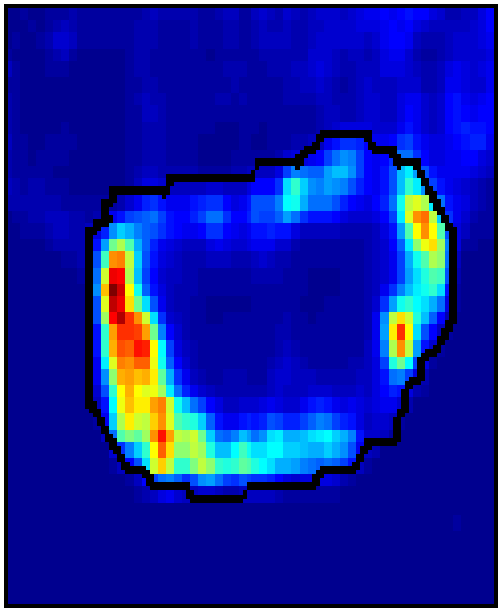


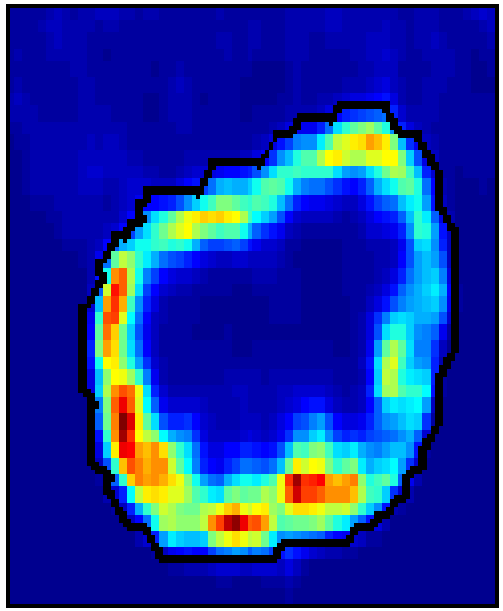
ZOOM

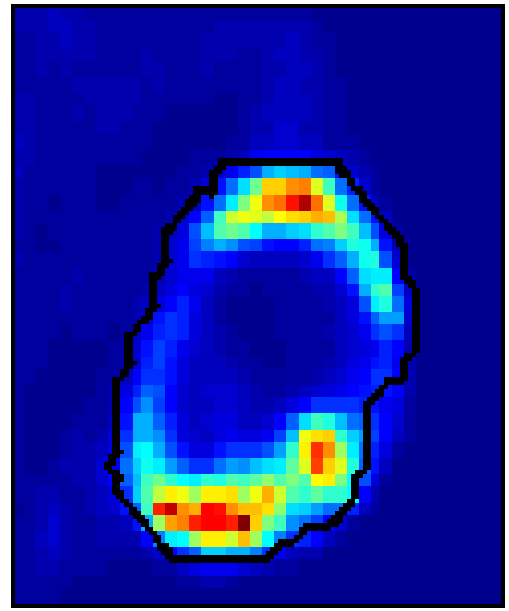
Numerical results

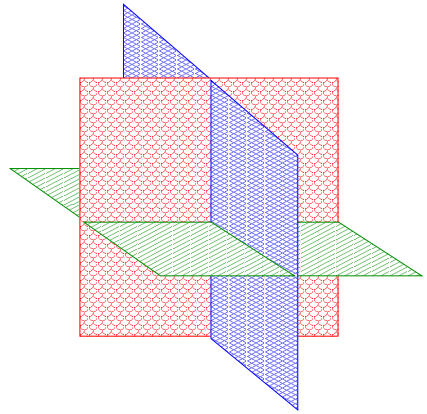
Reconstruction on 3D SPECT image

🕮 NH, F. Hubert (2014)



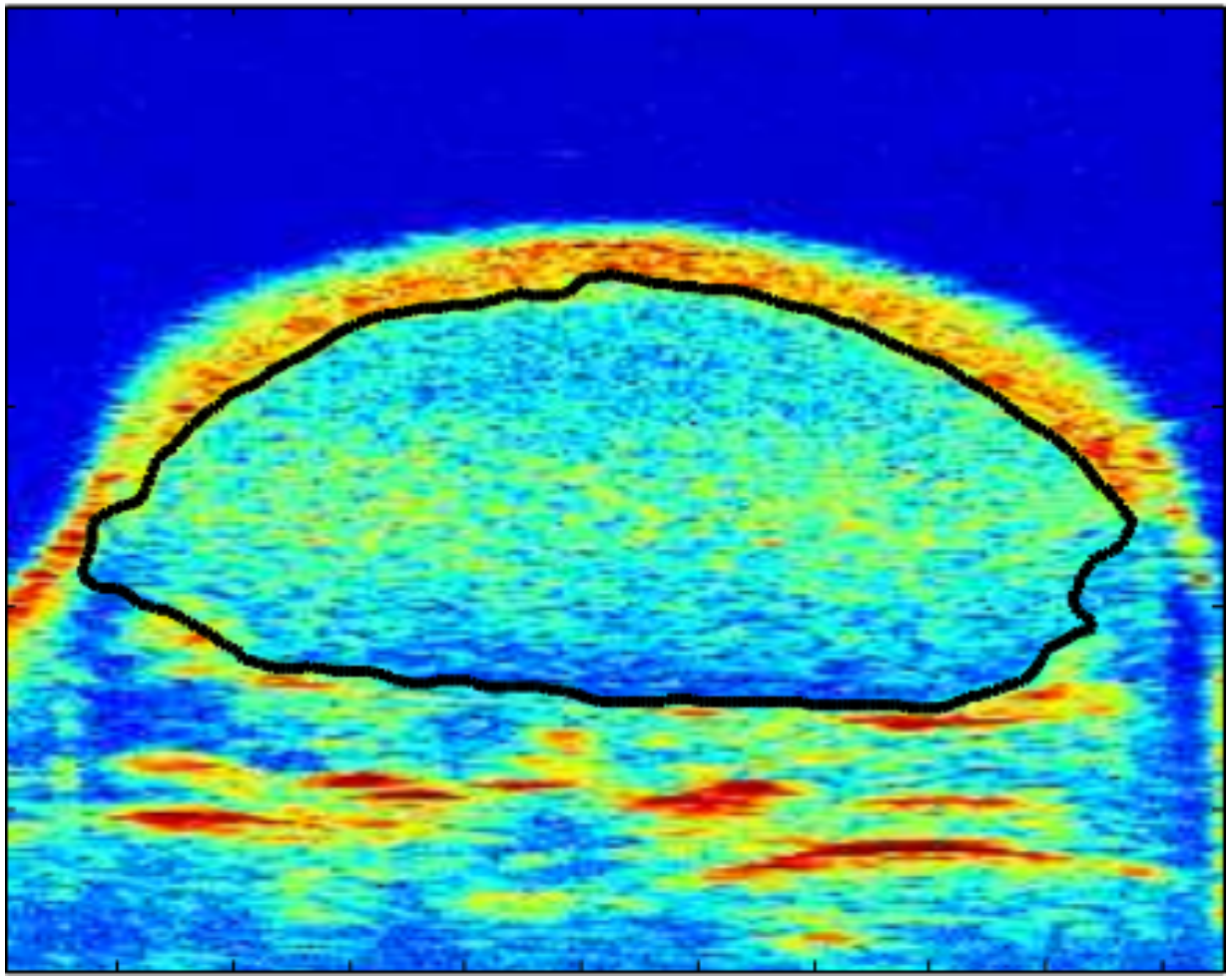






Numerical results

Reconstruction on 2D ultrasound image



Conclusion of Part 3

Conclusion

- implementation of DDFV schemes tailored to Cartesian grid
- efficient resolution of the subjective surfaces equation
- tumour boundary reconstructions obtained on medical images

↪ Hartung, N. and Hubert, F. *An efficient implementation of a 3D CeVeFE DDFV scheme on Cartesian grids and an application in image processing*, **Proceedings of Finite Volumes for Complex Applications VII**, 2014.

Perspectives

- (semi-)automatisation of reconstruction
- comparison to other space discretisation methods
- refinement / coarsening

THANK YOU FOR YOUR ATTENTION