

## A Scale Separation Approach Applied to a Mathematical Model of Solid Tumour Growth

#### Barbara de Melo Quintela,

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### PRIMAGE Project

- PRedictive In silico Multiscale Analytics to support cancer personalized diaGnosis and prognosis, Empowered by imaging biomarkers
- Patient specific models of the tumour growth to personalize treatment
  - Neuroblastoma (NB) Most frequent solid tumour outside of the brain in children



(Martí-Bonmatí et al. 2020)



## Continuous Model - Tumour growth and chemotherapy outcome





#### Motivation





## Question

How to separate the scales?



### Definition of scale

- **Grain** which is the largest value between the lower limit of spatial/temporal resolution allowed by instrumentation, and the smallest/fastest feature of interest.
- Extent the smallest value between the upper limit of spatial/temporal resolution and the size of the largest/slowest feature to be observed.

$$\begin{cases} \boldsymbol{\pi}_{\boldsymbol{\gamma}_{k}}^{*}(\boldsymbol{k}(\boldsymbol{X}),\boldsymbol{T}_{l},\boldsymbol{t}) = \boldsymbol{\pi}_{\boldsymbol{\gamma}_{k}}(\boldsymbol{I}_{k},\boldsymbol{\alpha}_{k},\boldsymbol{\tau}_{k},\boldsymbol{S}_{1},\dots,\boldsymbol{S}_{J},\boldsymbol{t}) \cdot \boldsymbol{\pi}_{\boldsymbol{\gamma}_{k}}^{treat}(\boldsymbol{T}_{l}) & (1) \\ r_{i}^{dV_{X}}(\boldsymbol{X},t) = \frac{dc_{i}^{dV_{X}}(\boldsymbol{X},\boldsymbol{S}_{1},\dots,\boldsymbol{S}_{J},t)}{dt} \\ \dot{\boldsymbol{S}}_{j}(\boldsymbol{X},t) = \sum_{k}^{N \in dV_{X}} \boldsymbol{\chi}_{k}^{j}(\boldsymbol{I}_{k},\boldsymbol{\alpha}_{k},\boldsymbol{\gamma}_{k},\boldsymbol{\tau}_{k},t) + \sum_{k}^{N \in dV_{X}} \sigma_{k}^{j}(\boldsymbol{I}_{k},\boldsymbol{\alpha}_{k},\boldsymbol{\gamma}_{k},\boldsymbol{\tau}_{k},t) \\ r_{i}^{dV_{X}}(\boldsymbol{X},t) = f_{p}^{i,a}(\boldsymbol{X},t) - f_{d}^{i,a}(\boldsymbol{X},t) = \frac{dC_{i}^{dV_{X}}(\boldsymbol{X},t)}{dt} \\ \frac{\partial C_{i}^{dV_{X}}(\boldsymbol{X},t)}{\partial t} + \nabla \cdot \left(C_{i}^{dV_{X}}(\boldsymbol{X},t)\frac{\partial u(\boldsymbol{X},t)}{\partial t}\right) = r_{i}^{dV_{X}} \\ \frac{\partial V}{\partial t} = k^{ia} \left(\frac{\partial C^{V}}{\partial t}\right) = k^{ia} \left(\frac{\partial C^{V}_{S}}{\partial t} + \frac{\partial C^{V}_{n}}{\partial t}\right), \end{cases}$$

# STUD DU DU DU DU

#### Single Scale Infinite Resolution Mathematical Model

$$\begin{cases} \pi_{\gamma_{k}}^{*}(k(X), T_{l}, t) = \pi_{\gamma_{k}}(I_{k}, \alpha_{k}, \tau_{k}, S_{1}, \dots, S_{J}, t) \cdot \pi_{\gamma_{k}}^{treat}(T_{l}) & (1) \\ r_{i}^{dV_{X}}(X, t) = \frac{dc_{i}^{dV_{X}}(X, S_{1}, \dots, S_{J}, t)}{dt} \\ \dot{S}_{j}(X, t) = \sum_{k}^{N \in dV_{X}} \chi_{k}^{j}(I_{k}, \alpha_{k}, \gamma_{k}, \tau_{k}, t) + \sum_{k}^{N \in dV_{X}} \sigma_{k}^{j}(I_{k}, \alpha_{k}, \gamma_{k}, \tau_{k}, t) \\ r_{i}^{dV_{X}}(X, t) = f_{p}^{i,a}(X, t) - f_{d}^{i,a}(X, t) = \frac{dC_{i}^{dV_{X}}(X, t)}{dt} \\ \frac{\partial C_{i}^{dV_{X}}(X, t)}{\partial t} + \nabla \cdot \left(C_{i}^{dV_{X}}(X, t)\frac{\partial u(X, t)}{\partial t}\right) = r_{i}^{dV_{X}} \\ \frac{\partial V}{\partial t} = k^{ia}\left(\frac{\partial C^{V}}{\partial t}\right) = k^{ia}\left(\frac{\partial C_{s}^{V}}{\partial t} + \frac{\partial C_{n}^{V}}{\partial t}\right), \end{cases}$$

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• Tumour

• Finite Element Method

• Tissue

• Agent-Based Model

• Cell

• Machine learning





**Temporal extent ->** duration of chemotherapy

**Temporal Grain** -> minimum distance to successive imaging controls

- Tumour
  - Finite Element Method

#### • Tissue

Agent-Based Model

• Cell

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Spatial extent -> size of tumour

**Spatial Grain** -> limited by image resolution and number of degrees of freedom the FEM can solve

Tumour

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**Spatial extent ->** conveniently set to grain of tumour model A tumour model with 300000 Finite Elements requires 300000 executions of the ABM • Tumour

• Finite Element Method

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• Tumour

• Finite Element Method

Binning Interpolation 1

• Tissue

• Agent-Based Model

• Cell

• Machine learning

Spatial extent -> conveniently set to grain of tumour model A tumour model with 300000 Finite Elements requires 300000 executions of the ABM - available HPC resources include 100 GPUs simultaneously





**Spatial and temporal extent of cell model ->** conveniently set to grain of tissue model

Tumour

• Finite Element Method

Binning Interpolation

• Tissue

• Agent-Based Model

Not coupled, run once

Cell

• Machine learning



#### Scale separation applied to solid tumour growth





#### Considerations

- The aim of this study was to find the scale separation of a new multiscale tumour growth model that minimises the modelling complexity, while respecting the experimental resolution and computational constraints that limit the scale ranges.
- Reduction of hundreds of thousands of FE to a hundred ABM is a major simplification.
- Every paper that describes a multiscale model should provide justification for its scale separation based on the resolution of the experimental methods available to inform the model and the computational power available for its solution.



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Thanks!

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