



HPC/Exascale
Centre of
Excellence in
Personalised
Medicine

Practical session with PhysiCell

José Carbonell Caballero
Thalia Diniaco



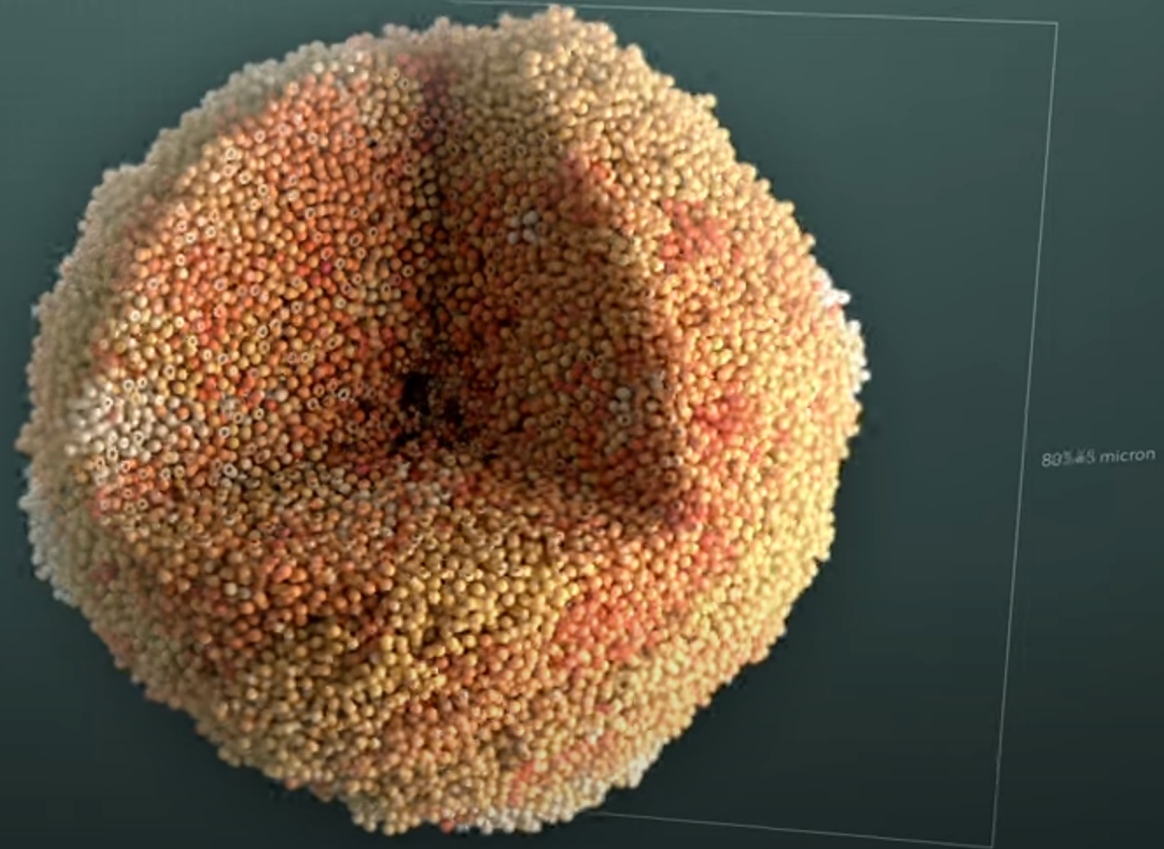
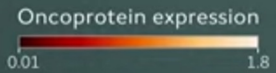
The PerMedCoE project has received funding from the European Union's Horizon 2020 research and innovation programme under the grant agreement N°951773



These materials are free cultural works licensed under a Creative Commons [Attribution 4.0 International \(CC BY 4.0\) license](https://creativecommons.org/licenses/by/4.0/)

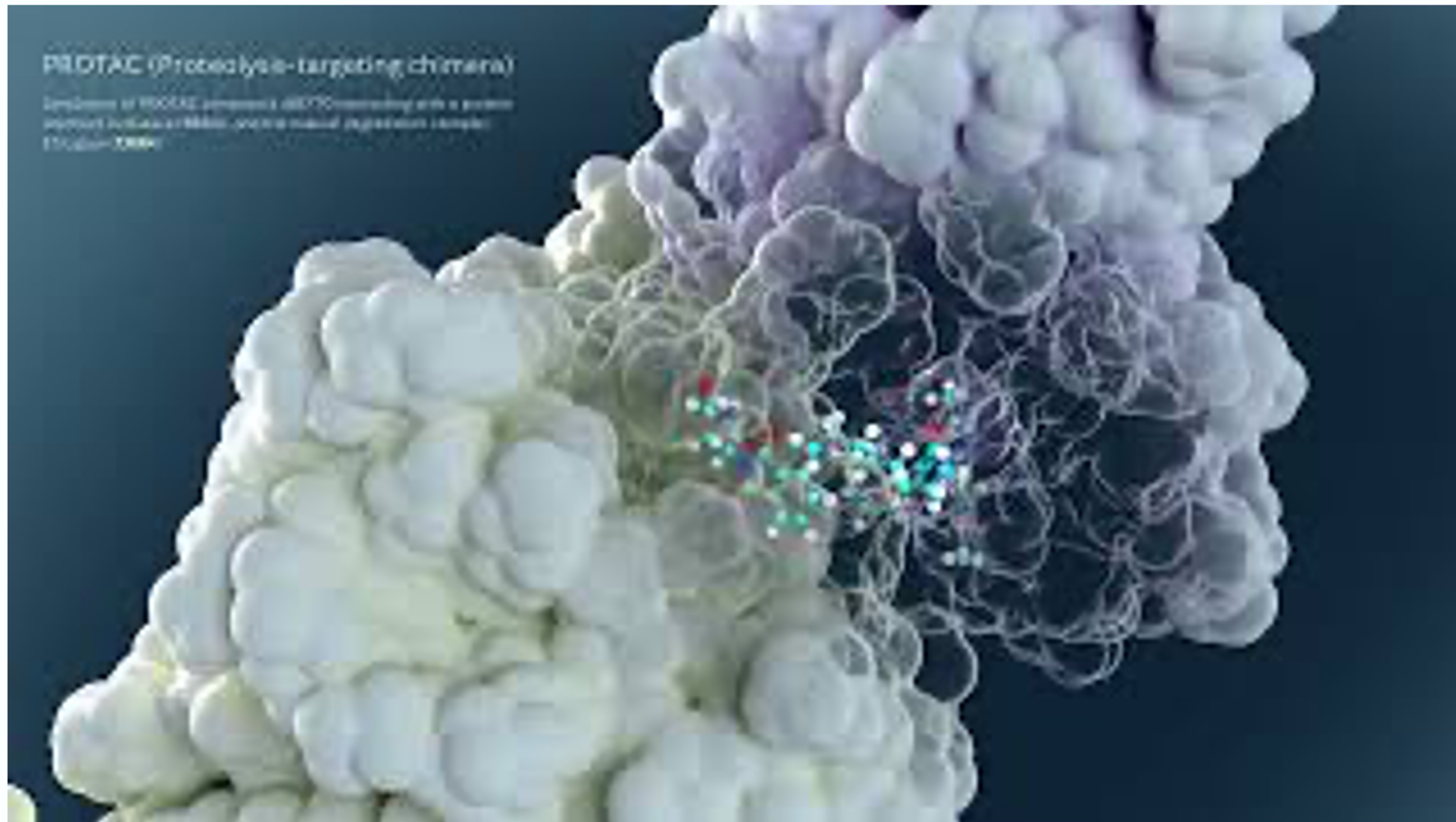
Simulating a cellular microenvironment

Representation of tumor heterogeneity due to genomic instability



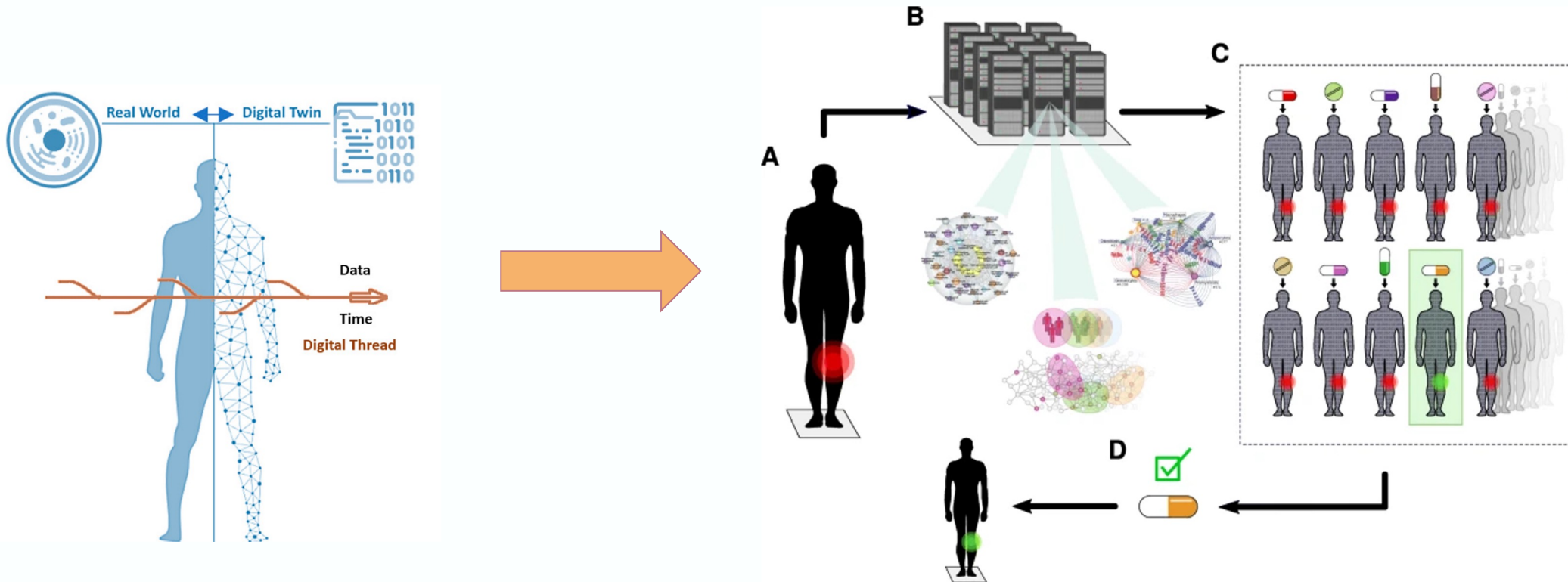
Simulating 1 cm³ of cancer tissue takes **15 days** on a supercomputer
About **16 years** on a 12-core home computer
If this computer would have enough memory

Simulating a cellular microenvironment



Personalised Medicine and Digital Twins

Towards patient-specific treatments

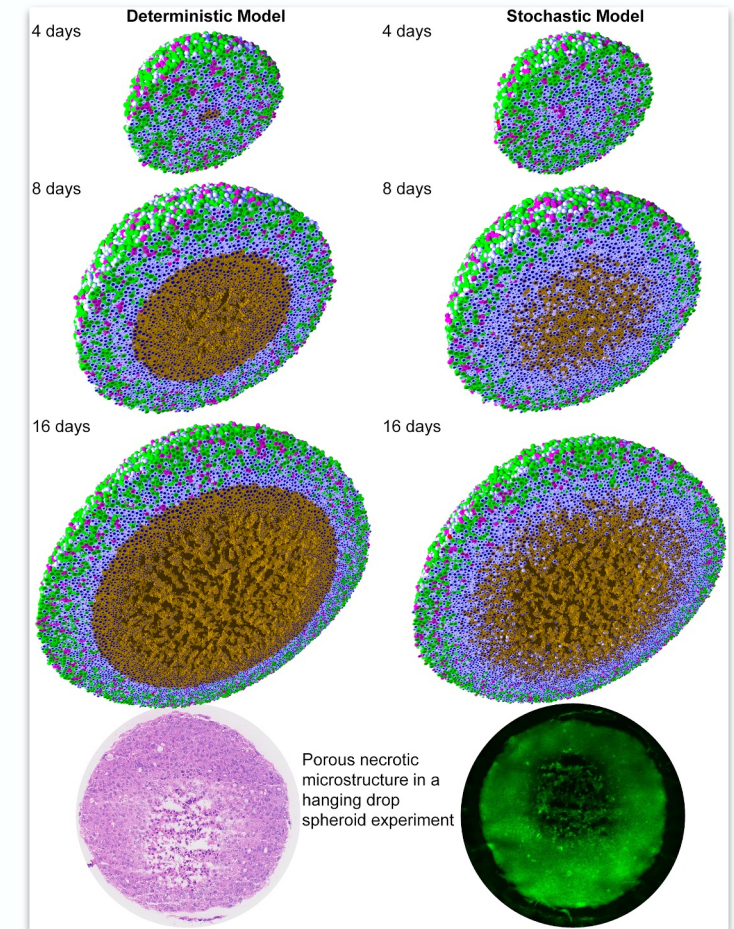
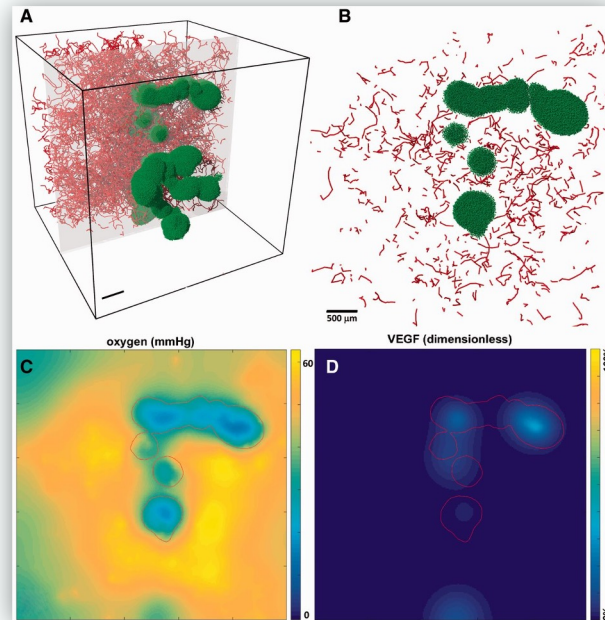


Björnsson, B., Borrebaeck, C., Elander, N. et al. Digital twins to personalize medicine. *Genome Med* 12, 4 (2020).

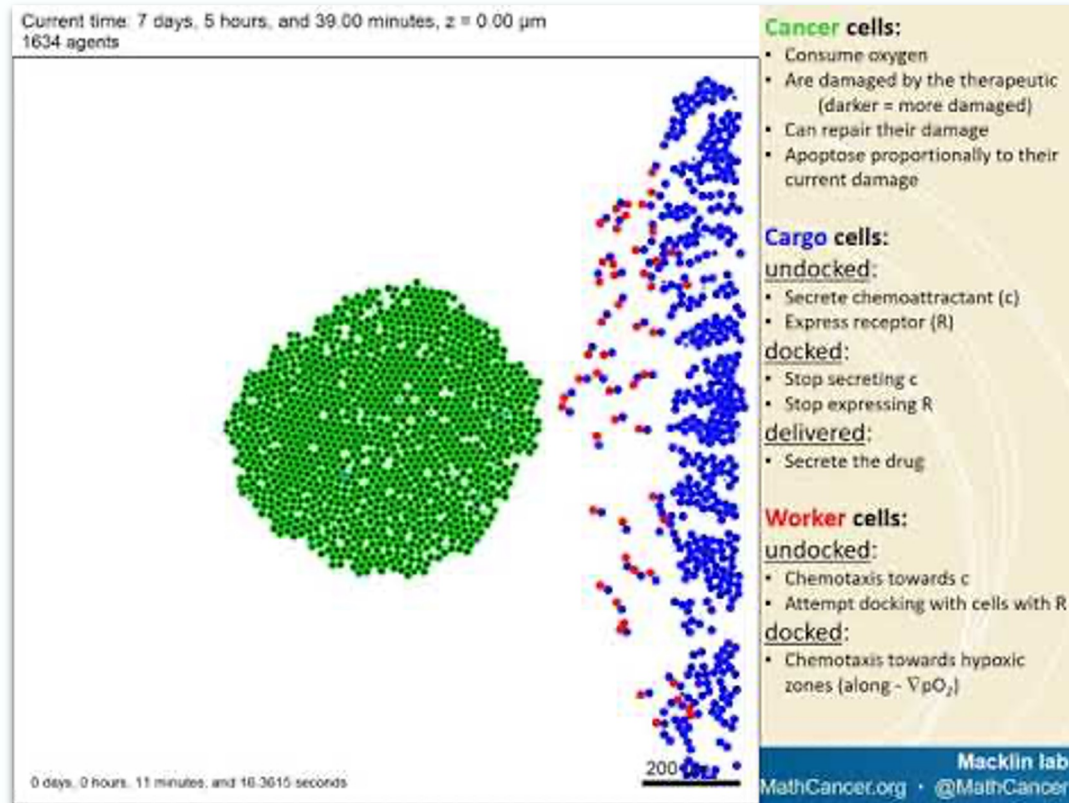
Core tools

PhysiCell

- Physics-based virtual microscope
- Implements Agent-Based programming
- Cell phenotype and cell-cell interactions
- Diffusion transport solver



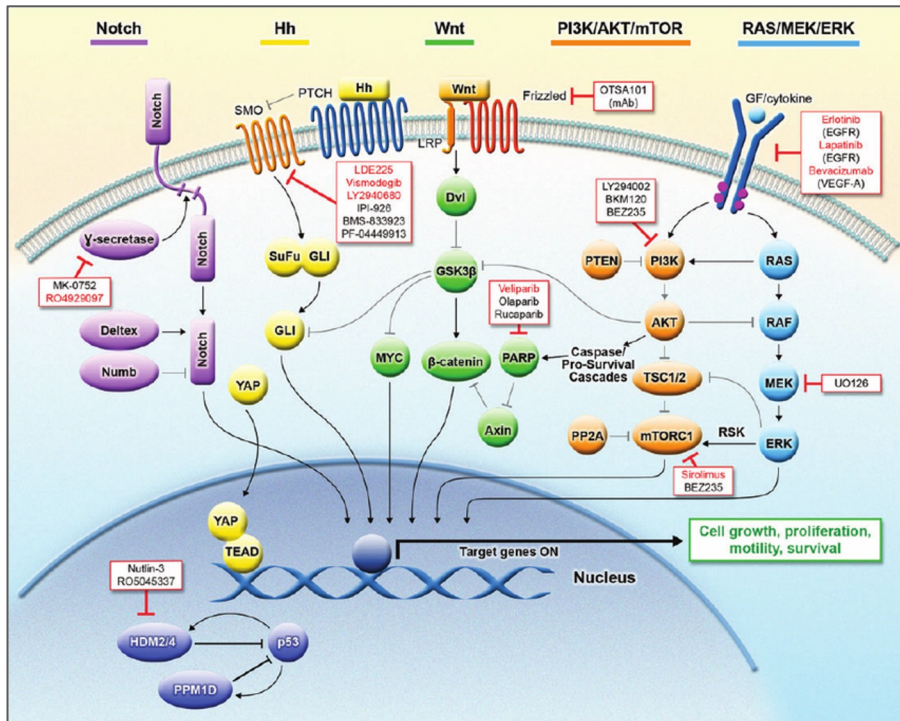
The framework recapitulates main cellular features



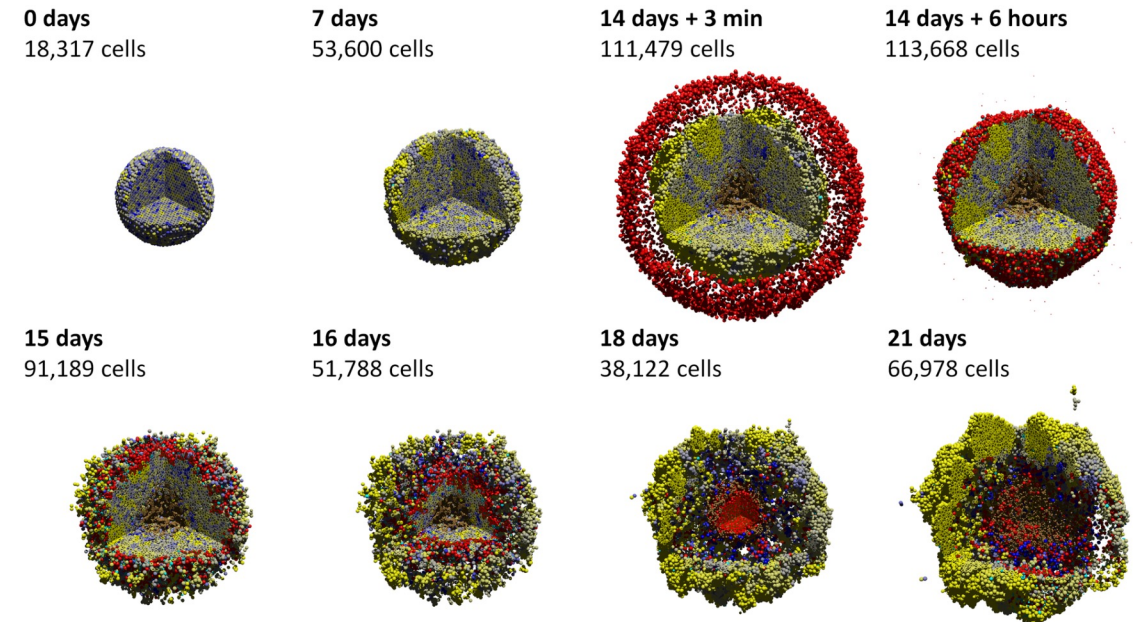
- Cell motility (and chemotaxis)
- Cell cycle phases (G0/G1, S, G2, M)
- Cell death (apoptosis and necrosis)
- Cell volume (nucleus and cytoplasm)
- Cell growth
- Substrate production/consumption
- Physical interaction between cells
- Phagocytosis

Extending PhysiCell

Introducing molecular pathways into multiscale agents

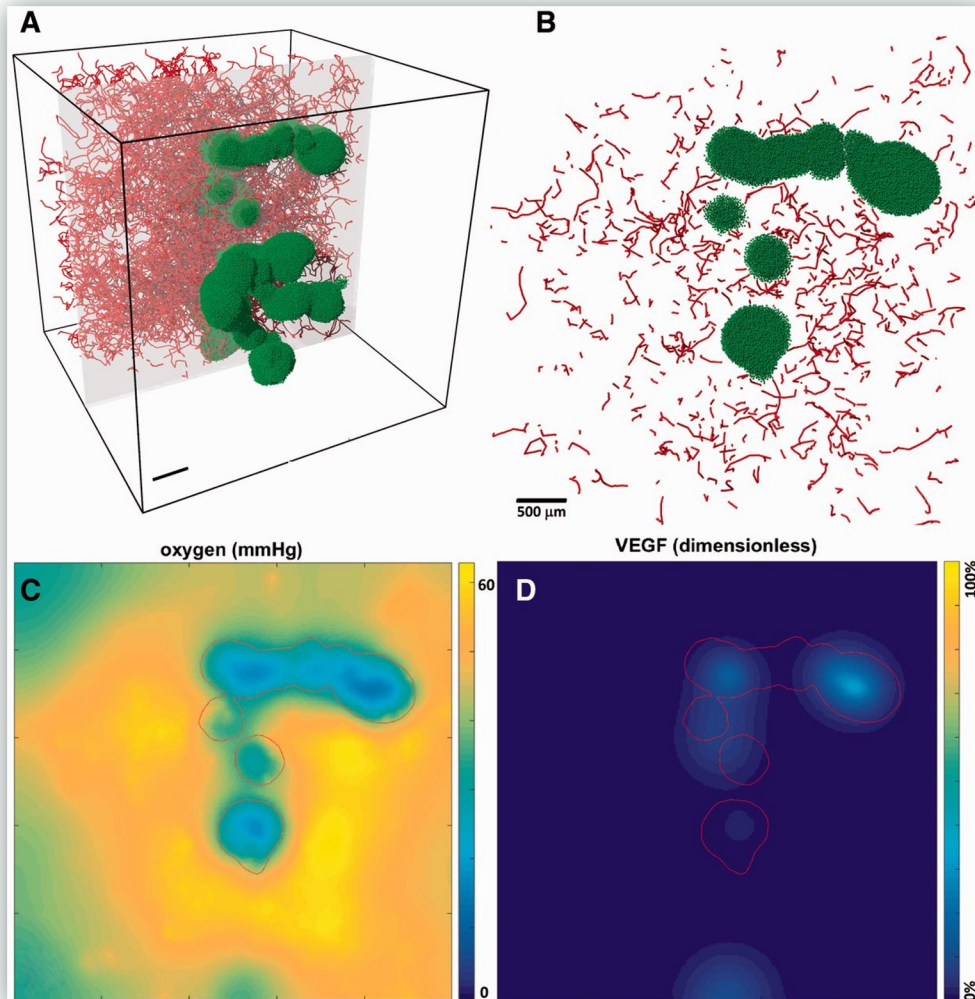


Tobey J et al. *Neuro-Oncology*, Volume 16, Issue 1, (2013)



Ghaffarizadeh A et al. *PLoS Comput Biol*. 2018

BioFVM (diffusive transport solver)



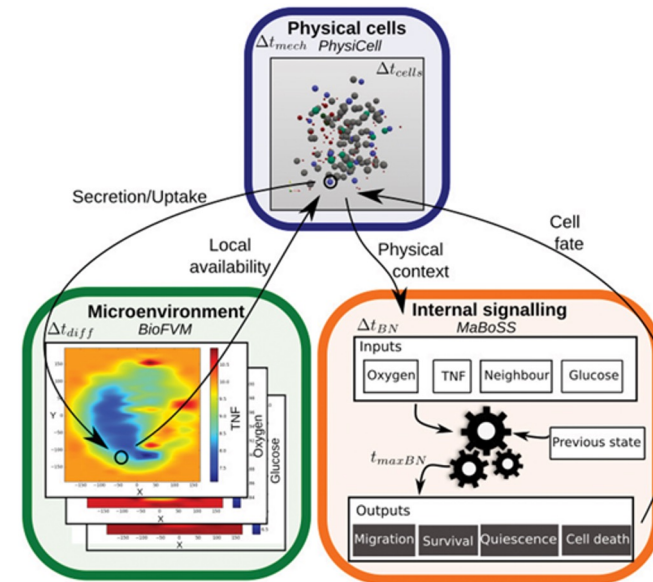
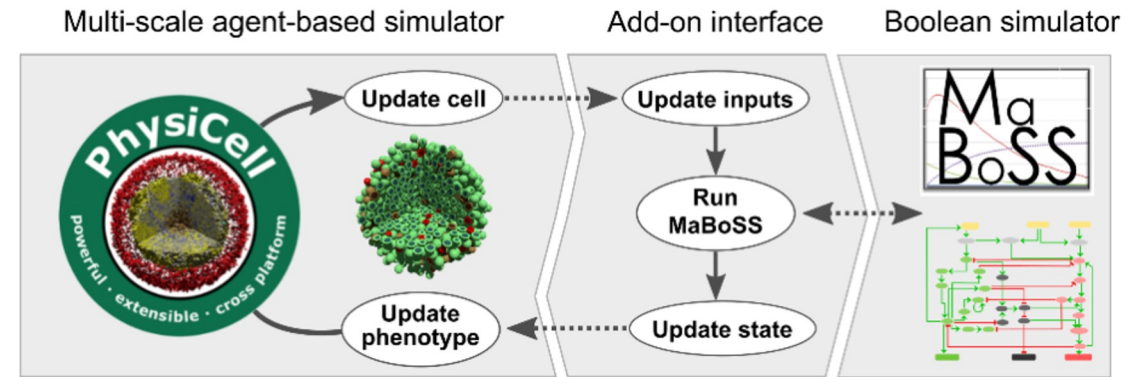
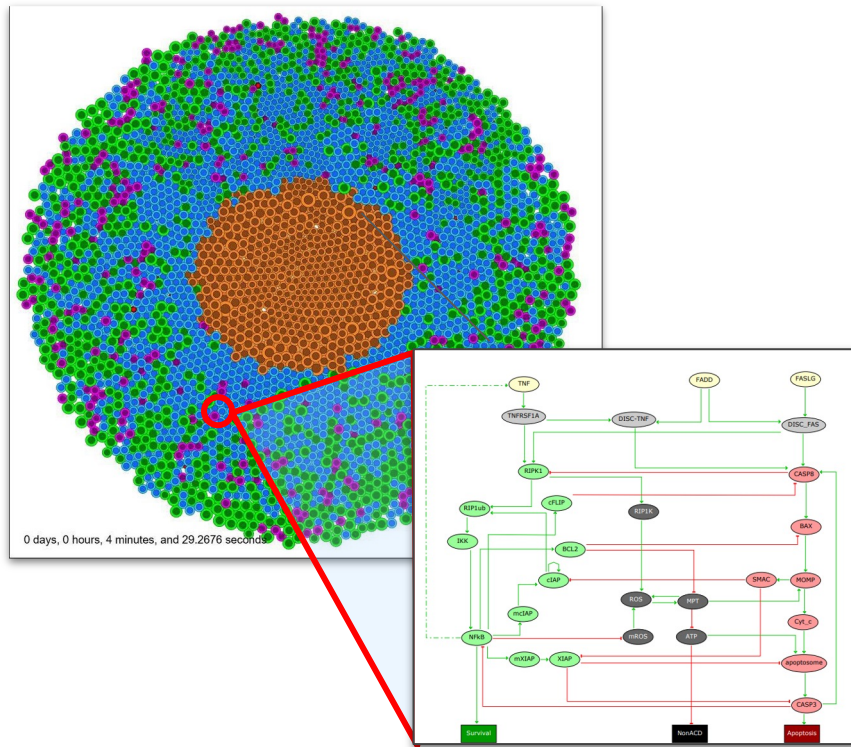
$$\frac{\partial \vec{\rho}}{\partial t} = \overbrace{\vec{D} \nabla^2 \vec{\rho}}^{\text{diffusion}} - \overbrace{\vec{\lambda} \vec{\rho}}^{\text{decay}} + \overbrace{\vec{S}(\vec{\rho}^* - \vec{\rho})}^{\text{bulk source}} - \overbrace{\vec{U} \vec{\rho}}^{\text{bulk uptake}}$$

$$+ \underbrace{\sum_{\text{cells } k} 1_k(\vec{x}) \left[\vec{S}_k(\vec{\rho}_k^* - \vec{\rho}) - \vec{U}_k \vec{\rho} \right]}_{\text{sources and uptake by cells}} \text{ in } \Omega$$

Extending PhysiCell

PhysiBoss (PhysiCell + MaBoSS)

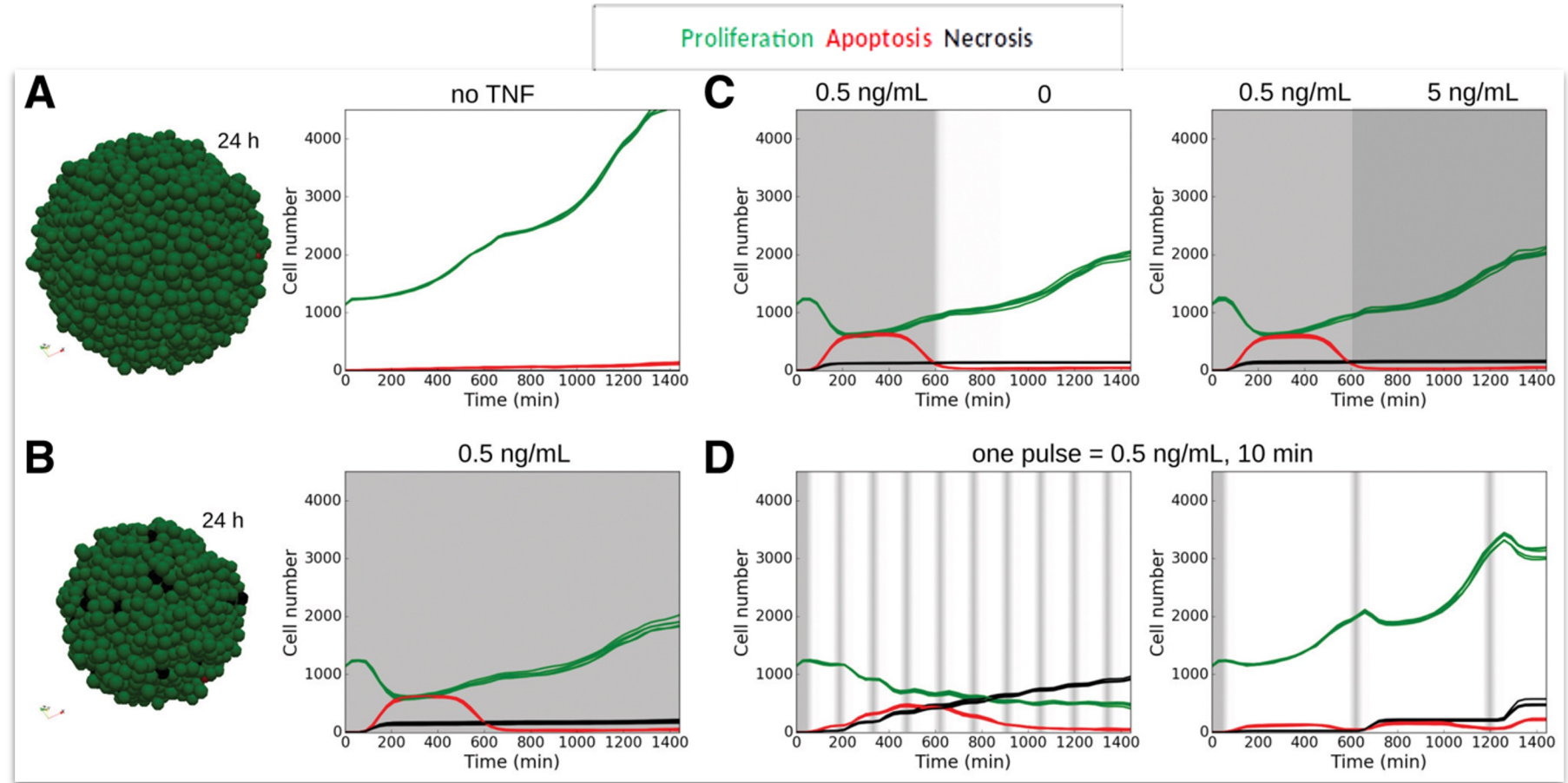
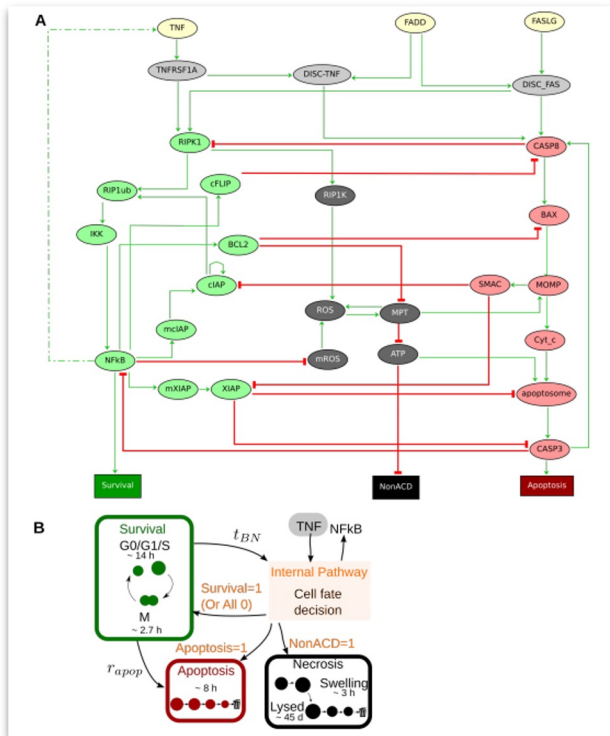
Cell state and decisions depend on embedded boolean models



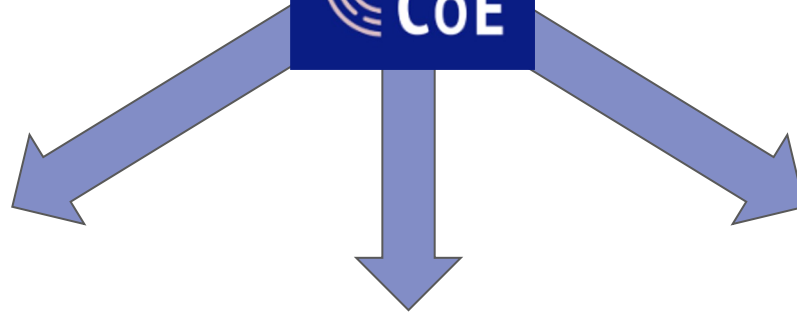
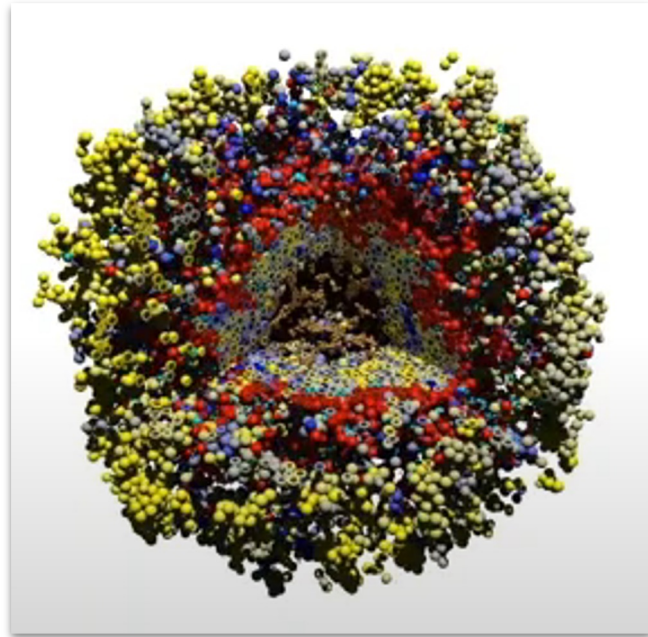
Extending PhysiCell

Agent-based + probabilistic logical models (PhysiCell + MaBoSS)

PhysiBoSS



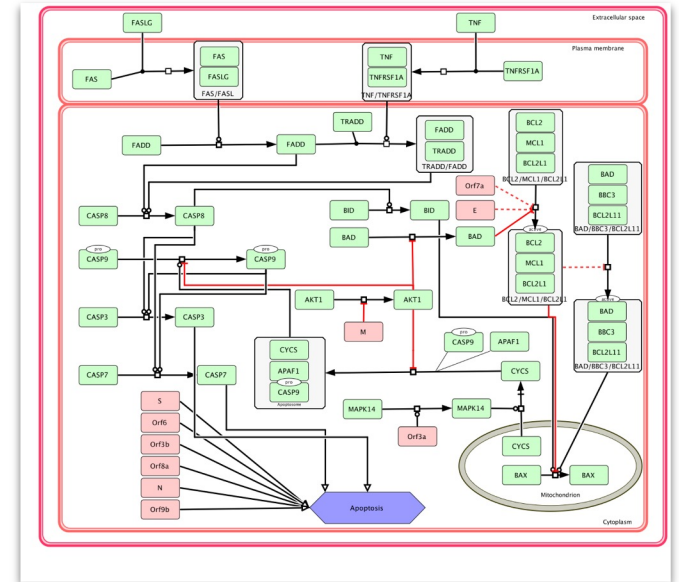
Cell level simulations



HPC



Molecular Pathways

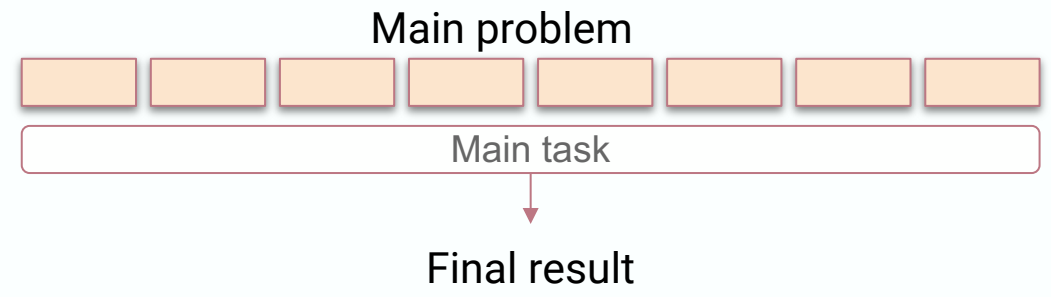


Parallel computing

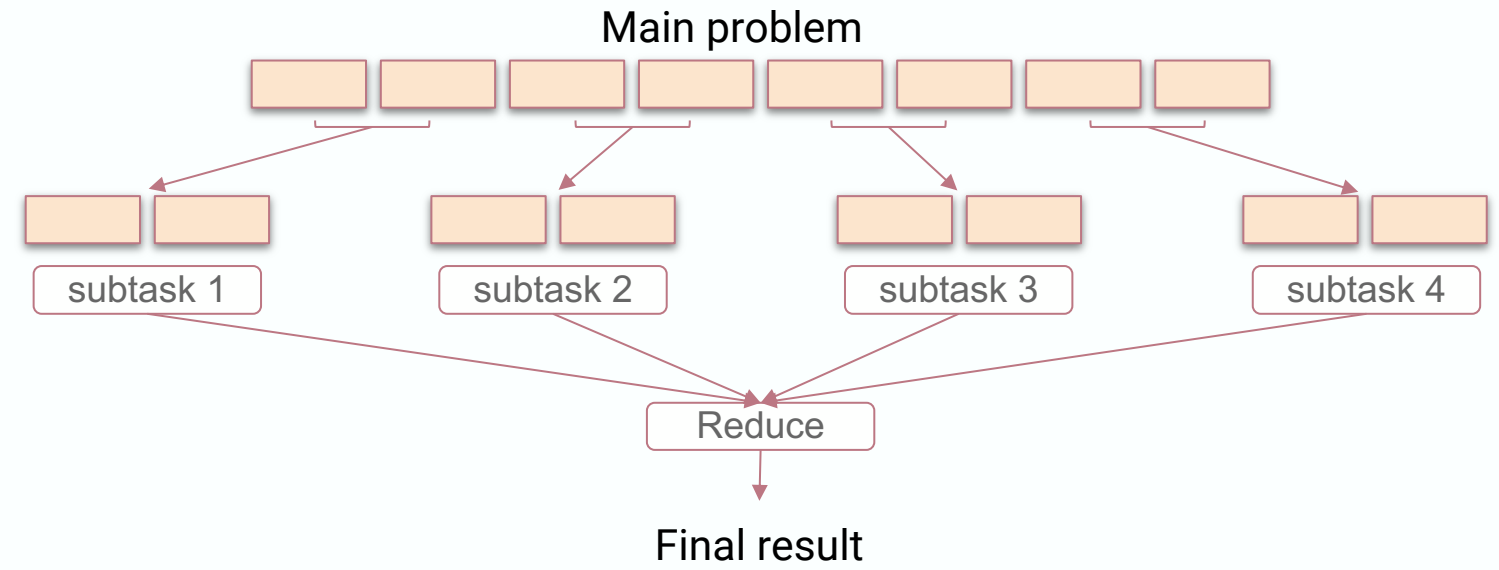
Traditional approaches

- Native support
- Based on logical threads
- POSIX threads (IEEE)

Serial computing

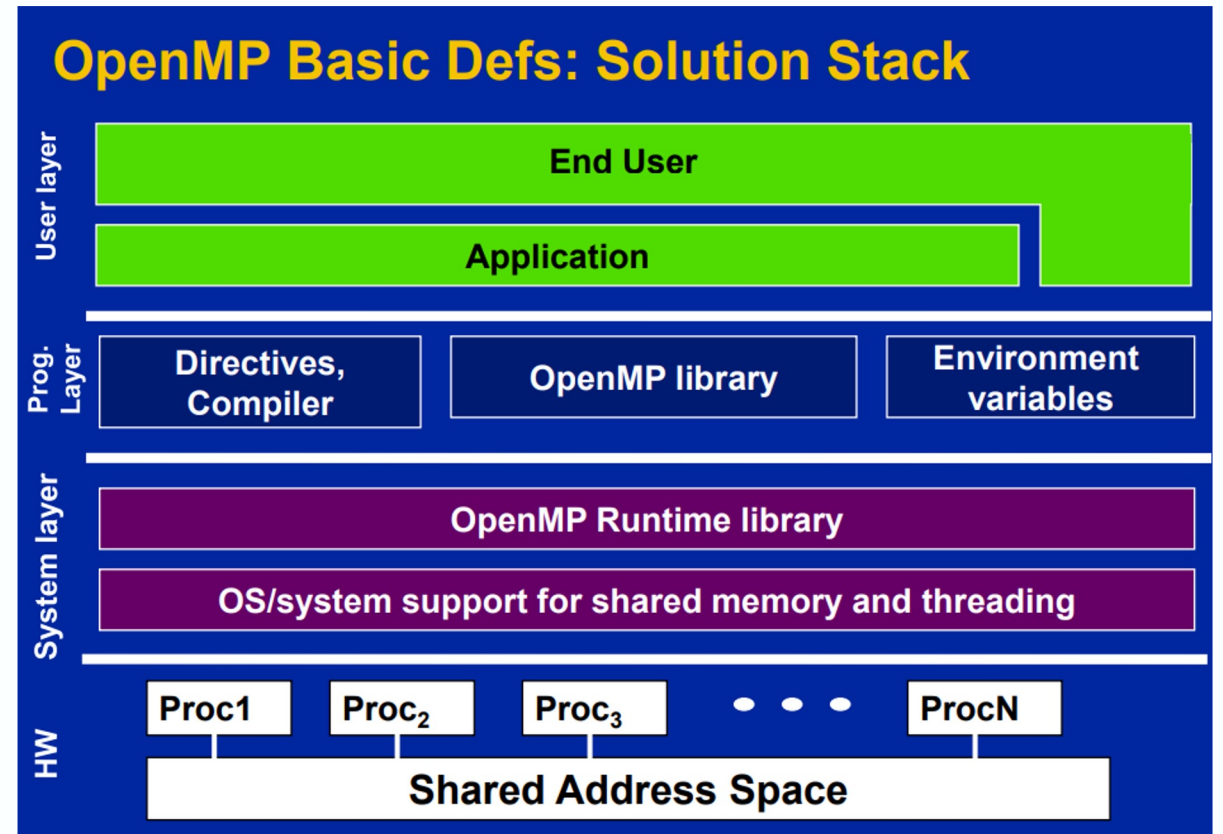


Parallel computing



OpenMP

- Directive-based
- Simple and flexible interface for developing parallel application
- API for direct multi-threaded, shared memory parallelism
- Comprised of three primary API components:
 - Compiler Directives
 - Runtime Library Routines
 - Environment Variables



Tim Mattson

Parallel computing

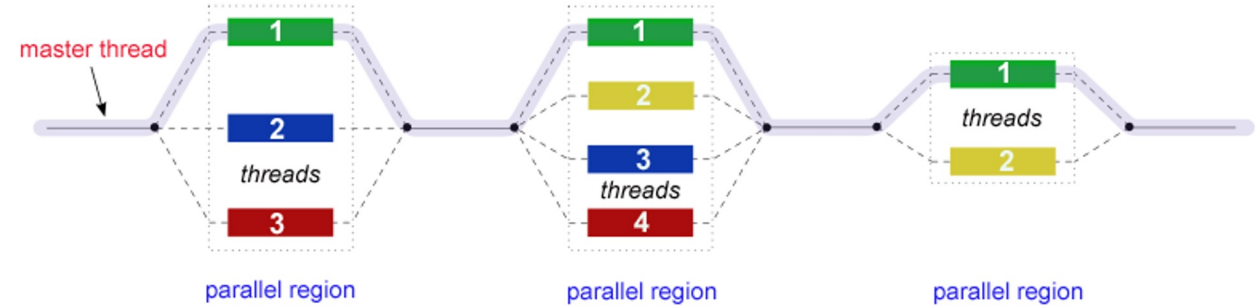
```
#include <stdio.h>
#include <omp.h>

int main(int argc, char** argv){
    int partial_Sum, total_Sum;

    #pragma omp parallel private(partial_Sum) shared(total_Sum)
    {
        partial_Sum = 0;
        total_Sum = 0;

        #pragma omp for
        {
            for(int i = 1; i <= 1000; i++){
                partial_Sum += i;
            }
        }

        //Create thread safe region.
        #pragma omp critical
        {
            //add each threads partial sum to the total sum
            total_Sum += partial_Sum;
        }
    }
    printf("Total Sum: %d\n", total_Sum);
    return 0;
}
```



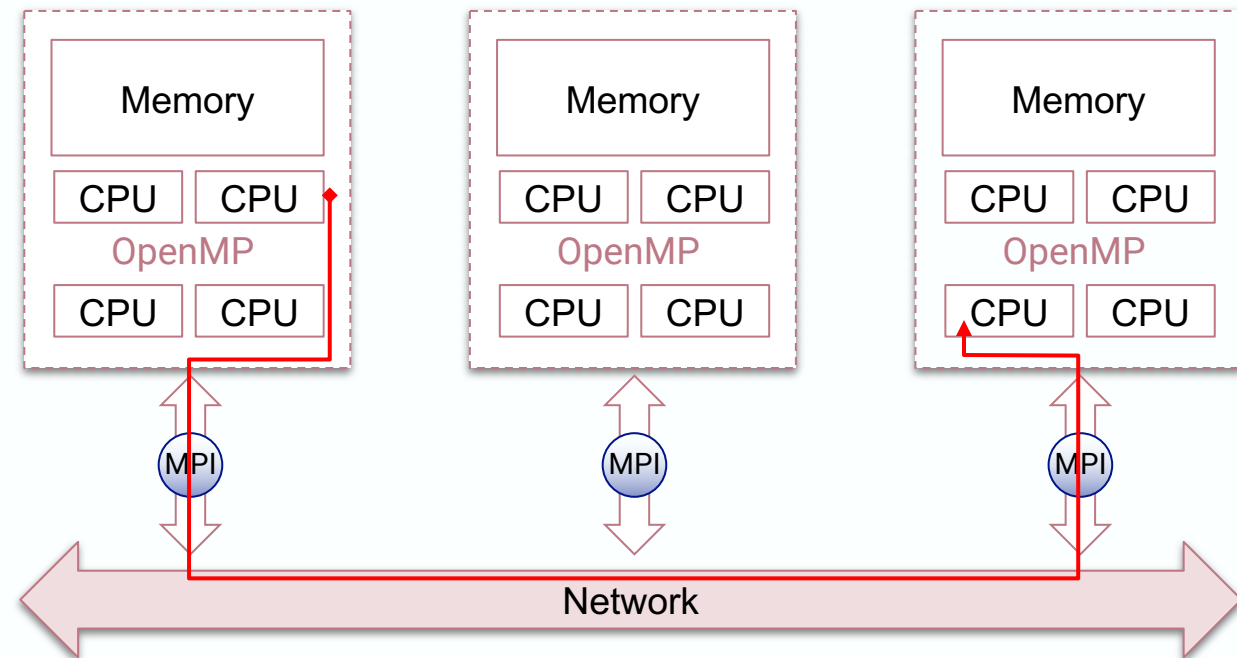
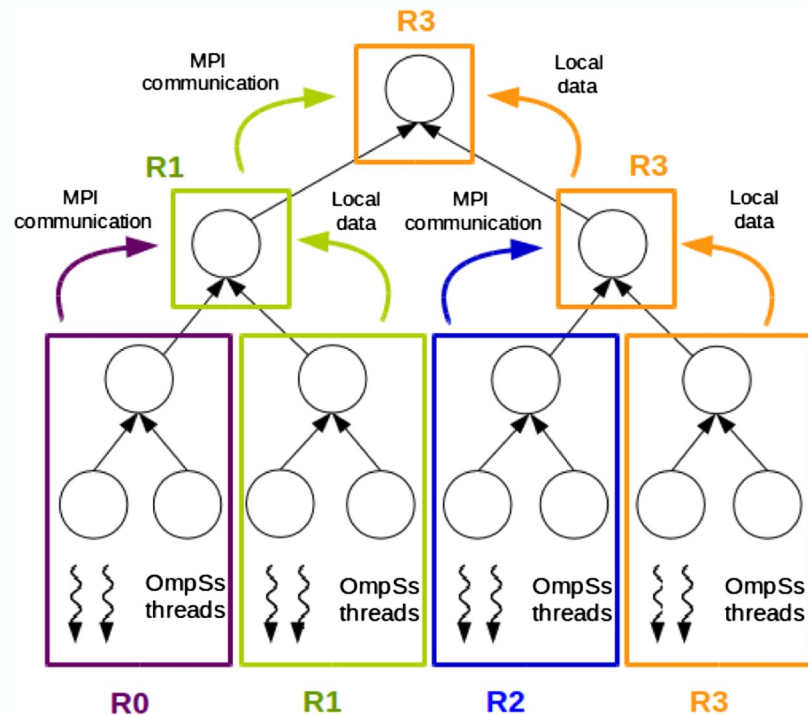
Example ploop.1.c

```
S-1 void simple(int n, float *a, float *b)
S-2 {
S-3     int i;
S-4
S-5     #pragma omp parallel for
S-6         for (i=1; i<n; i++) /* i is private by default */
S-7         b[i] = (a[i] + a[i-1]) / 2.0;
S-8 }
```

Distributed computing

Message Passing Interface (MPI)

- API for coordinating different nodes to jointly perform a given task
- Communication via the local network (latency is an issue)
- Several nodes work as a single machine
- Different implementations (OpenMPI, Intel MPI)



Distributed computing

Message Passing Interface (MPI)

```
#include <stdio.h>
#include <mpi.h>

int main(int argc, char** argv){
    int process_Rank, size_of_Cluster;

    MPI_Init(&argc, &argv);
    MPI_Comm_size(MPI_COMM_WORLD, &size_of_Cluster);
    MPI_Comm_rank(MPI_COMM_WORLD, &process_Rank);

    for(int i = 0, i < size_of_Cluster, i++){
        if(i == process_Rank){
            printf("Hello world from process %d of %d\n", process_Rank, size_of_Cluster);
        }
        MPI_Barrier(MPI_COMM_WORLD);
    }

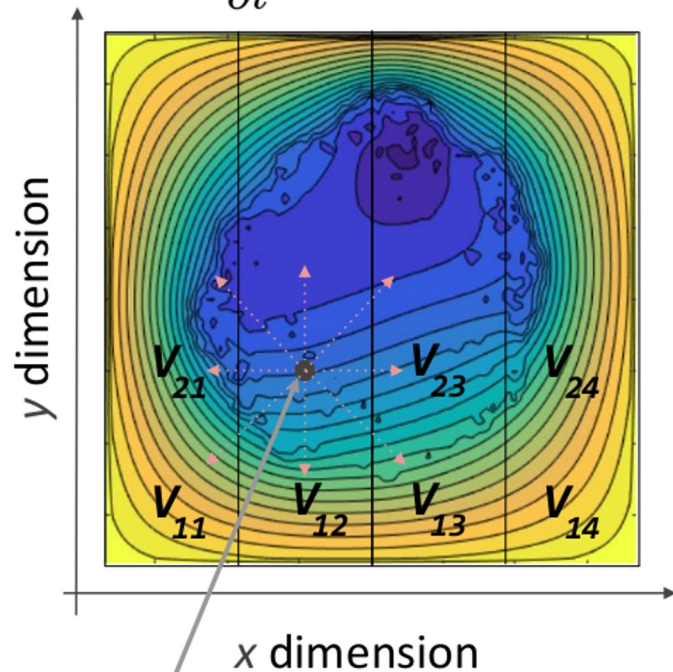
    MPI_Finalize();
    return 0;
}
```

<https://curc.readthedocs.io/en/latest/index.html>

Refactoring strategies in PhysiCell

PhysiCell-MPI

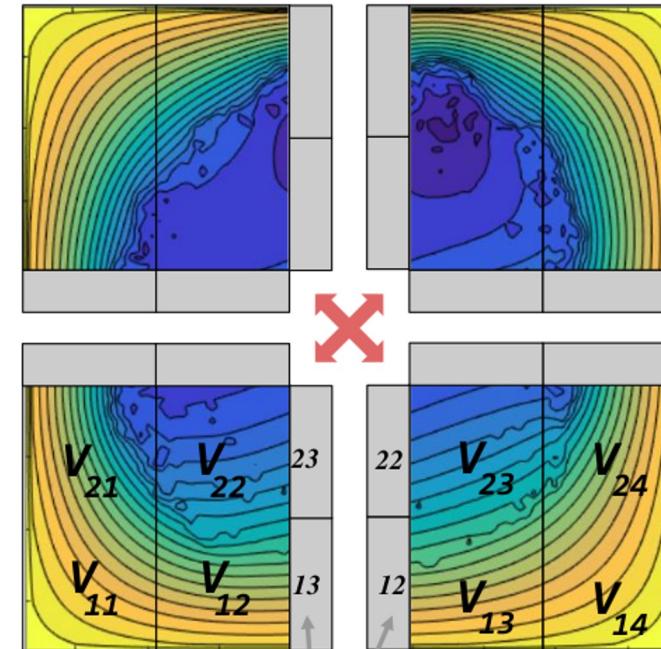
$$\text{Full Domain } \left(\frac{\partial \rho}{\partial t} = D \nabla^2 \rho - \lambda \rho \dots \right)$$



Individual Voxel: stores the values of each molecule concentration. Connected to other voxels through Moore neighborhood (PDE solver)

Domain
Decomposition

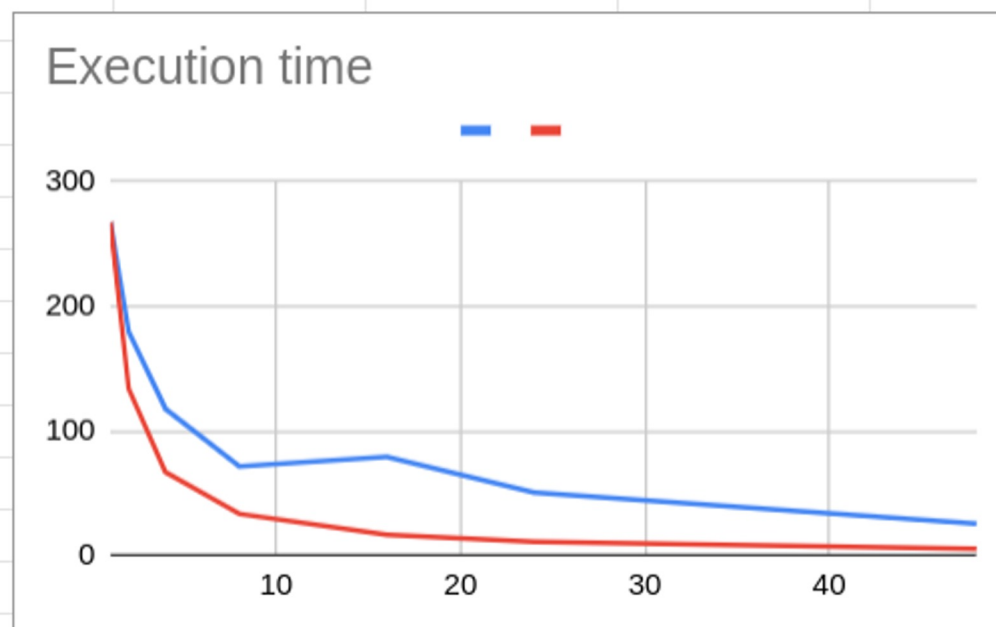
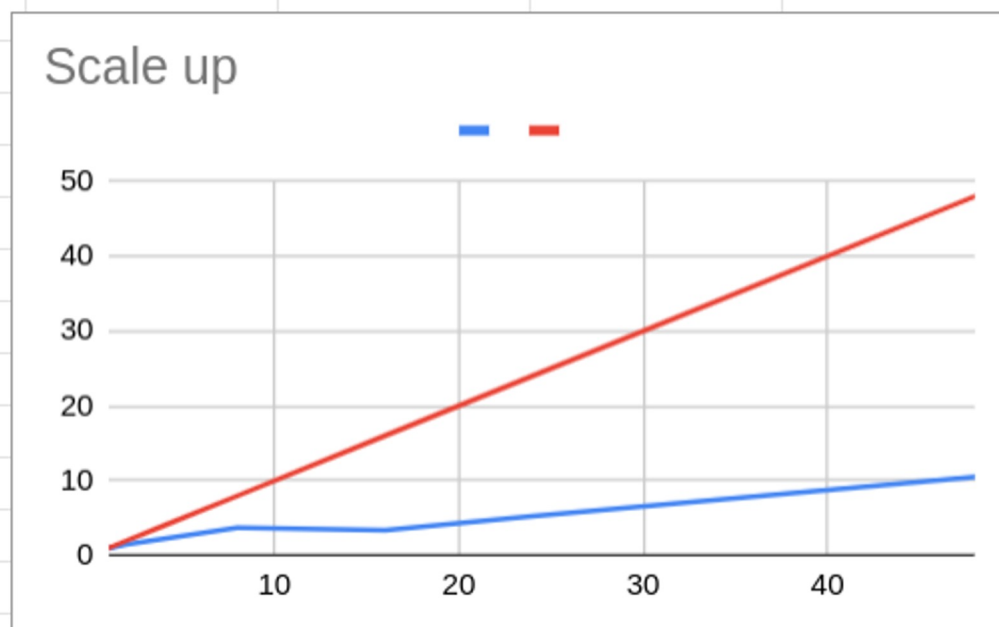
Sub-Domains i ($i = 1 \dots 4$)



Ghost (Halo) Cells: needed to update boundary voxels in a transparent way. Needed to exchange information between neighbour voxels

Hands-on

		CORES						
		1	2	4	8	16	24	48
NODES	1	266.942	179.2124	117.6434	71.4096	79.2203	50.5011	25.387
	2	123.5726	85.8754	60.0800271	39.0463			
	4	99.2707	77.2388	56.7724				



THANK YOU



HPC/Exascale
Centre of
Excellence in
Personalised
Medicine

www.permedcoe.eu

Follow us in social media:



www.linkedin.com/company/permedcoe

@permedcoe



The PerMedCoE project has received funding from the European Union's Horizon 2020 research and innovation programme under the grant agreement N°951773