# VITAE

# VIrTual brAin pErfusion

ERC Proof of Concept VITAE (GA 825829)

JCAD 2020


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# Outline

Context

Software

Benchmarks & results

Return on experience

Perspectives

# Context

## Problem

Blood flow is vital for feeding and cleansing neurons

## Recent discovery

Blood flow decrease before measurable cognitive decline in Alzheimer's Disease (2016)

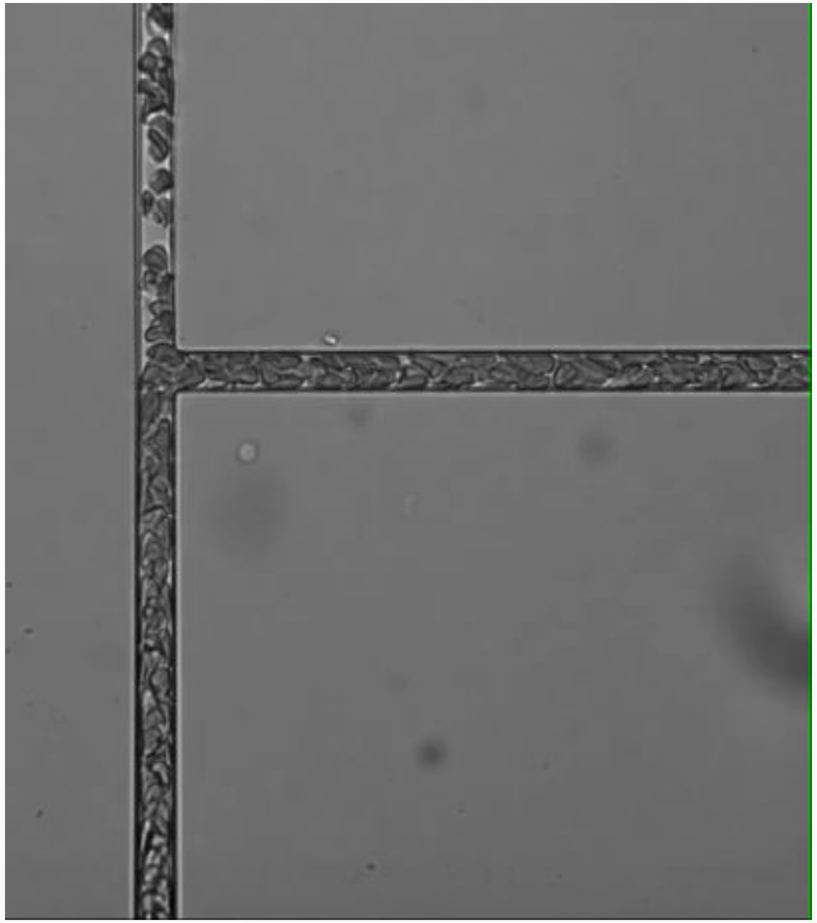
## Novel therapeutic strategy

development of drugs targeting the vascular system

## Idea

Use HPC simulation of cerebral blood flow to accelerate vascular targeted drug development

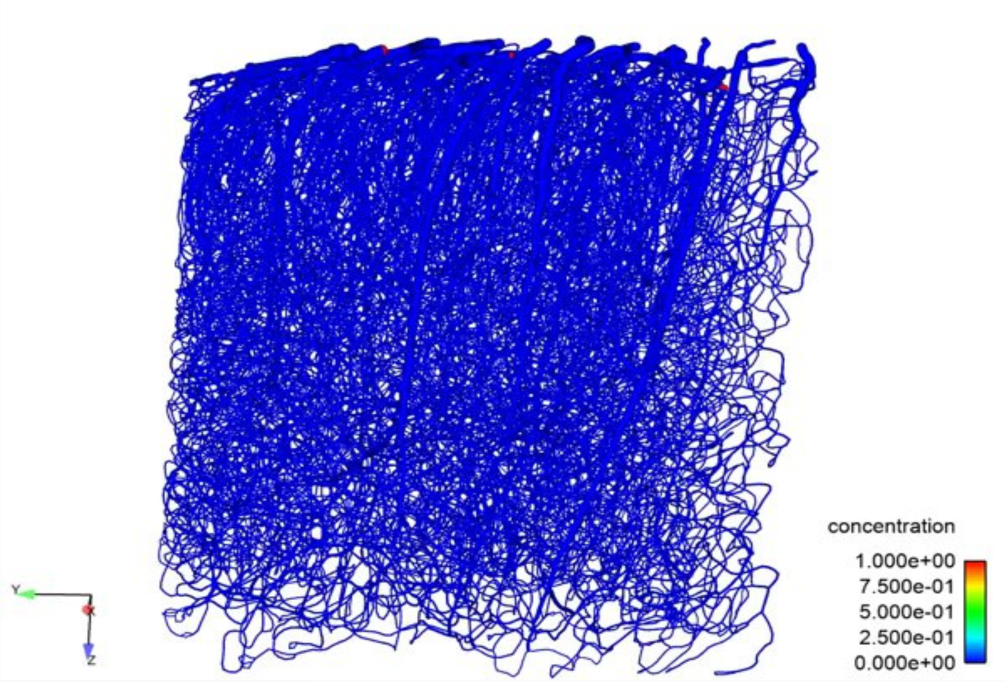
# Background


PhD IMFT Adlan Merlo

## Blood flow study

- Vascular networks have a complex topology
- Blood itself is a complex fluid

# Blood flow simulations




PhD IMFT Maxime Berg, Berg et al. 2020

1 $mm^3$ mouse brain

## Previous Simulations (using V1.0)

14k vessels

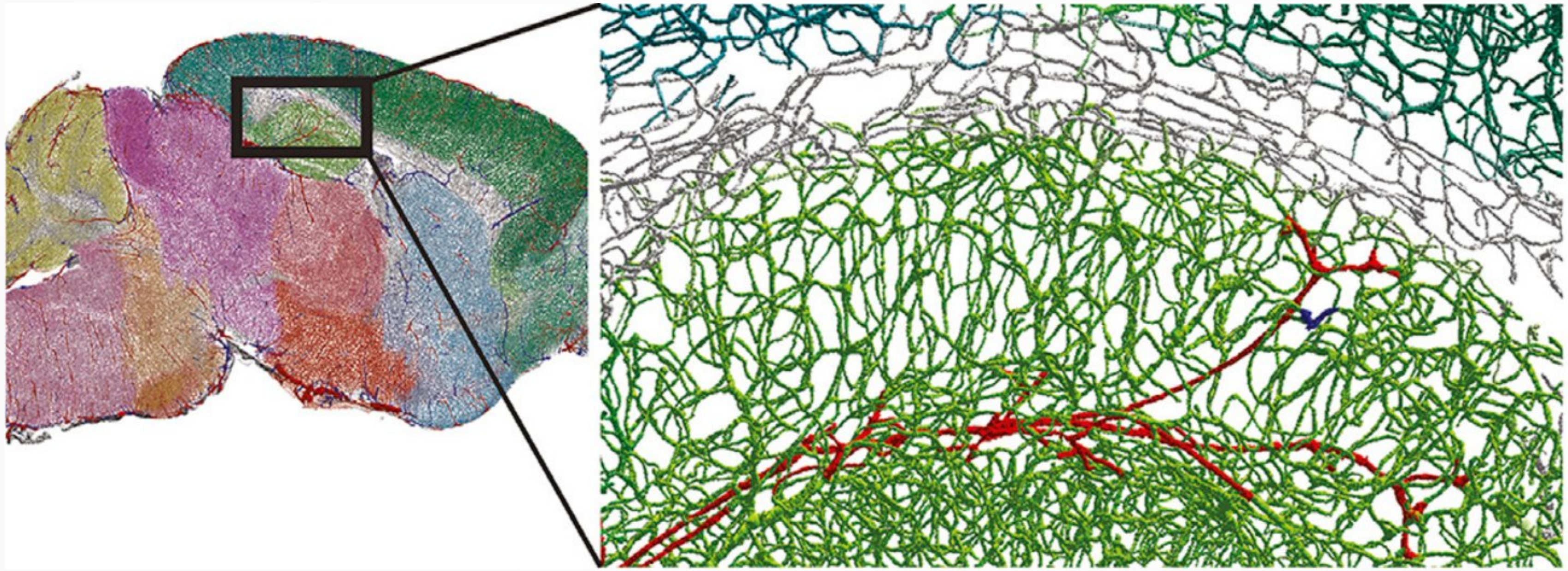
## Issue

Does not scale up for large vascular networks

# Whole mouse brain imaging

International effort to acquire whole mouse brain vascular networks

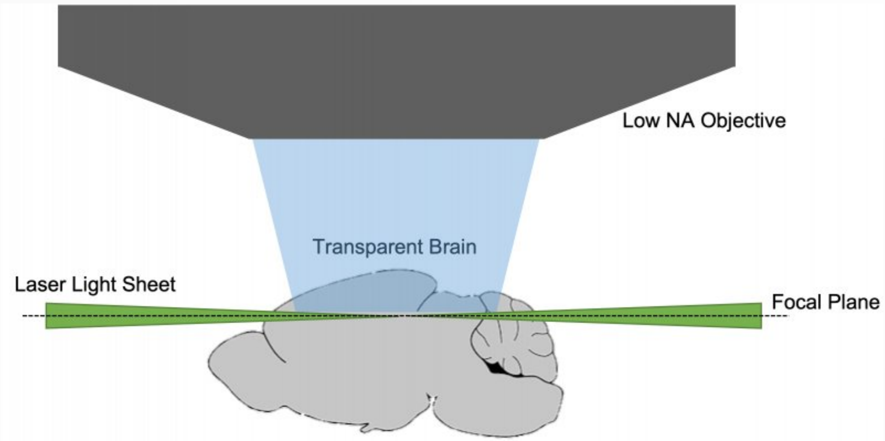
2020: publication of a pipeline reconstructing the full vascular network of a mouse brain at *Institut du Cerveau et de la Moelle épinière (ICM)*



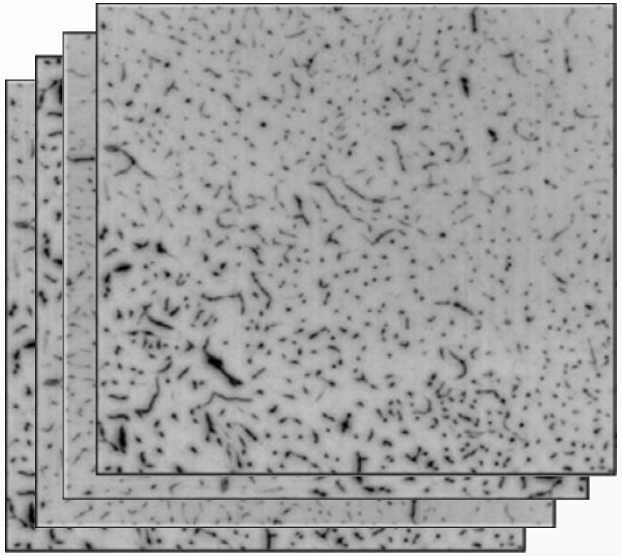
Kirst et al. 2020

# Whole mouse brain imaging

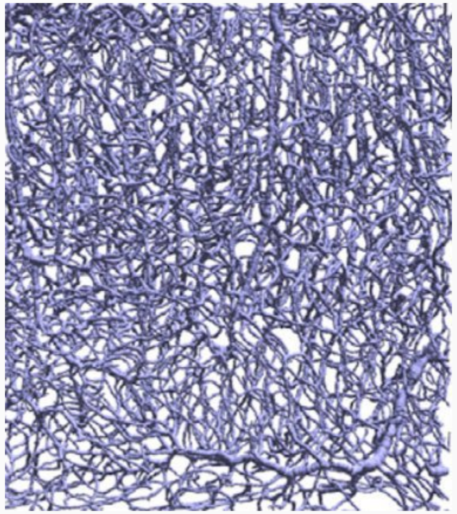
## Example: Lightsheet microscopy




visikol.com



Kirst et al. 2020

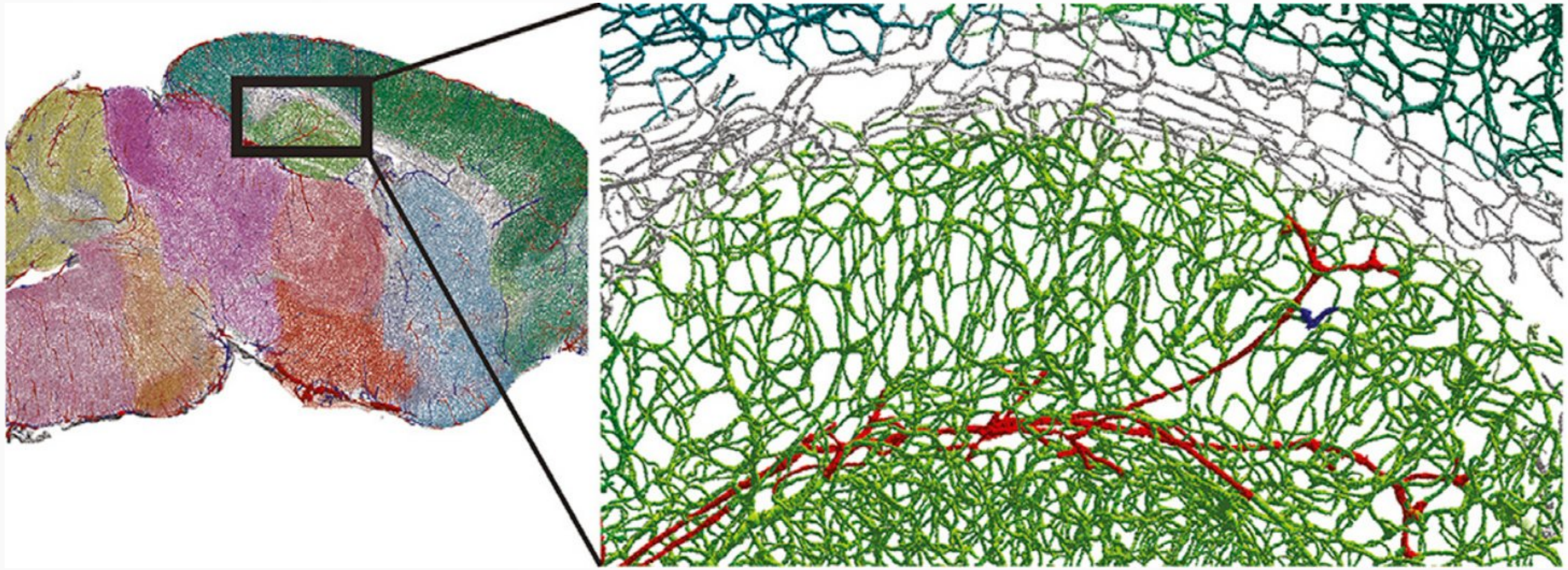


Kirst et al, 2020

# Whole mouse brain imaging

## Simulation goals :

- 5M to 10M vessels
- Pressure and blood flow
- Distribution of red blood cells
- Nutrient and drug delivery

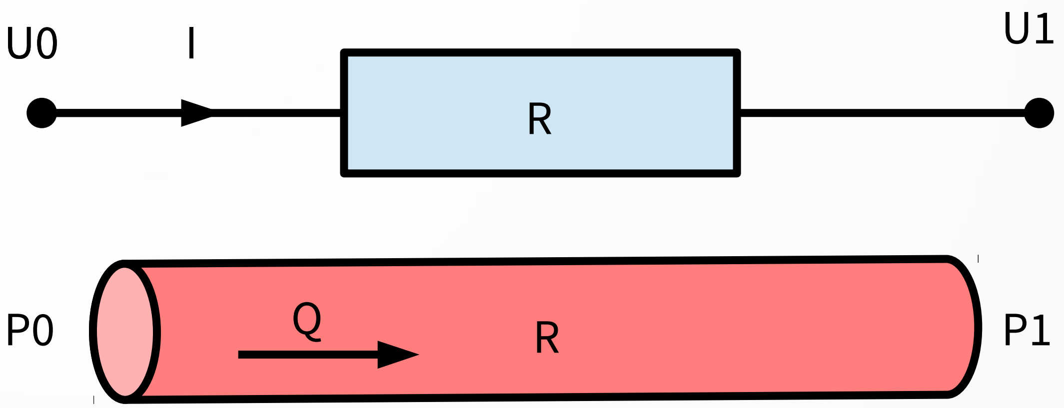


Kirst et al. 2020

# Flow solving

## Electrical analogy

- $\Delta U = RI$
- $\Delta P = RQ$




## Matrix formulation for full brain

- Inversion of a ~5Mx5M sparse square matrix M
- Requires gradient descent like algorithm
- Requires parallel calculation

$$Mp = y$$

# History

- 2014: V1 start
  - Research code in C++
  - Not scalable
  - Completely written on top of *PETSc*
- 2018: ERC POC grant
  - Scaling for full brain
  - Code industrialization
- 2019: V2 start
  - Hiring dedicated software engineer
  - Codebase mostly rewritten
- 2020: first tests on full brain data (Kirst et al.)

# The VITAE software

## Design goals

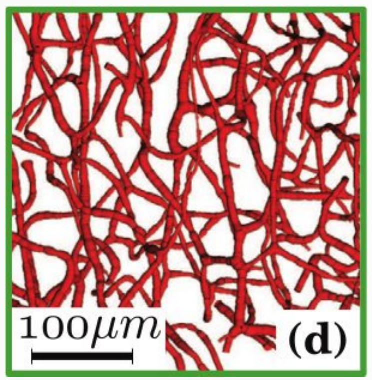
- Fully parallel processing
- CPU efficient
- Modern C++
- Modular API
- User friendly
- Fully documented

## Dependencies

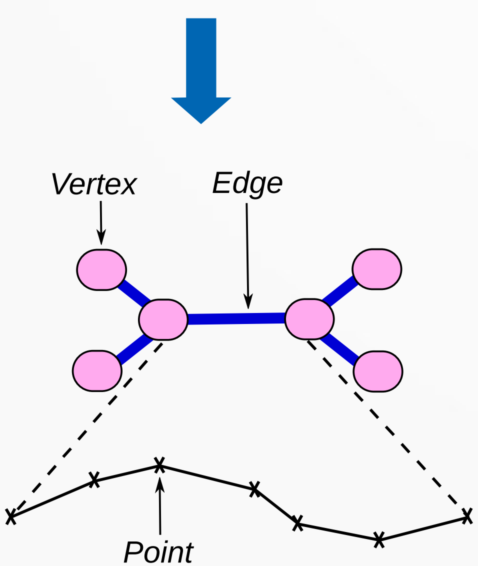
- std=c++14 (gcc9, ICC 18 & 19)
- Compilation (cmake-3.10)
- MPI (OpenMPI-2.1.1, MPICH-3.3.2)
- Parallel IO (HDF5-1.10.5)
- Linear algebra (PETSc-3.7.7)
- Graph partitioning (Parmetis-4.0.3)
- JSON Config (nlohman-json-3.7)
- JSON Schema #7 (pboettch-2.0)
- Unit tests (cxxtest-4.4)

# Data model

## Vascular networks have a graph structure




Peyrounettte et al. 2018

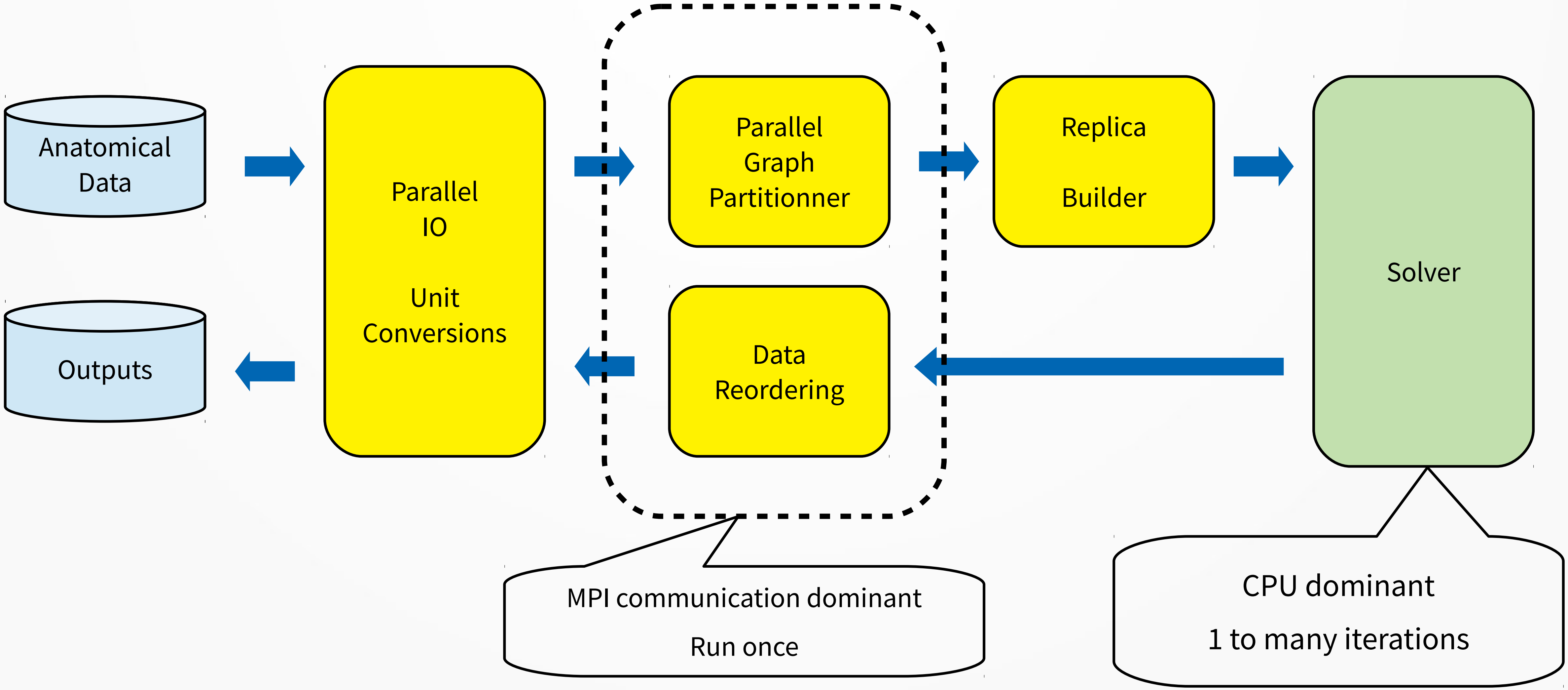



Three major categories

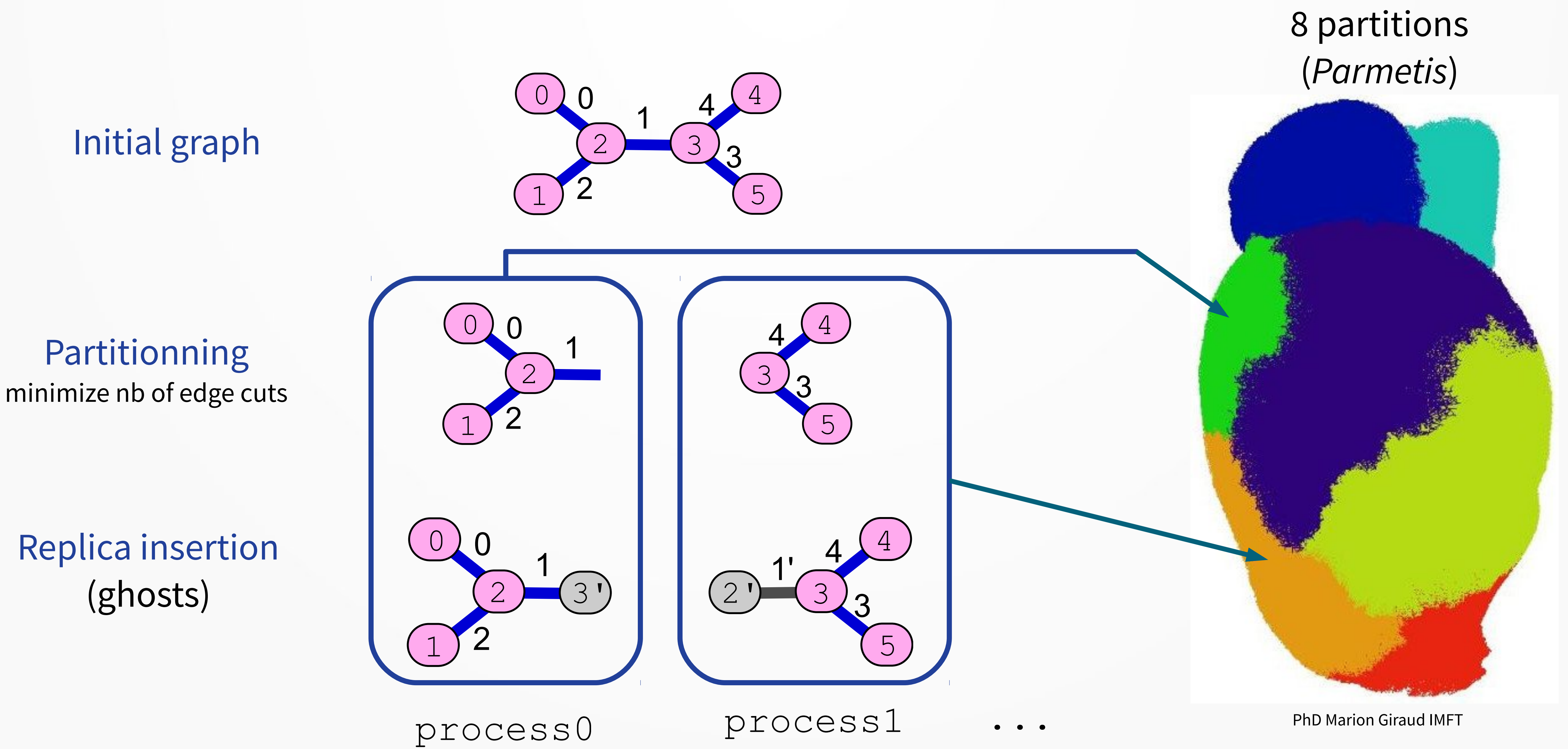
- `vertex` for bifurcations
- `edge` for vessels
- `point` for vessels path (grouped by edge)

| Network | Size [vertex] | Memory footprint estimation |
|---|---|---|
| [V1] Kleinfeld (mouse) | 10 k | 11.7 MiB |
| [V2] Average mouse brain | 5 M | 6.1 GiB |
| Average Human brain | > 1 G | > 1.2 TiB |

# Data flow

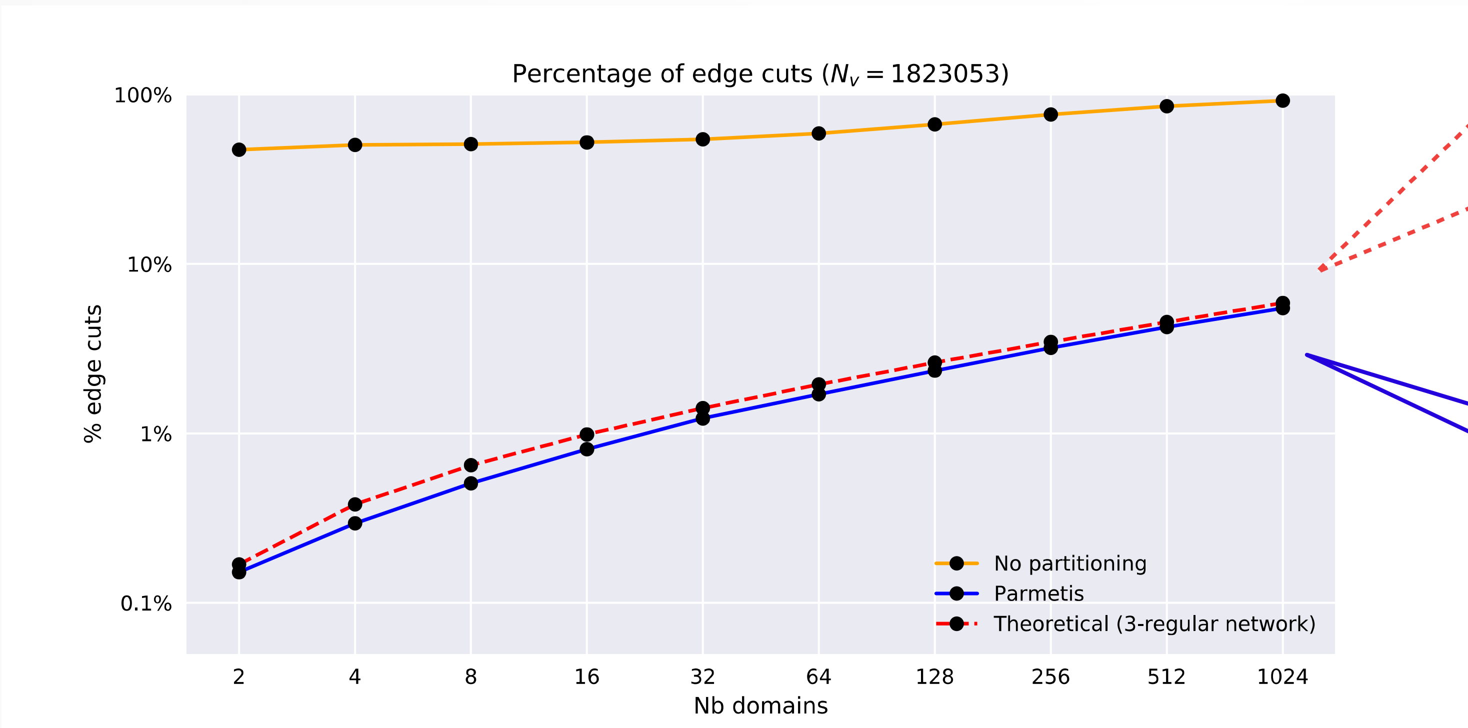

Anatomical Data
Outputs
Parallel IO
Unit Conversions
Parallel Graph Partitionner
Data Reordering
Replica Builder
Solver
MPI communication dominant
Run once
CPU dominant
1 to many iterations

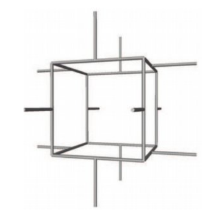
# Graph Partitioning



# Benchmarks

## Efficiency of graph partitionning



*3-regular*
*Synthetic network*

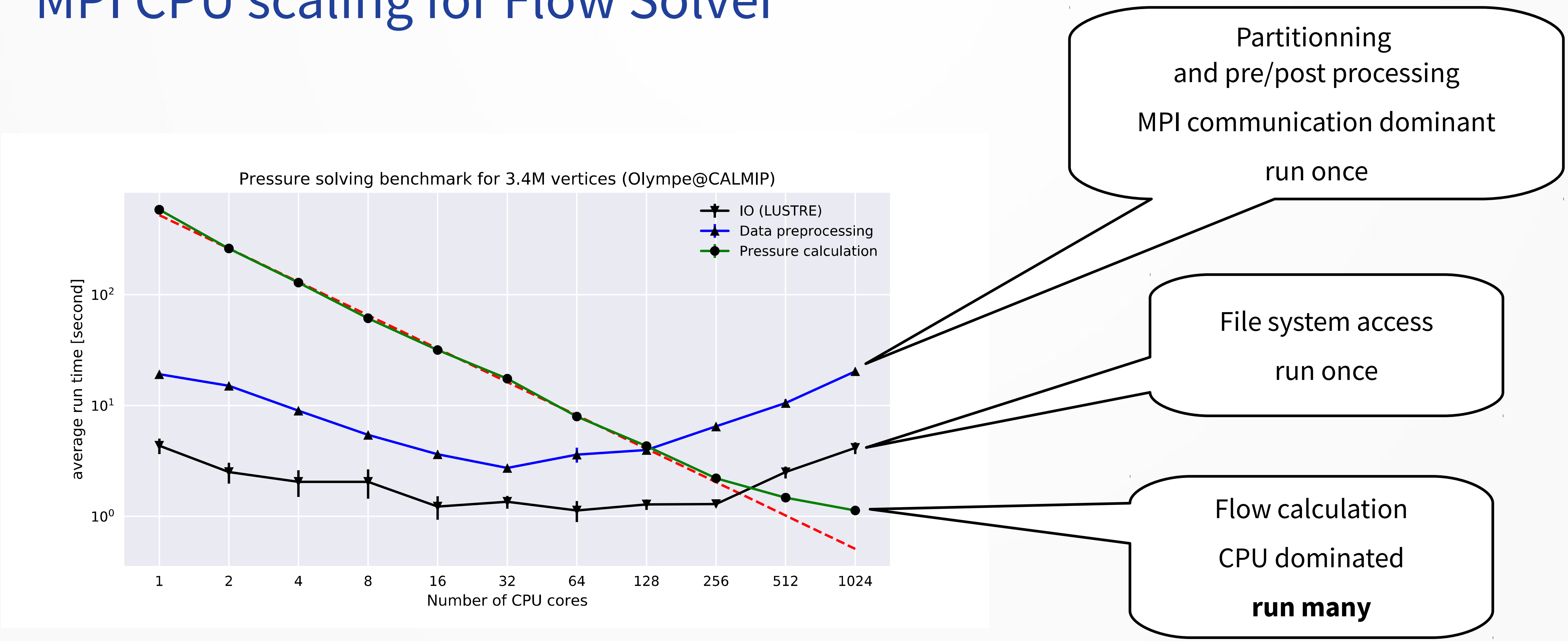
$$ncut \sim O\left(N_d^{1/3} \times N_v^{2/3}\right)$$

***1.8M vertex network***
***(Kirst 2020 CU)***

Lower is better

# Benchmarks

## MPI CPU scaling for Flow Solver

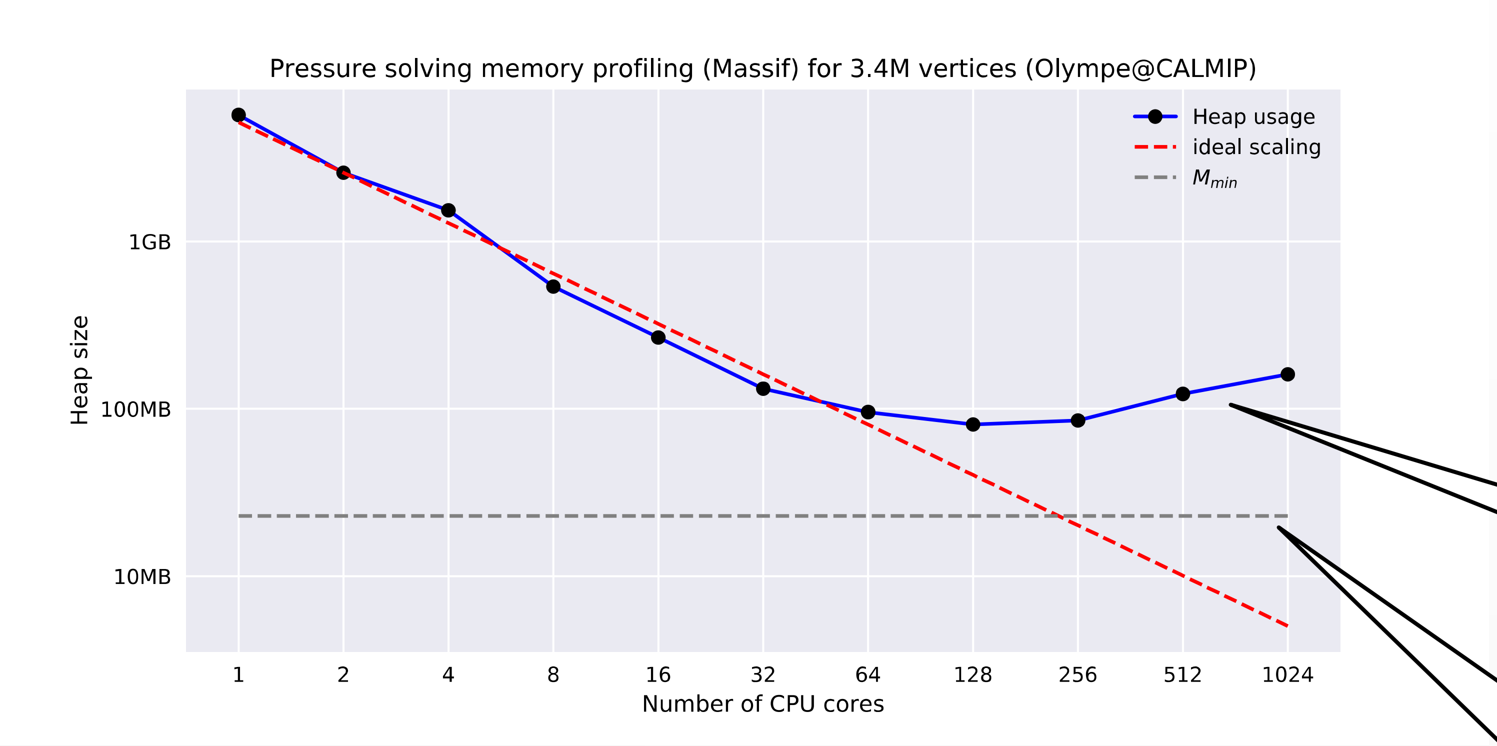



Lower is better

# Benchmarks

## MPI peak memory scaling for 1 process

Profiling tool: `valgrind --tool=massif`




`ms_print massif.out`

Lower is better

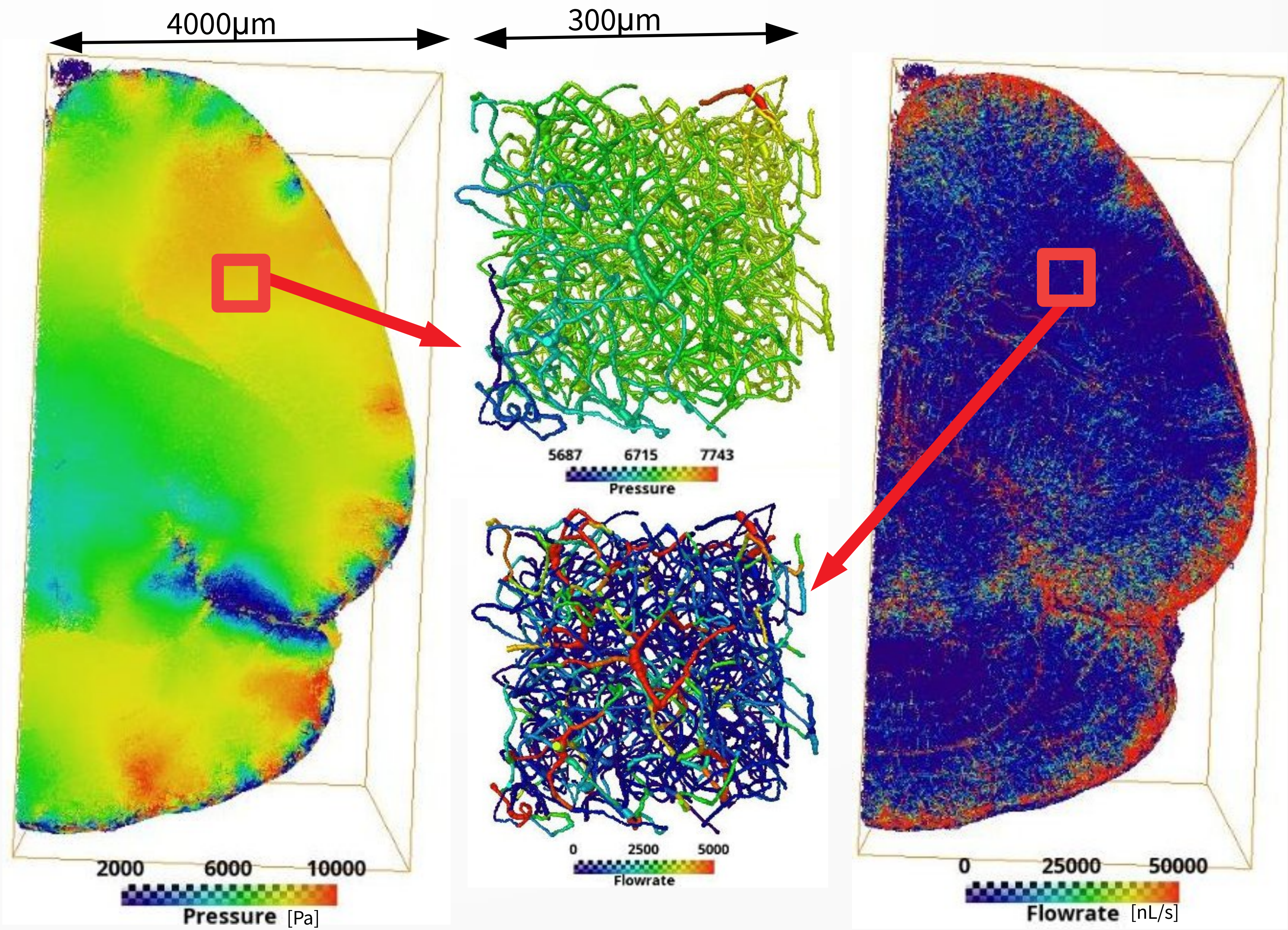
Memory excess
Dominated by
*Parmetis MPI buffers*

*Minimum*
*Process size*

# Results

## Full brain pressure and flow rate calculation

- Half mouse brain
- Data source:
  - ICM (Kirst et al. 2020 CU)
  - HDF5 File size: 507MB
  - Nb vertices: 3.4M
  - Nb edges: 4.7M
- Calculation
  - Olympe@CALMIP
  - ~10 minutes
  - one process
- Visualization
  - Avizo




PhD Marion Giraud IMFT

# Issues

## Technical

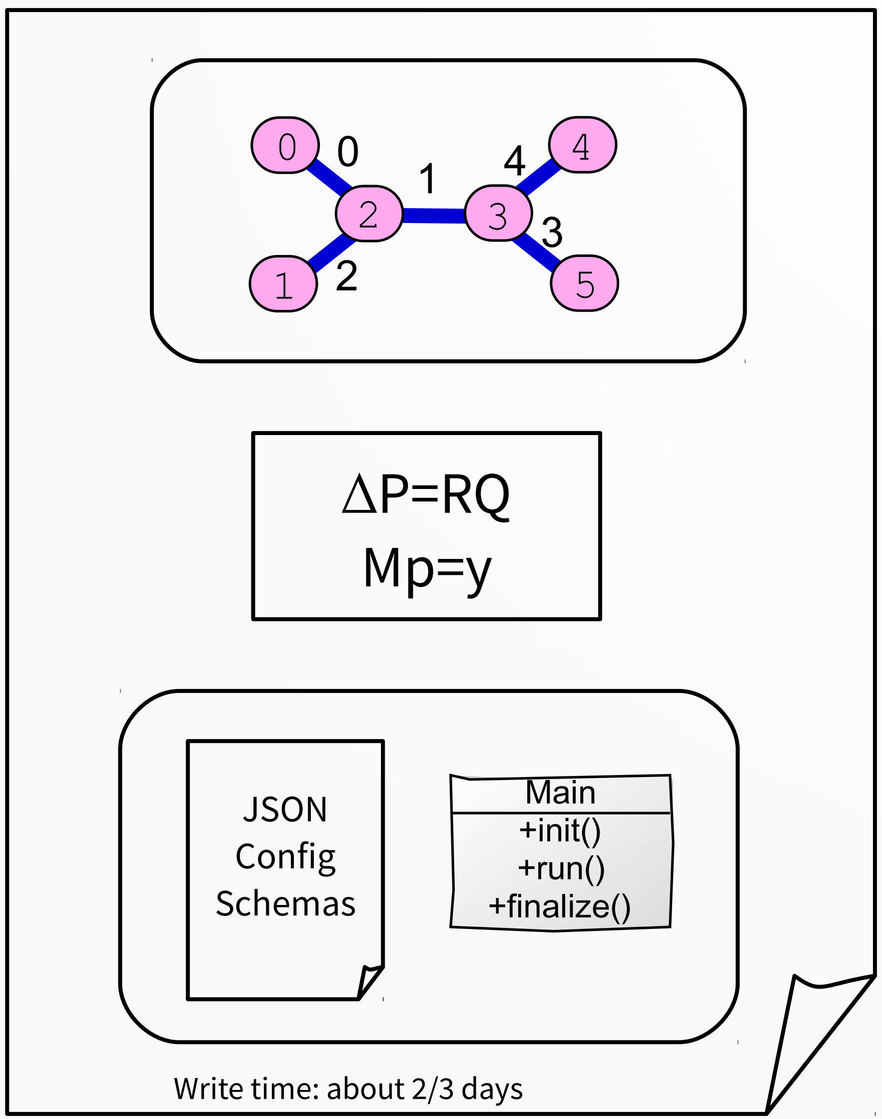
- PETSC installation & config
- Direct use of HDF5 instead of PETSc wrapping
- MPI is not very well suited for graph manipulation
  - Graph structure requires to call various mixtures of `Mpi_Alltoall()` and `Mpi_Alltoallv()`
  - Average nb of connected domains is 13 which may require specific optimizations
- Intel ICC18 compiler (std::shared_ptr<std::array>, etc.), ICC19 easier
- CMake steep learning curve, one has to use modern version
- C++ version of dependencies often not available or incomplete
  Example: HDF5, PETSc, MPI, etc.

## Other

- Semantic
  - Example: disambiguate UIDs versus global offset and local offset

# Solver teamwork

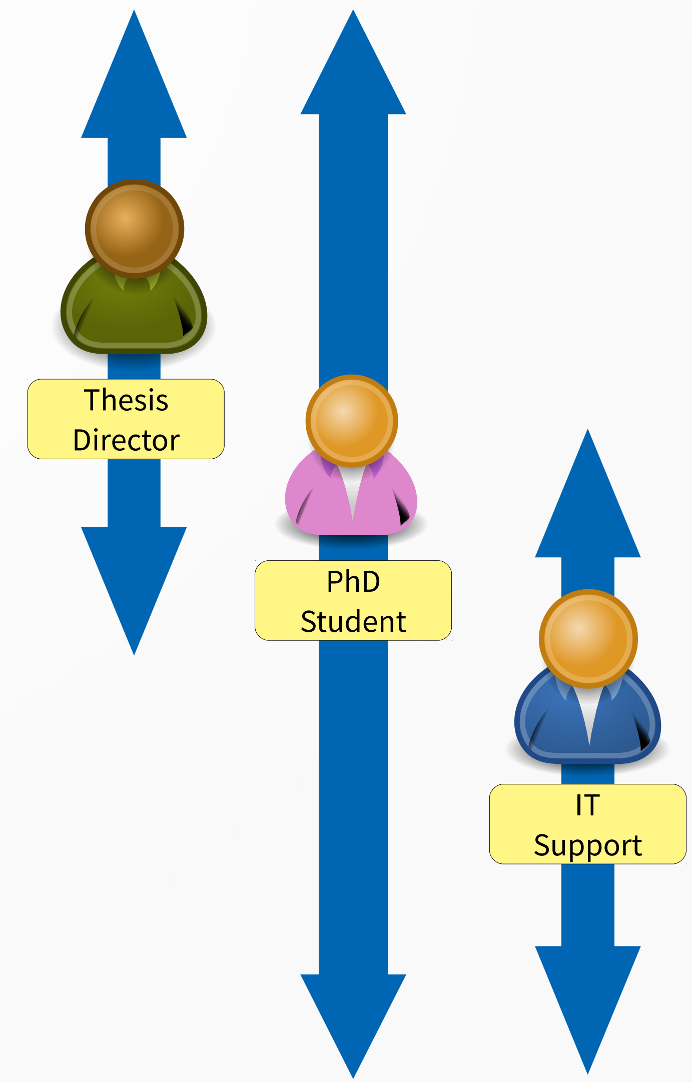
## Solver specifications




1) Scientific goal
   Mesh definition

2) Numerical scheme
   Algorithm

3) Code Specifications
   Data, Object Model

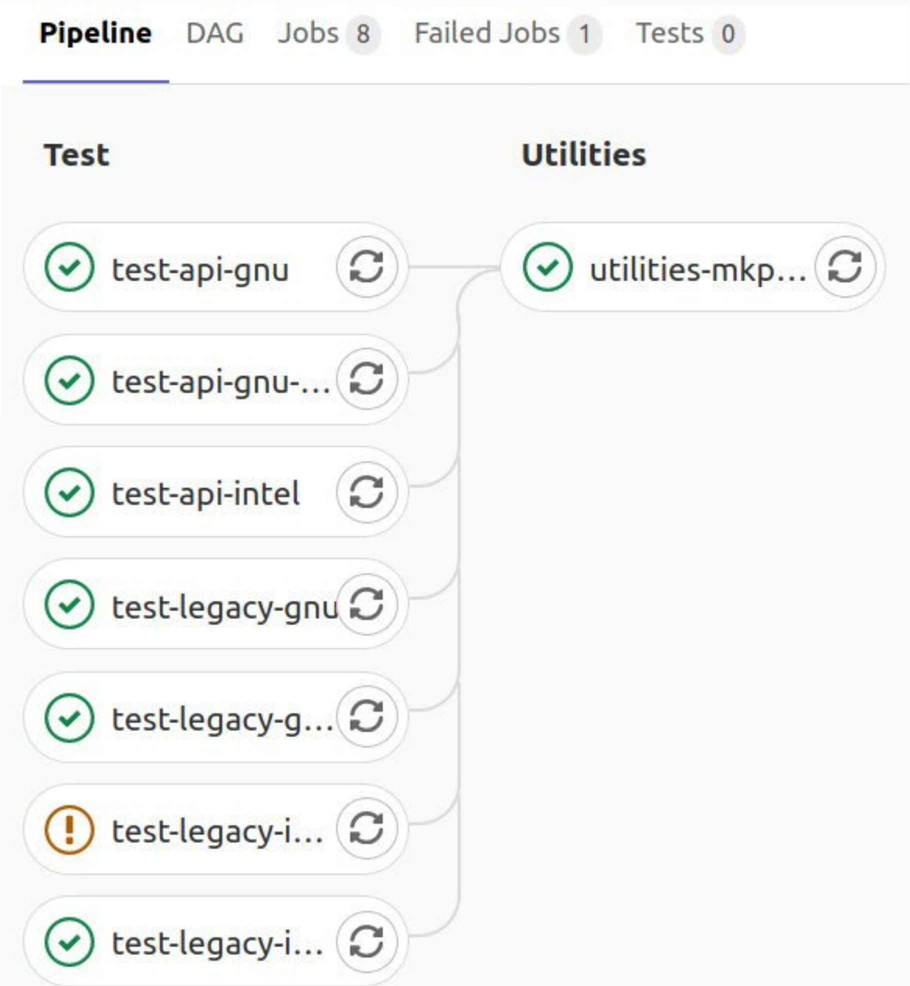


# Software quality

## Continuous integration

- Git versionning
- Wiki
- Runners
- unit tests

GitLab




## Naming convention document

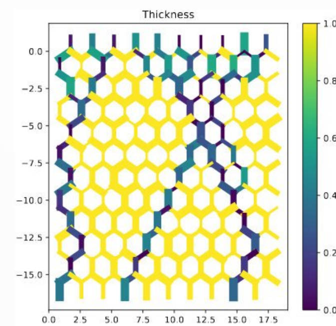
## Schema validation

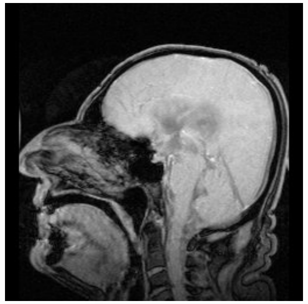
## Documentation

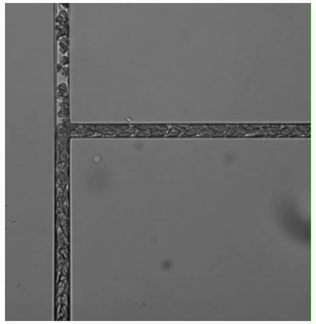
- Latex manual
- Rich doxygen code snipets

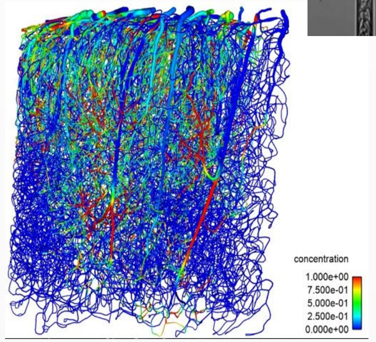
# Scheduled Projects

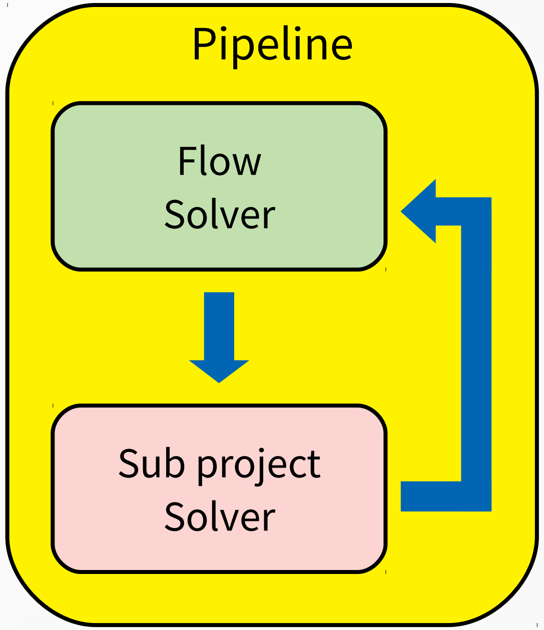
- Solver: *BrainPulse*
  - Solver for blood pulsatility
  - Project lead: Alexandra VALLET (univ. oslo)
- Solver: BioGrow
  - Simulation of bacterial growth
  - Project lead: Jean-Daniel Julien
- Solver: *PhaseSeparation*
  - Calculation of blood cells concentration in plasma
  - Initial author: Maxime Berg
  - Porting to VITAE API V2: Maxime Pigou
- Solver: *MassTransport*
  - Simulation of solute transport into blood
  - Initial author: Maxime Berg
  - Porting to VITAE API V2: Alexandre Sauvé







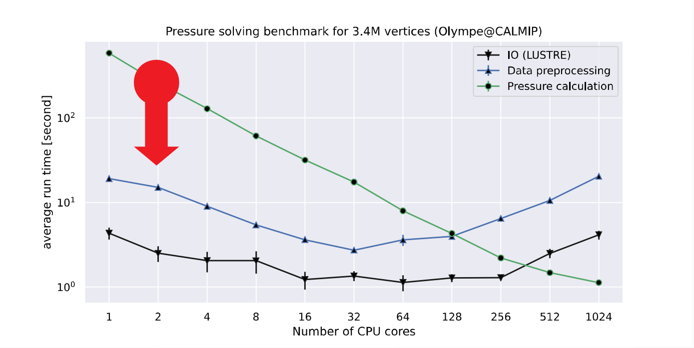



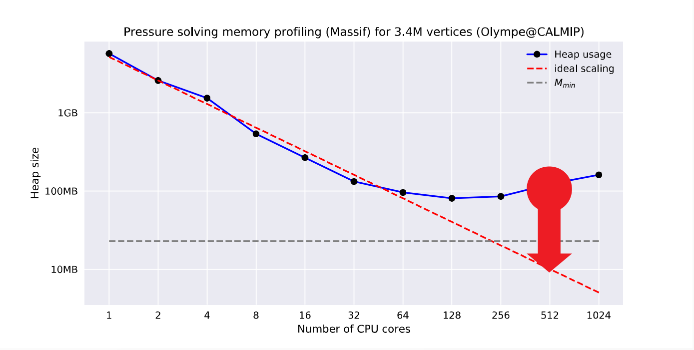

depth 2
iterative solvers

# Evolutions

## Technical

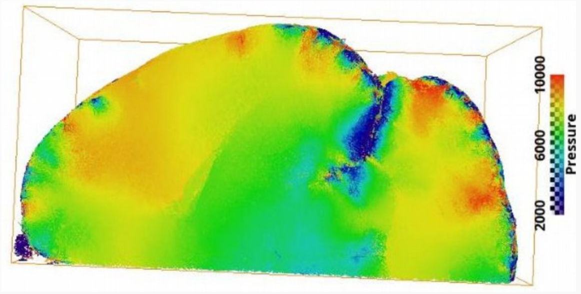
- Improve flow solver convergency time (*PETSc* KSP methods)
- Improve partitioning scaling (Example: test *PT-SCOTCH*)




## Data exploitation

- New vascular networks  from various collaborations
- Reduction of full brain results




Questions