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University of Canterbury Super Computer

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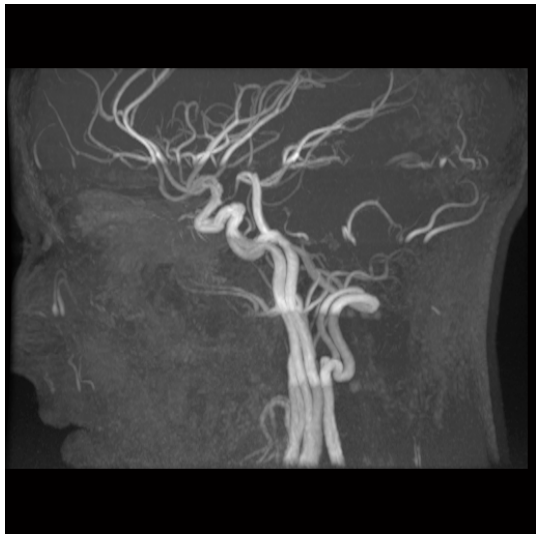
System Level Acceleration: Applications in Cerebro-vascular Perfusion.

Tim David and Steve Moore



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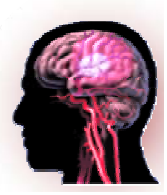
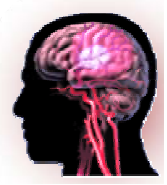
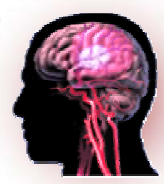


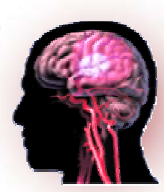
- What is system level acceleration?
- "the deployment of diverse compute resources to solve the problem of a single work stream, all with the experience of a single server to the user."
  - System Level Accelerators: A Hybrid Computing Solution, Matthew Drahzal et al (IBM Red Book 4409)



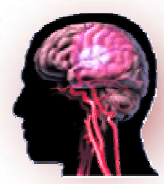
- Why should we investigate/use it ?
- Power issues
- real power of SLA approach is disparate systems each with specific functions such as computing, visualization, data storage
- improvement in the efficiency of the overall completion of a workflow



- The hypothesis of scales. From a physiological perspective
  - Scale lengths (macro to micro to macro)
  - Complexity
  - parallelism

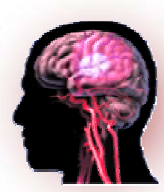


- System Level Acceleration
  - linking two different architectures on a single problem
  - MPP: Blue Gene for the micro scale
    - Cellular chemistry onto micro-vasculature
  - SMP: p-575 for the macro scale
    - 1D and 3D fluid dynamics
- System Level Acceleration for Multi-scale Modelling (SLAMM)

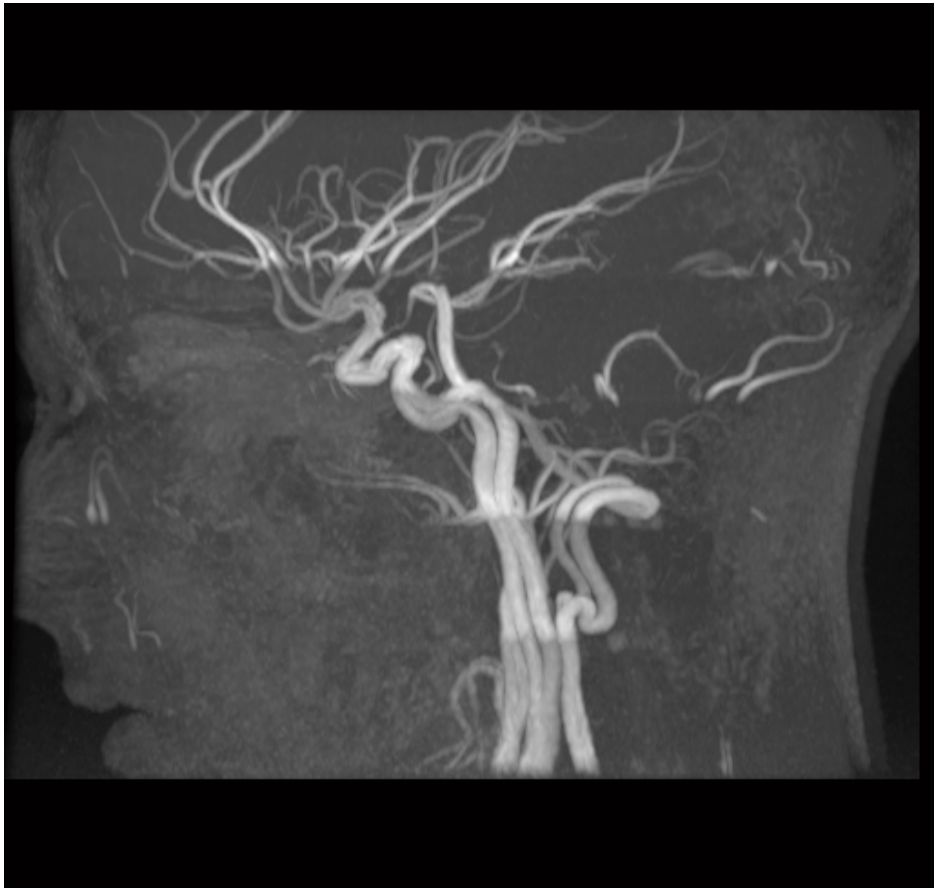


Biological Engineering problems have a multitude of physical scales:

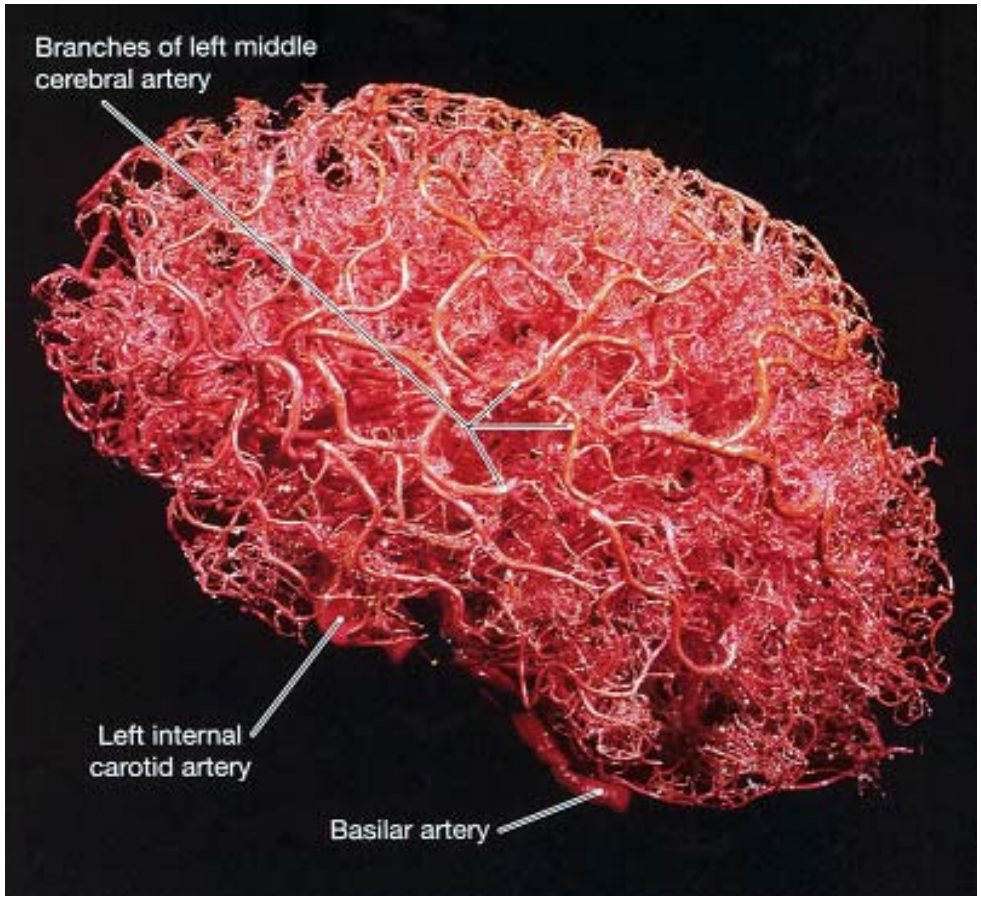
- Major arteries (25mm - 1mm)
- Vascular tree (1mm - 20μm)
- cellular biochemistry (100 nm)



- The visible (macro scale available to MRI)

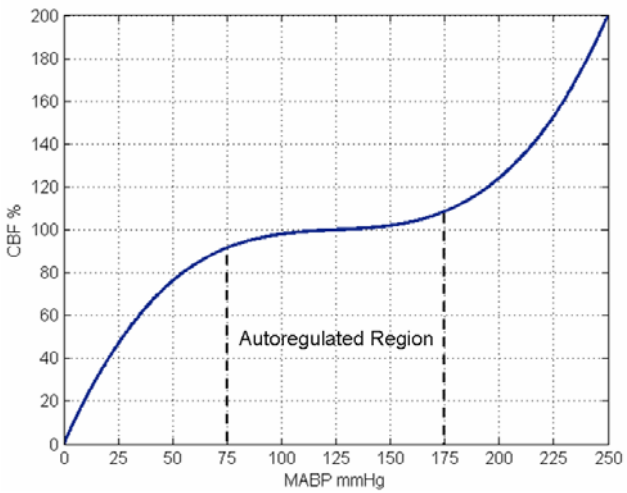


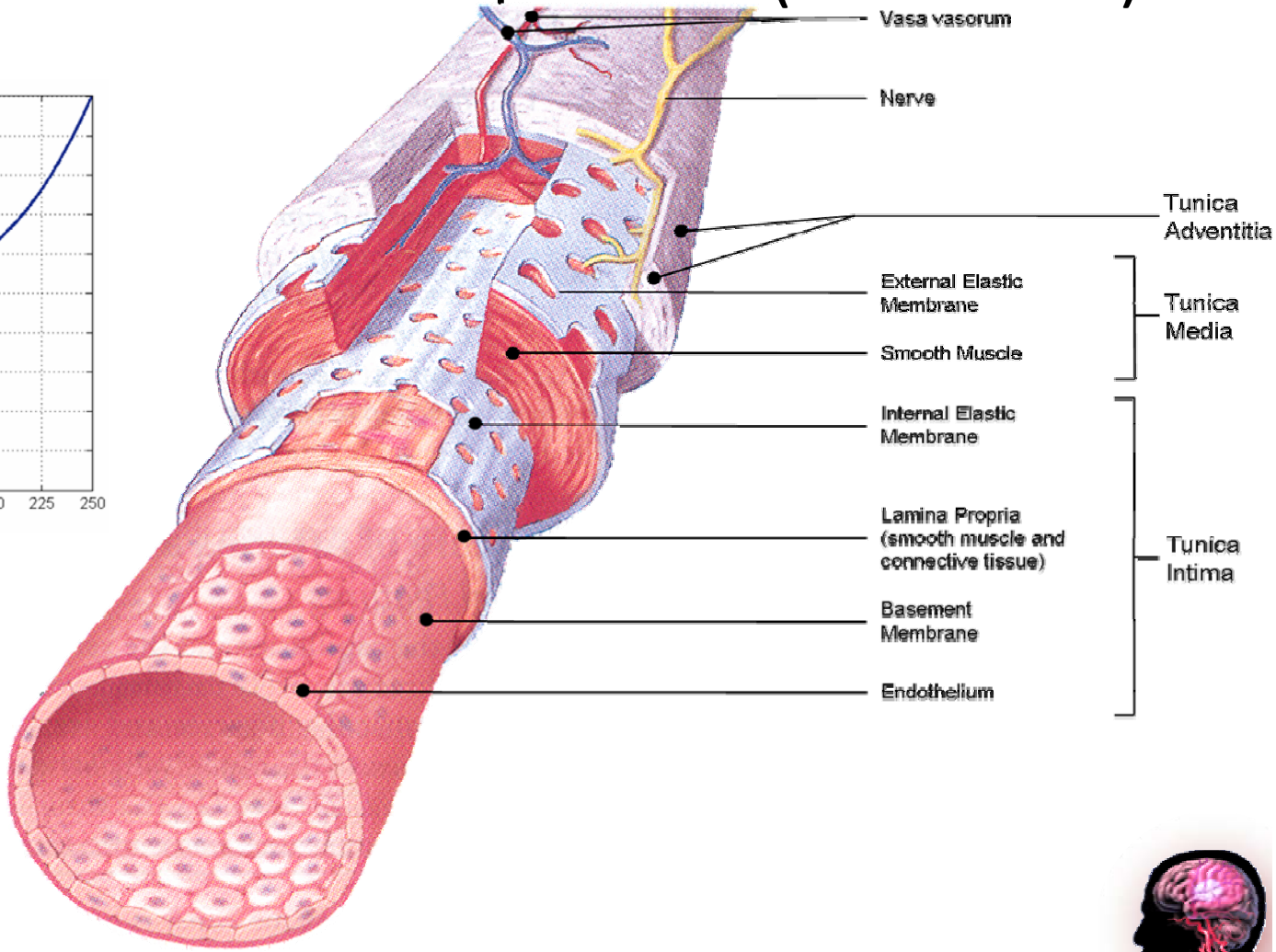
Complexity (partly visible)



F.H. Martini. *Fundamentals of anatomy & physiology*. Benjamin Cummings, 7th edition, 2005.

Complexity: Blood Vessel Composition ("invisible")





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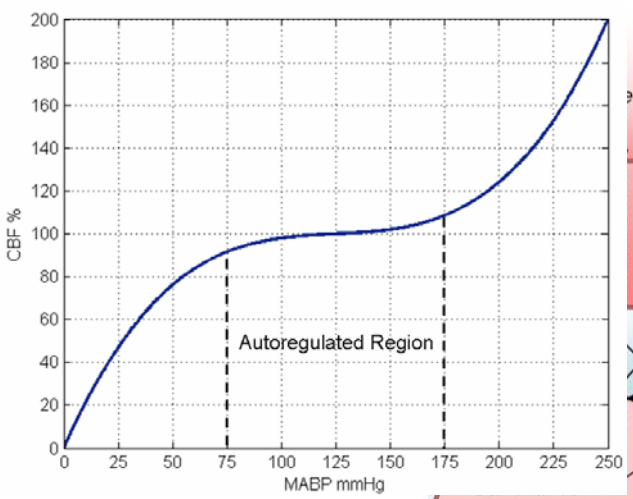
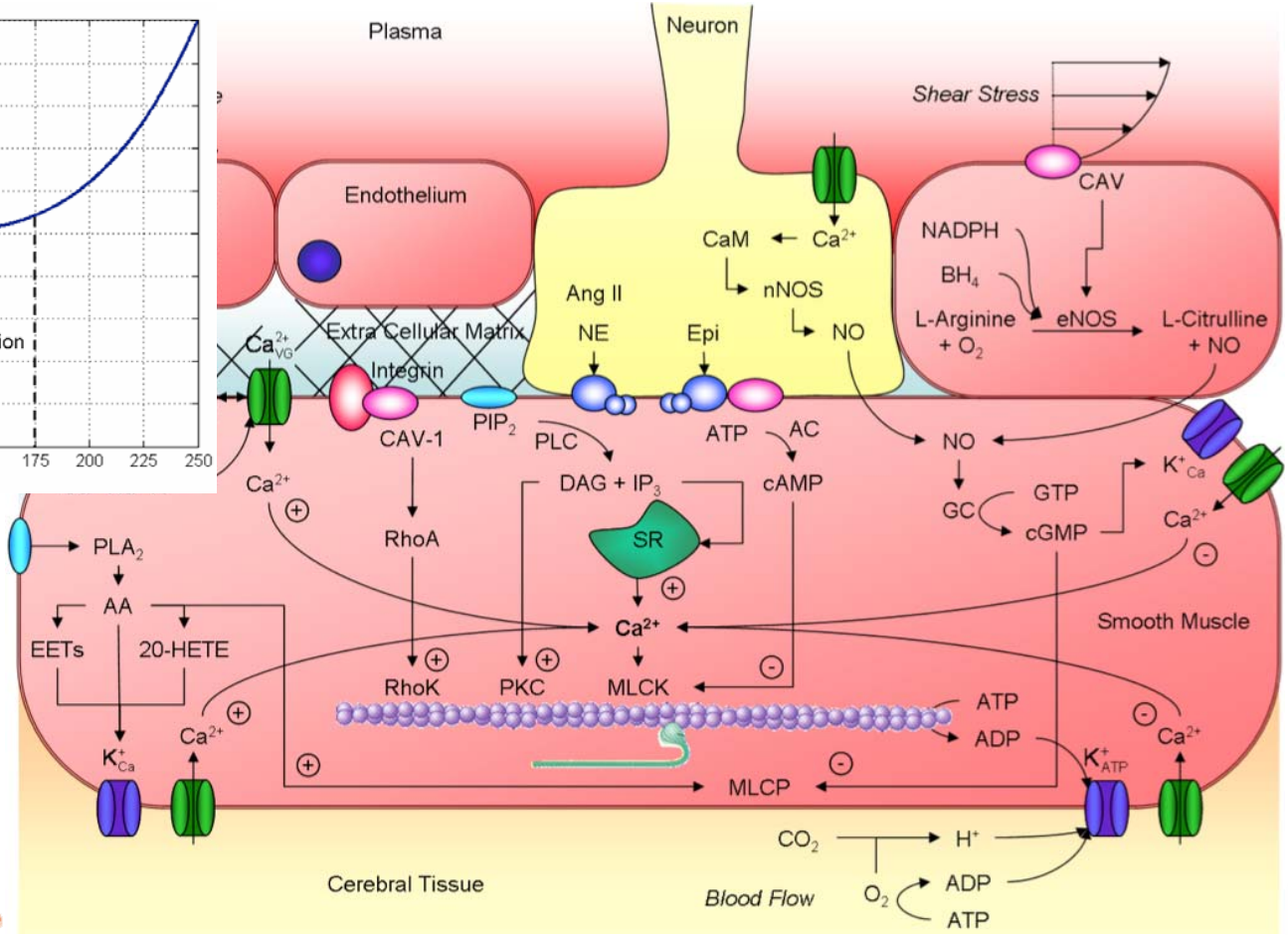
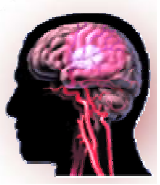
Complexity: Cellular Chemistry ("invisible")



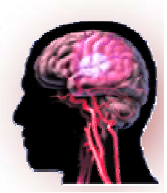




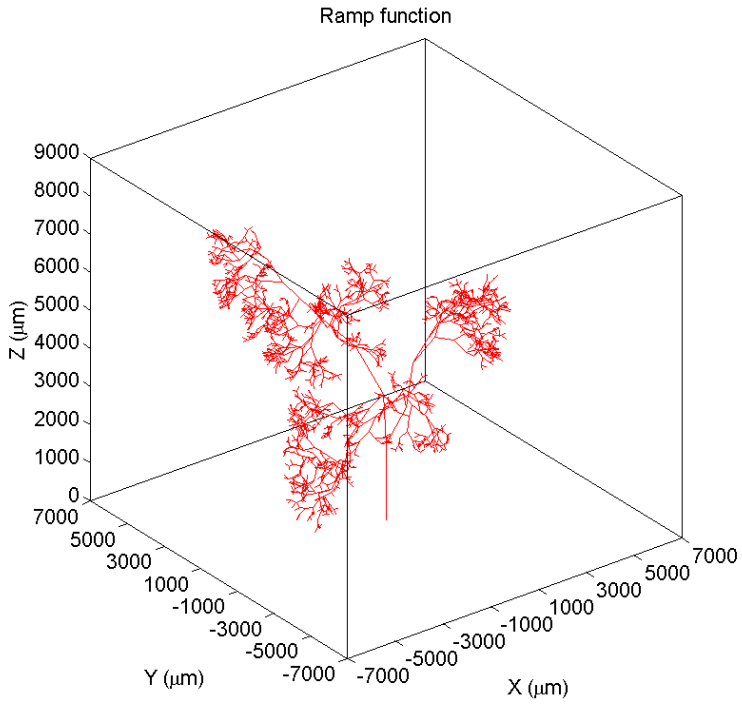
Start with modelling the vasculature .

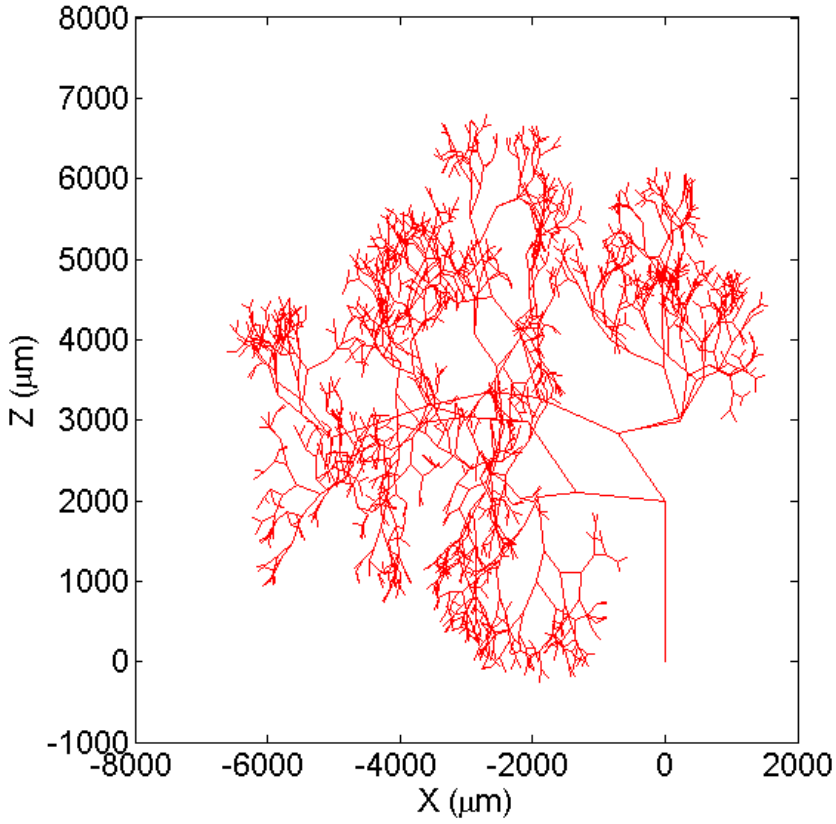
A single vascular tree in the brain providing blood to a volume of cerebral tissue:

- ~ 1 - 4,000,000 segments
- 500,000 – 2,000,000 “leaves”
- Can connect a Capillary bed per “leaf”



- By using a combination of empirical, stochastic, vector field theory we produce 3D vascular trees





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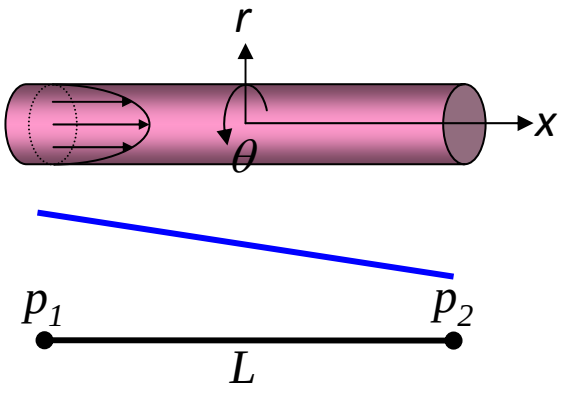
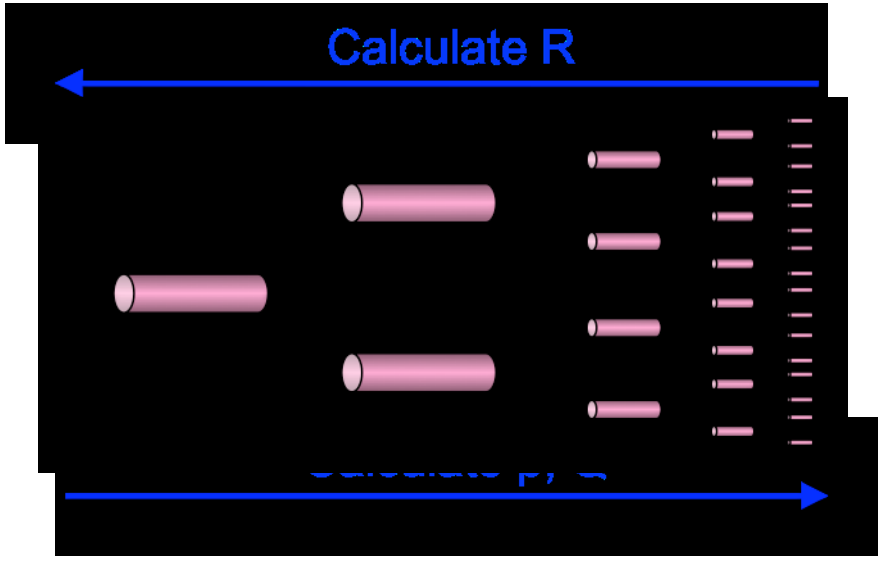
Flow in the tree: 0D Formulation



$$\frac{\partial \rho \mathbf{u}}{\partial t} + \nabla \cdot (\rho \mathbf{u}\mathbf{u}) = \mu \nabla^2 \mathbf{u} - \nabla p$$

$$\Delta p = QR \qquad R = \frac{8\mu L}{\pi r^4}$$



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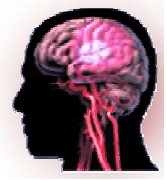
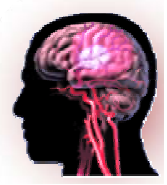


- Proof of principle
- Simple model of functional hyperaemia
- Autoregulation of the tree, based on conservation of Carbon Dioxide

$$\frac{dC_{O2}}{dt} = G_{CO2}\left(CMRO_2 + CBF\left(C_{CO2,artery} - C_{O2}\right)\right)$$

$$\frac{dr}{dt} = -G_r\left(\left(C_{CO2,sp} - C_{O2}\right)\right)$$

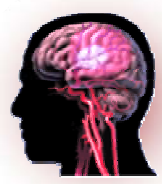


- Model can include more complexity in terms of o.d.e.s

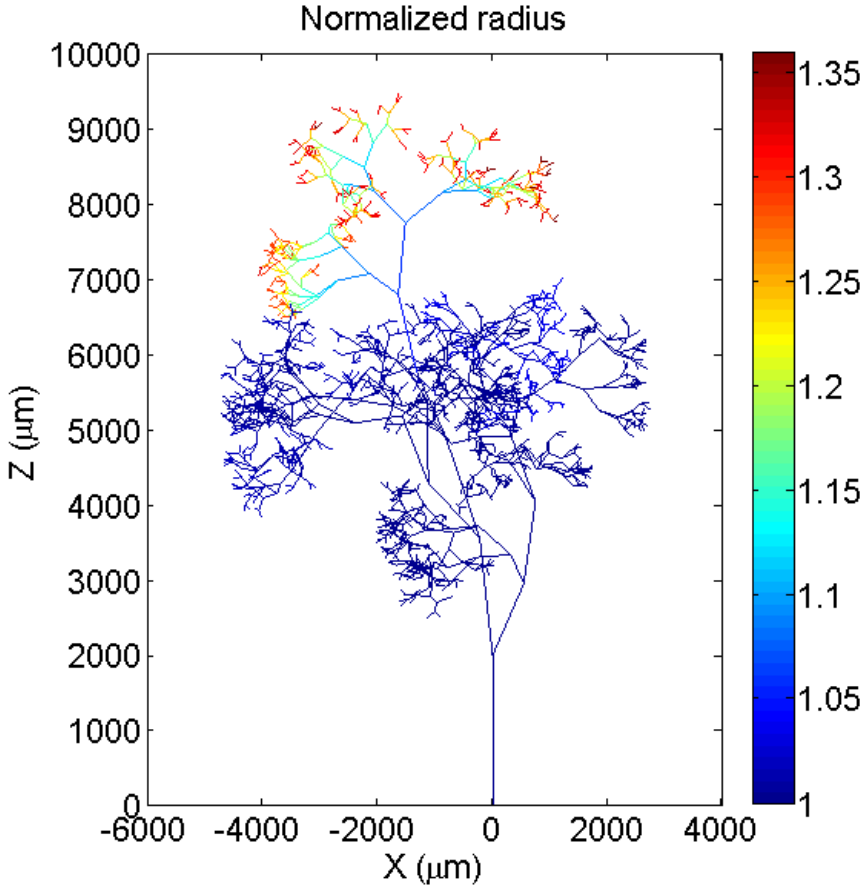
$$\frac{d}{dt}\left[Ca^{2+}\right]_i = \sum \text{sum of fluxes} = \sum_{k=1}^{N} J_k :$$

$$e.g.\ J_{channel} = \alpha\beta\, m_\infty\left(IP_3\right)\, n_\infty\left(\left[Ca^{2+}\right]_i\right) h(t)\left(C_s - \left[Ca^{2+}\right]_i\right)$$

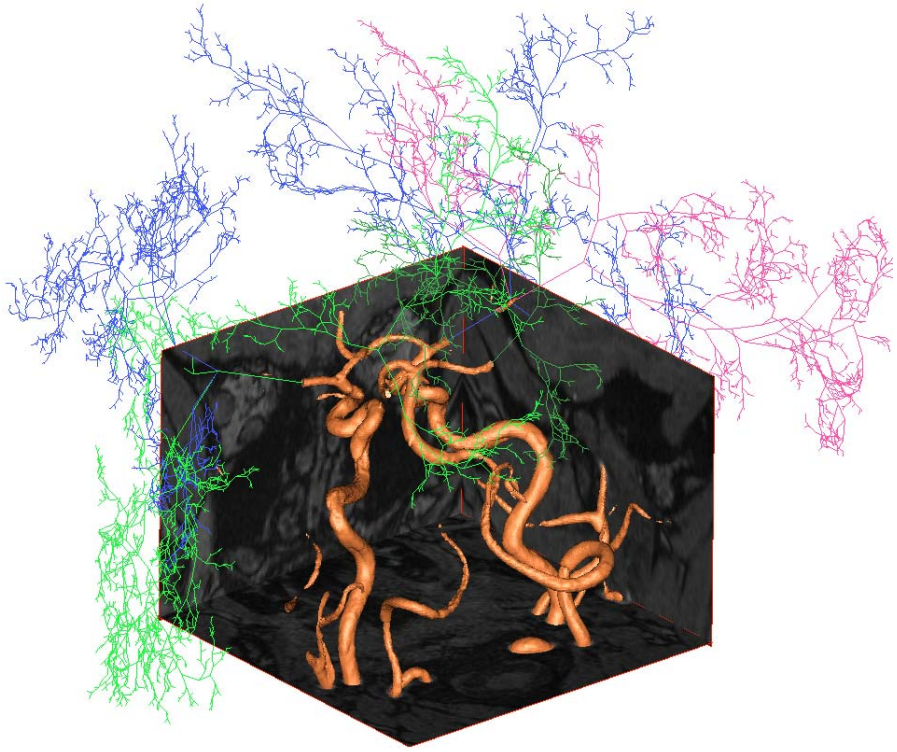
$$\frac{dV_m}{dt} = -G_{BK}\left(V_m - V_K\right) - G_{Ca}\left(V_m - V_{Ca}\right)\frac{1}{1+\exp\left\{-\frac{V_m - V_1}{2}\right\}}$$



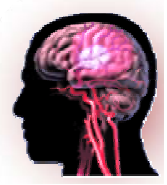
- Radius distribution in tree



- **Macro-micro -Macro:**
- **vascular trees => outlet b. c. for 1D or 3D fluid code**
- **Also 3D flow is the inlet b. c. for vascular tree**

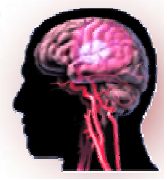


- Vascular tree mapped on to the BG
- 1D or 3D fluid dynamics code onto the power series (p 575)
- Communication needs to be fast without recourse to disk transfer via GPFS



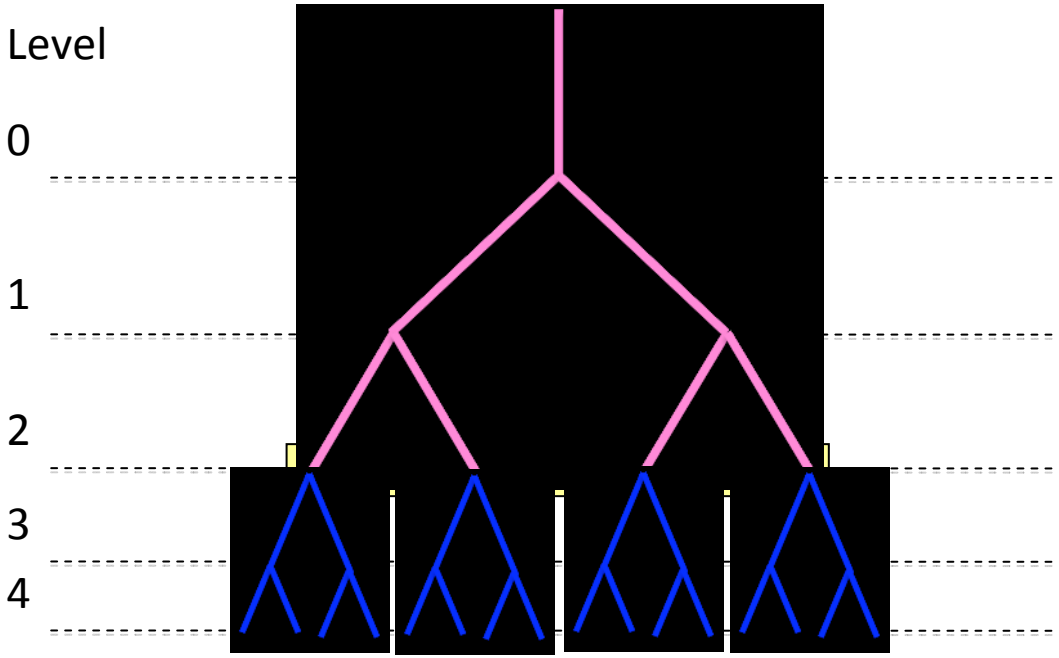
• Connecting BG and p-575

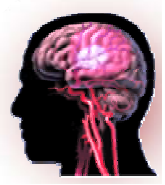
- BG:Read input file (artery labels => port numbers)
- BG/p575: creating communicators
  - Domain decomposition(p-575), subtrees (BG)
- BG: creating the trees (each processor creates a portion of a tree)
- BG: root processors connect to p575
  - New C++ class utilising Unix socket
- BG: loop waiting for p575 to send pressure request

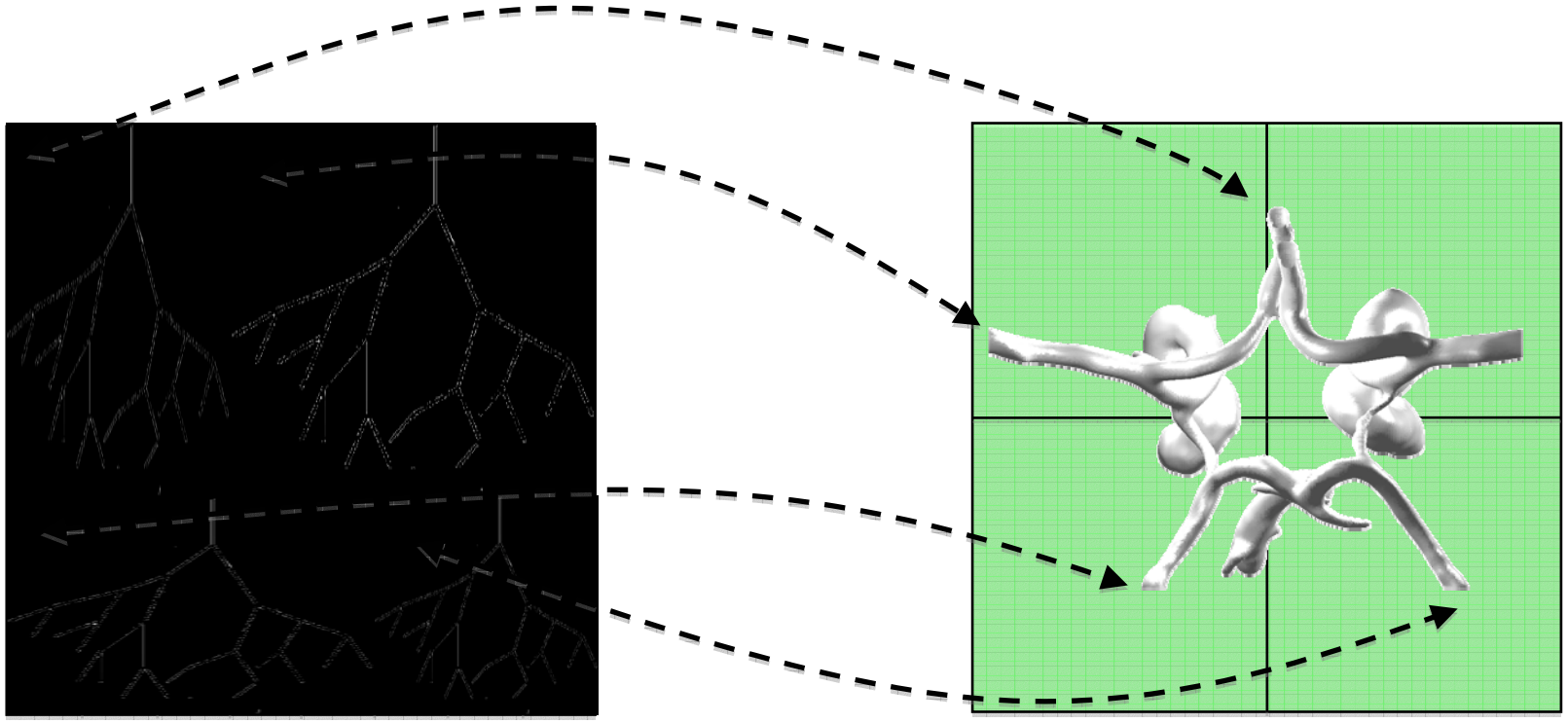


Partitioning a Tree for parallelism

$$\text{Num segments Per Tree} = \sum_{i=1}^{N} 2^i + 1$$



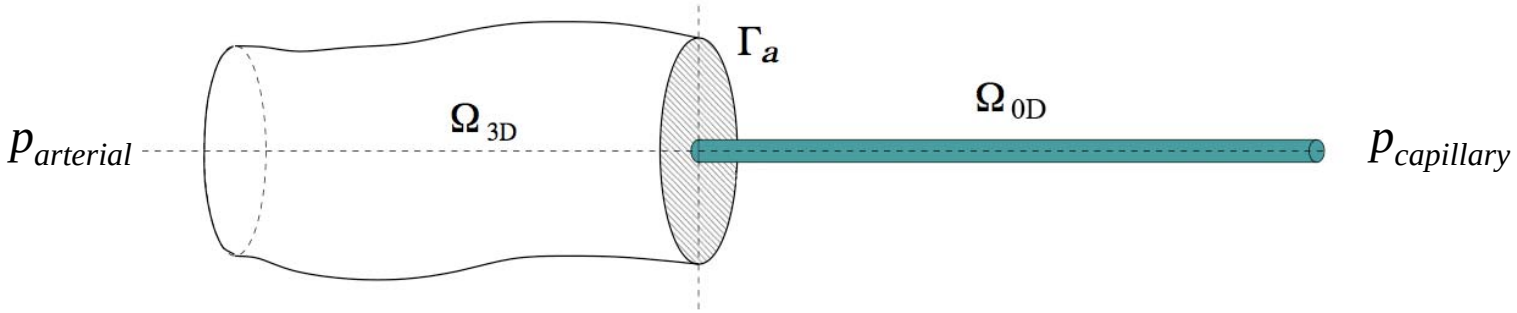




Blue Gene/L

Power Series

0D – 3D Coupling (inner iteration per time step)

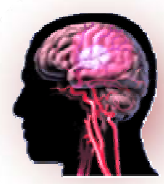


$$A_{3D} = A_{0D}$$

[redacted]

$$Q_{3D} = \int_{\Gamma_a} \mathbf{u} \cdot \mathbf{n} dA = Q_{0D}$$

$$\bar{p}_{3D} = \frac{1}{\Gamma_a} \int_{\Gamma_a} p dA = p_{0D}$$



Blue Gene loop times

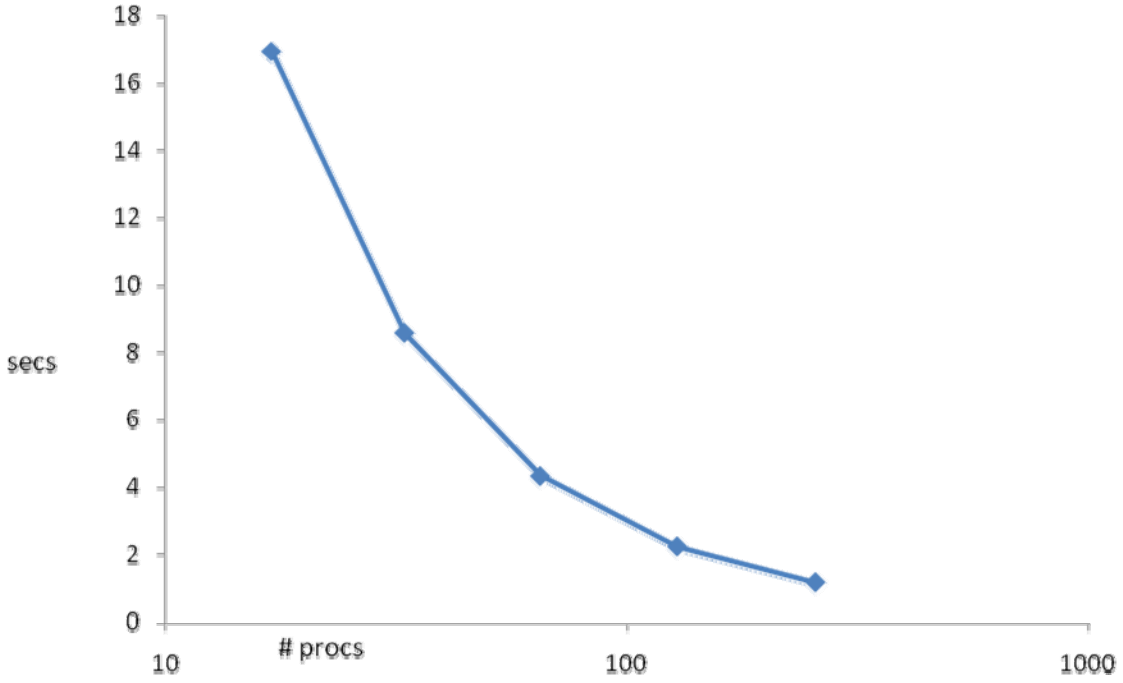
levels of tree		7	9	11	13	15	17	19	21		X6 efferent arteries
# proc	17	0.005	0.001	0.003	0.0108	0.0427	0.2354	0.7512	2.8218		**16.9308**
	33	0.007	0.001	0.002	0.0058	0.0217	0.1348	0.3919	1.4276		**8.5656**
	65	0	0.0015	0.0019	0.0039	0.0119	0.0764	0.2042	0.7195		**4.317**
	129	0	0.0026	0.0028	0.0038	0.0078	0.0482	0.1121	0.3688		**2.2128**
	257	0	0	0.005	0.0055	0.075	0.0317	0.0635	0.1911		**1.1466**

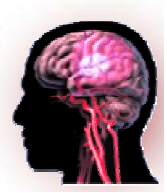
P-575 iteration times (3D code)

# elements (millions)	# proc	1	4	8	16
0.5		76.37	18.07	8.98	6.83
1		140.4	38.1	19.56	13.95
2.5		398.7	92.89	47.01	31.8
5		758.1	183.98	87.96	61.28
10		1516.2	367.96	175.92	**122.56**

Blue Gene: # procs vs iteration time (pass up and down the tree)

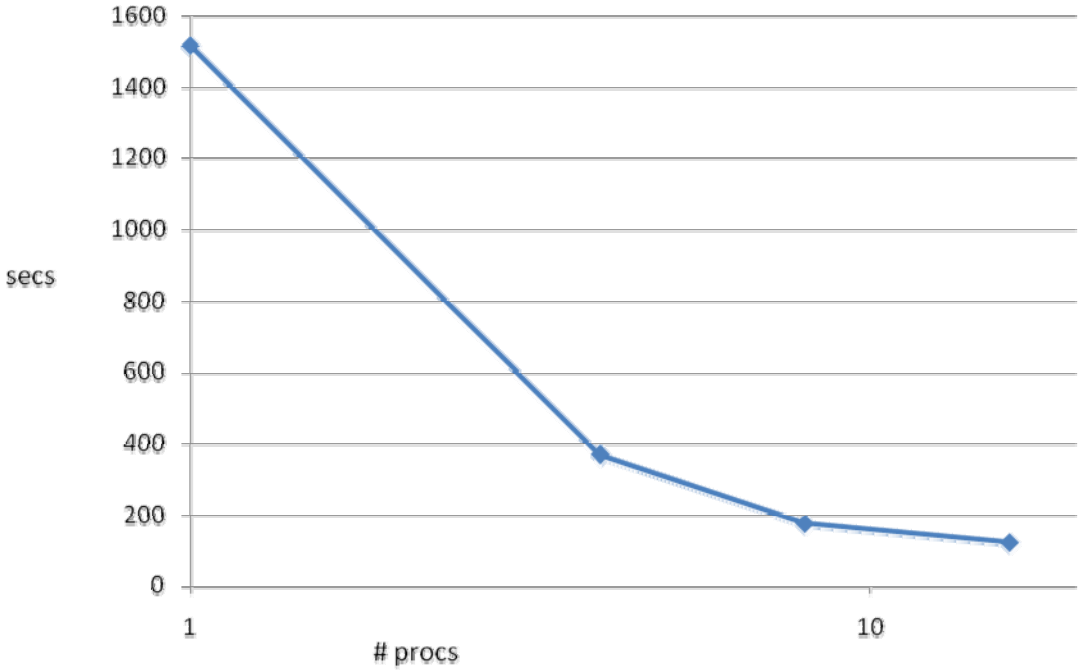
- Clearly a function of the tree mapping algorithm,
- communication is not the dominant issue.
- Root processor doing more work as a function of procs used.
- But present autoregulation is simple and complexity can increase significantly



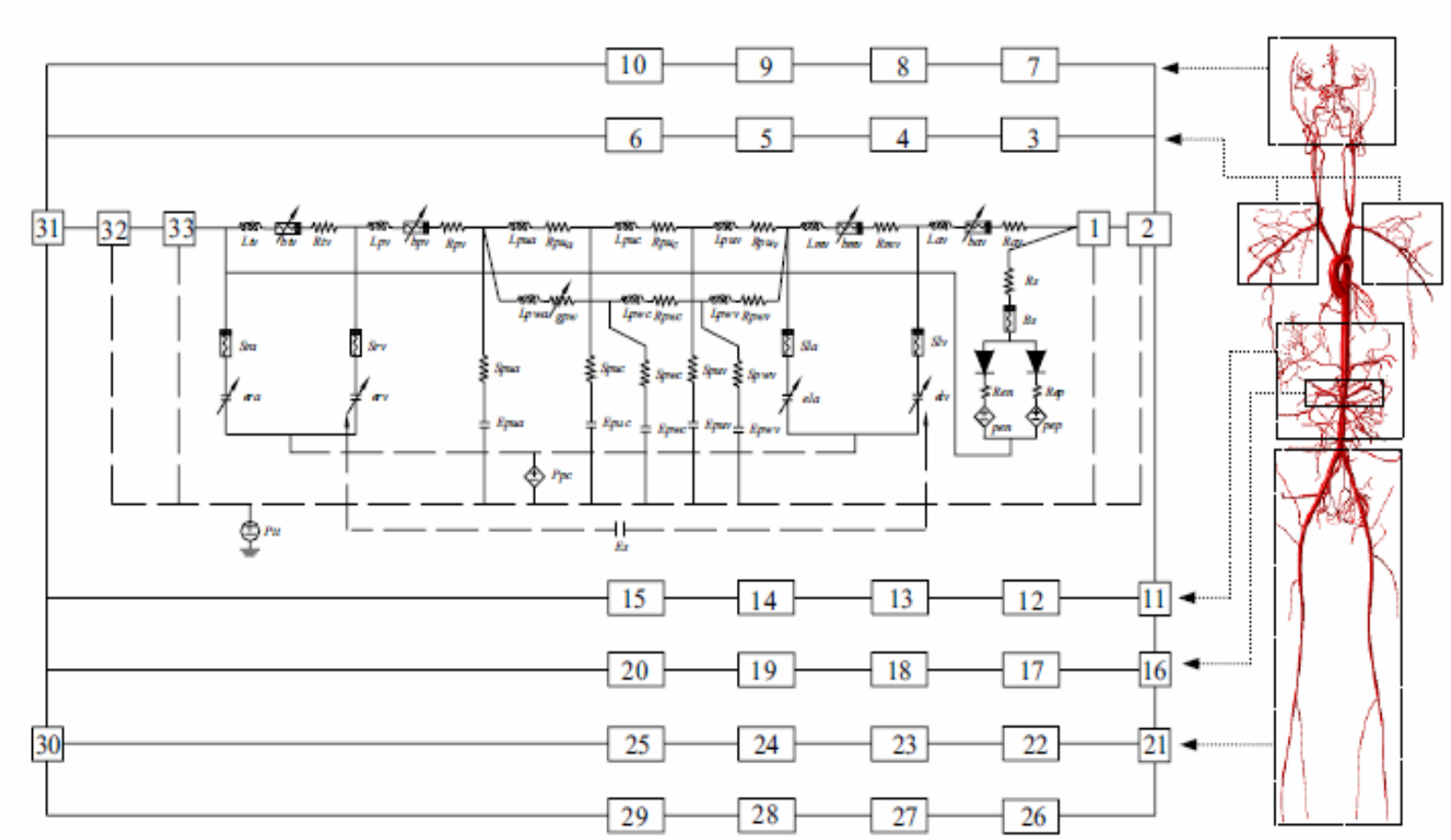


p-575: # procs vs iteration time

- Long iteration times for 3D fluids code
- BG: “twiddling thumbs”!
- Issue of load balancing



- human vasculature model (1D wave eqns)



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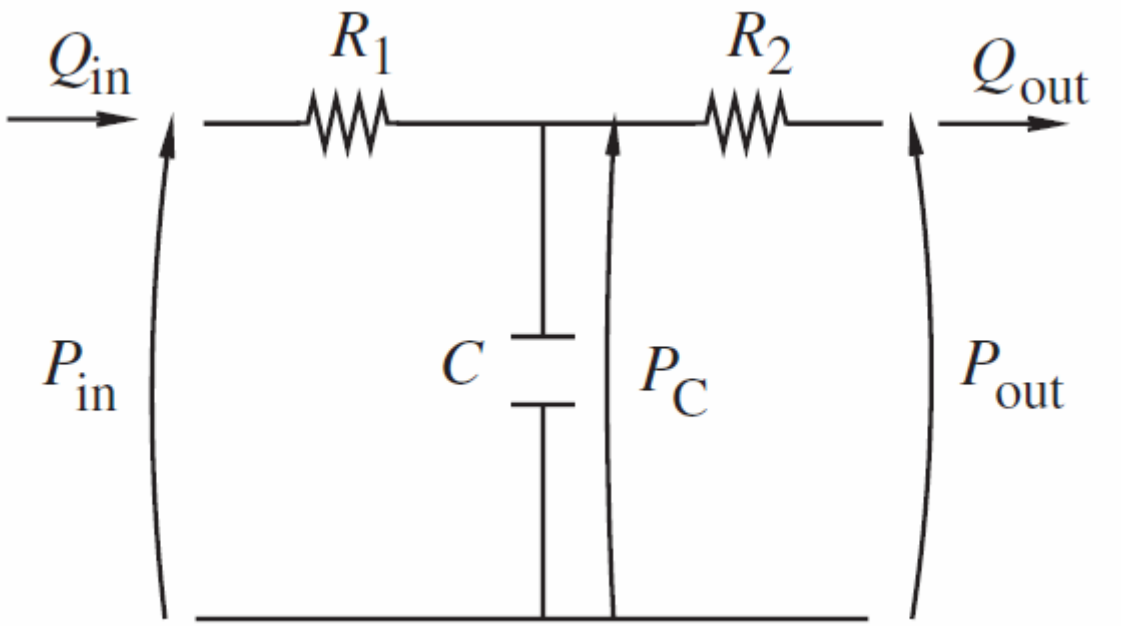
- 1D boundary conditions
- R1 (impedance matched) no wave reflections
- R2 (variable, evaluated by BG) tree resistance



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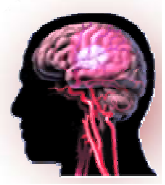
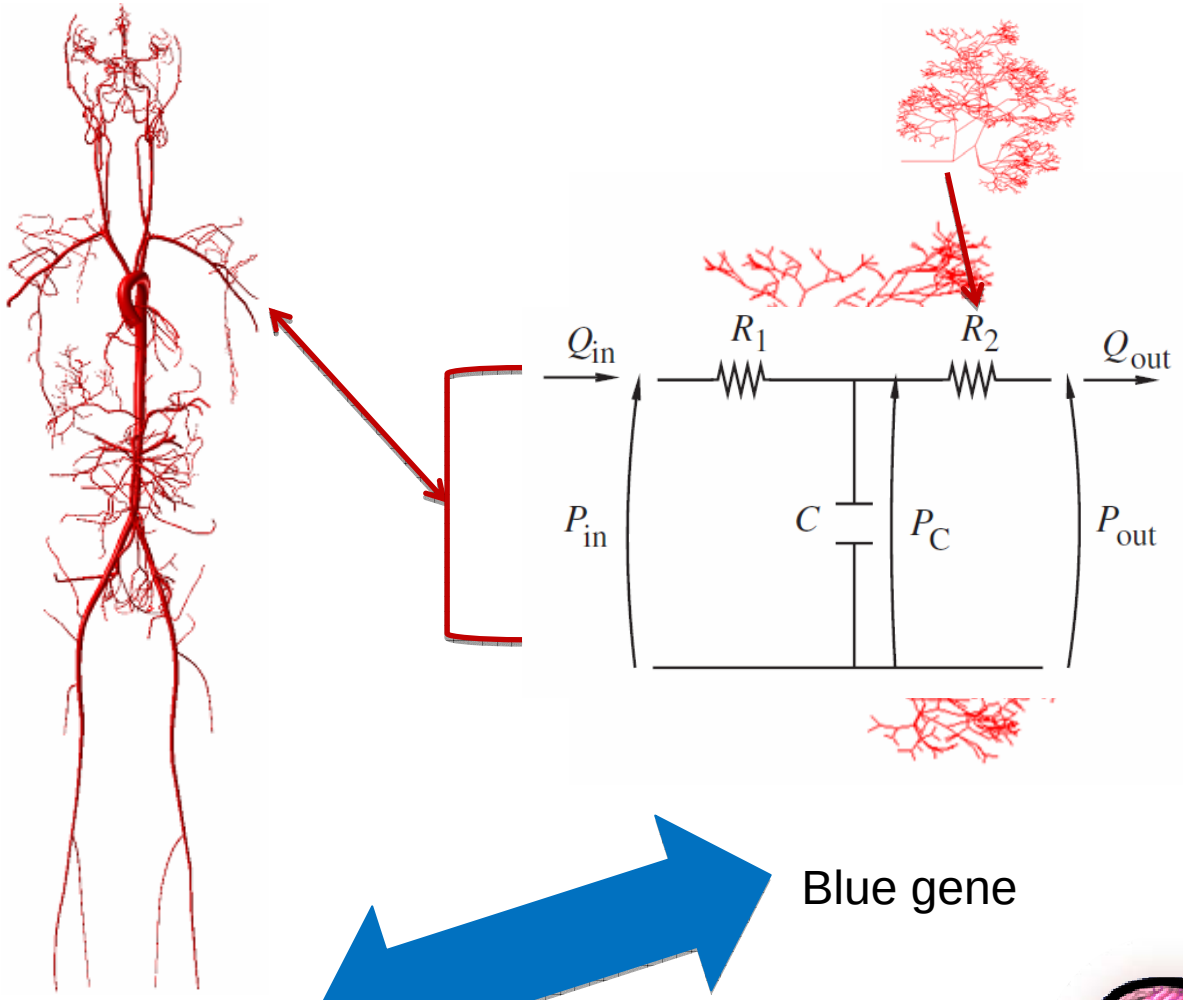
Alastruey, J., et al., *Reduced modelling of blood flow in the cerebral circulation: Coupling 1-D, 0-D and cerebral auto-regulation models.* Int. Jour. Num. Methods Fluids, 2008. **56**: p. 1061-1067.



- 1D code on p575
- Each sub-tree mapped to a particular sub-rack of BG.
- Downstream peripheral resistance(s) evaluated on BG



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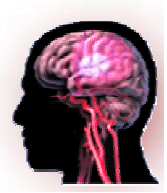
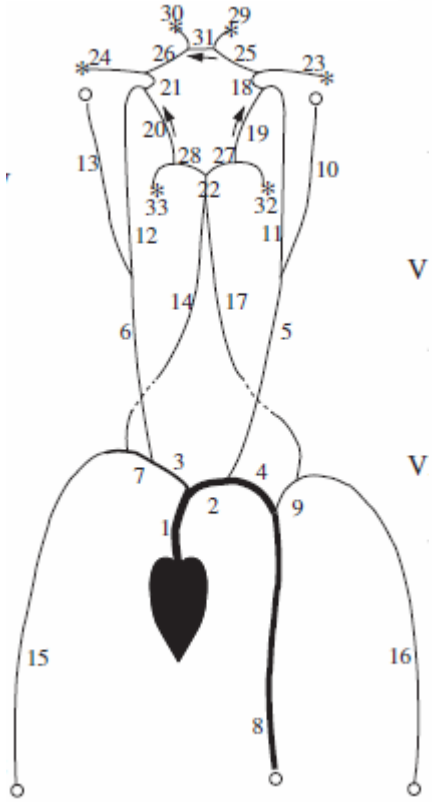
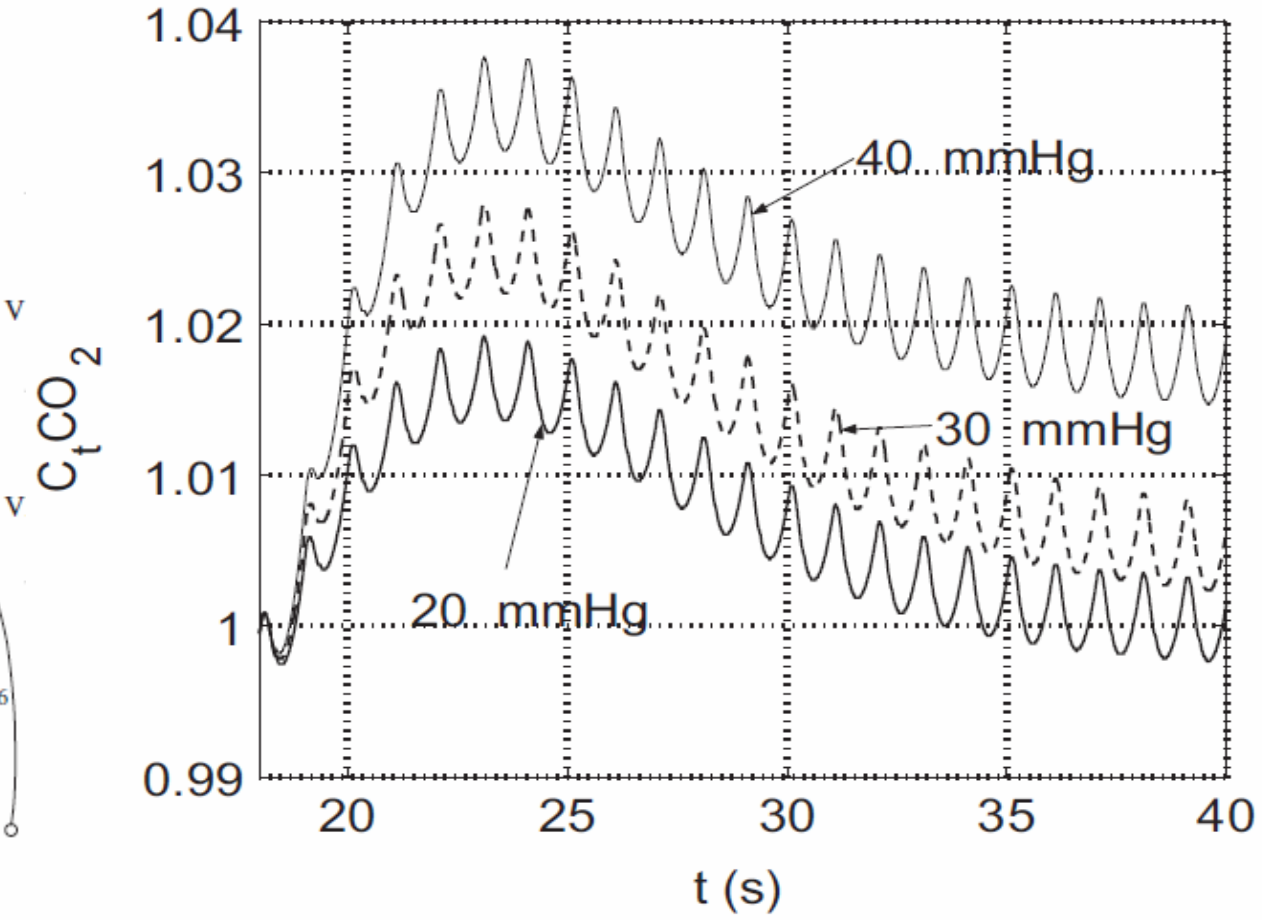
- **Does this require HPC?**
- 1D model (relatively simple physiologically !)
- ~ 55 major arteries
- => ~55 vascular trees
- => each tree ~1,000,000 segments
- => each segment requires ~ 30 o.d.e.s to model simple cellular chemistry.
- => 1,650,000,000 o.d.e.s



- Proof of principle Autoregulation in the cerebro-vasculature





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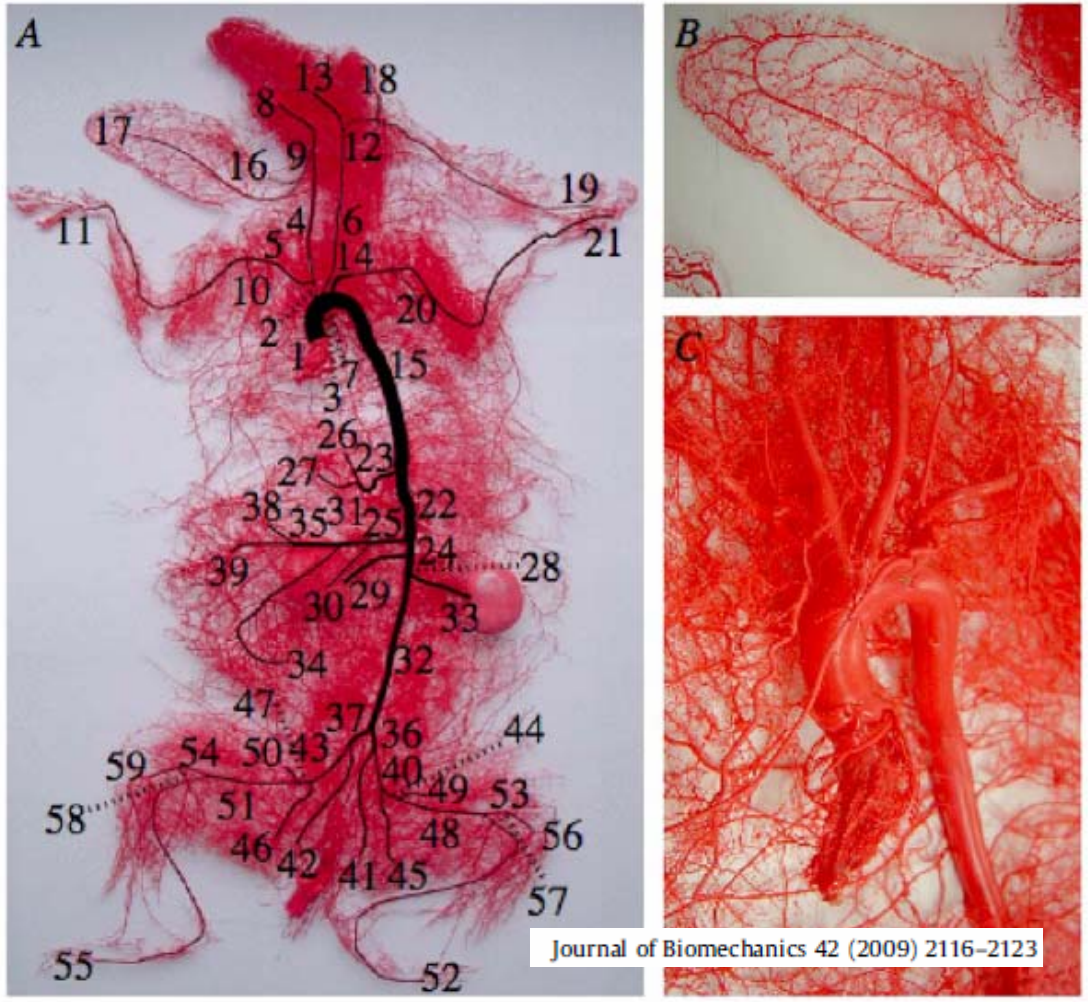
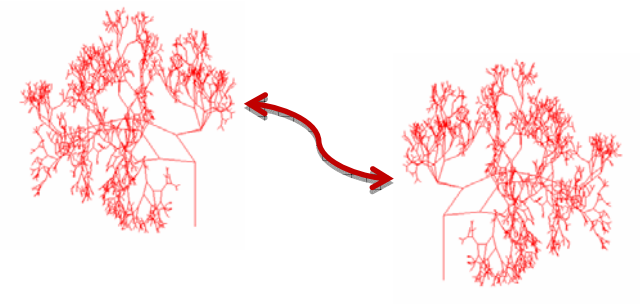
Int. J. Numer. Meth. Fluids 2008; ***56:1061–1067***

- Applied to animal models as well.

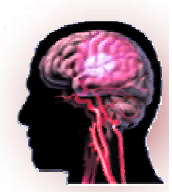


The Challenges

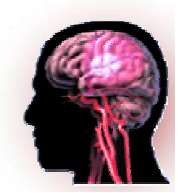
- Validation by in vivo experiments (blood flow makes a difference)
- Collateral arterial networks



- Load balancing
- Real-time simulation of the whole human vasculature



- Future Work
  - Improve tree growing algorithms to be constrained by regions of the brain
    - (morphing algorithms)
  - **Load balancing** and tree mapping algorithms
  - **Transparency of SLA and ease of use to the user (part of loadleveler?)**
  - Integrate more fully the cellular biochemistry. Role of the astrocyte and spatial K^+ buffering
    - (90% complete)
  - Implement a compliant 1D model between the 3D and 0D models
    - (50% complete)
  - Capillary network perfusion models at the terminal end of vascular tree (50% complete)



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  Jim Sexton and Kirk Jordan.

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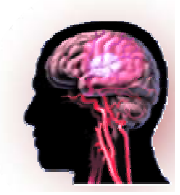
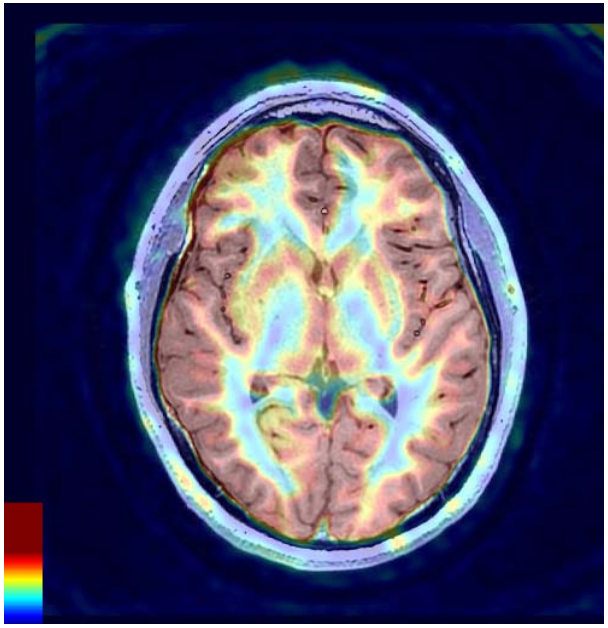
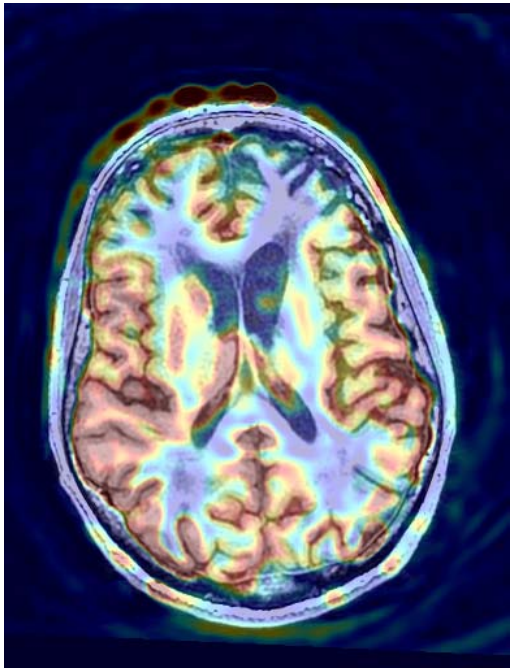
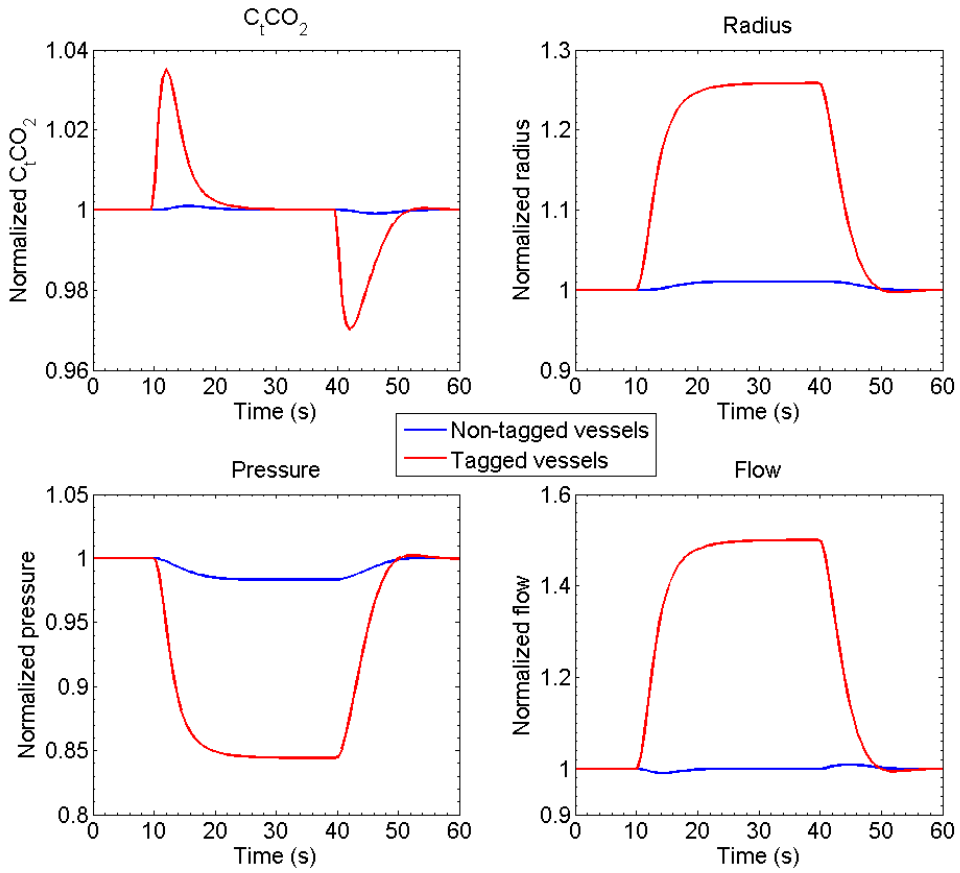


- Why is this important ?
- Left: healthy volunteer.
- Right : 65 year-old male with Alzheimer's disease.





- Full non-linear solutions for the “Tagged” Asymmetric tree
- Averaged radius plots (vs t) , metabolic rate increased at t=10, returned to original at t=40
- Red lines tagged vessels (average), blue lines untagged vessels



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