Patient-Specific Hemodynamics in FEniCS

Kent-Andre Mardal

Simula Research Laboratory

In collaboration with Susanne Hentschel, Anders Logg, Kristian Valen-Sendstad from Simula and Jørgen Isaksen and Tor Ingebrigtsen from University hospital in Nothern Norway

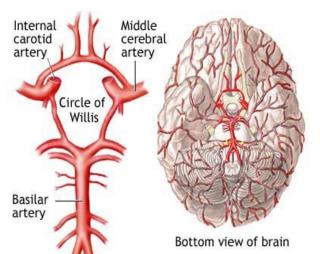
The circle of Willis

The circle of Willis is the brains main supplier of blood

It connects the carotid and vertebral arteries into a network that ensures the brain with a stable blood supply even if one vessel is occluded

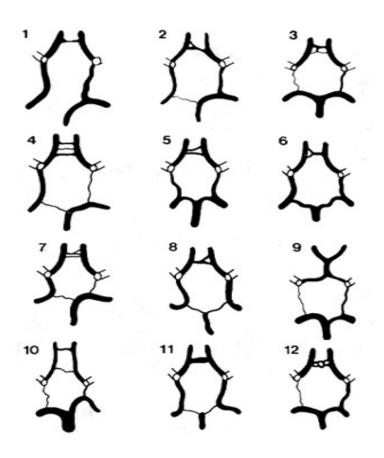
Unfortunately, aneurysms are often found in the circle of Willis (1-6%)

Aneurysms may rupture and cause a stroke Annual risk is assumed to be $\sim 1\%$



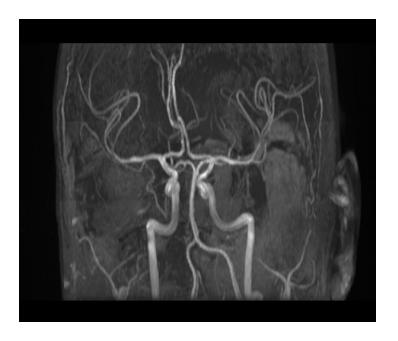


What causes aneurysm development and rupture?

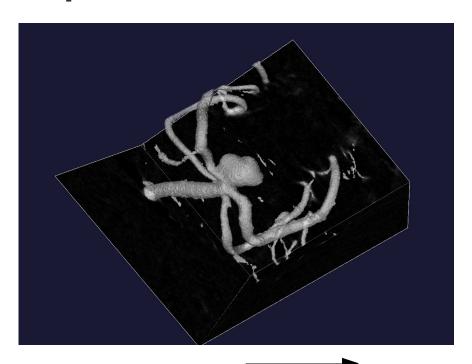


Differences in anatomy -> differences in flow

Great variations in anatomy Eg only 50% have a well-balanced circle

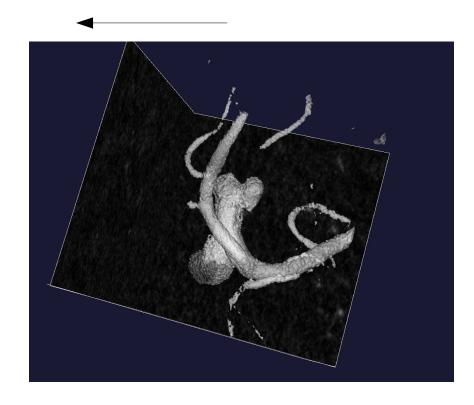


Clinical Problem: which aneurysms are at risk of rupture?



The one at the most (statistically) dangerous location?

The biggest?

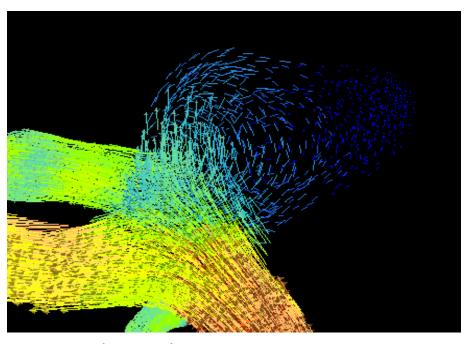


These are examples of two common risk indicators, unfortunately none of them very precise

Can we provide better risk indicators?

Stress computations based on fluid flow or fluid-structure interaction seem as a promising tool

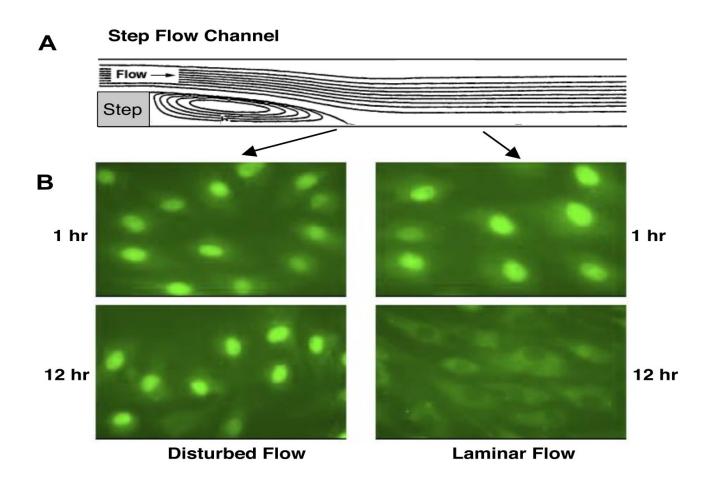
Patient-specific anatomies can be obtained with a reasonable accuracy



Popular computational risk indicators are low shear stress, high shear stress, oscillatory shear stress, and pressure

These indicators have been linked to remodeling of the vessel wall via the endothelium

The endothelium layer remodel itself according to the flow conditions



Chien, Am J Physiol Heart Circ Physiol, 2006

Validation and testing in a patient specific case

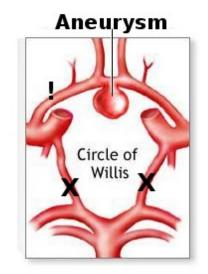
She has limited blood supply to the left part of the brain.

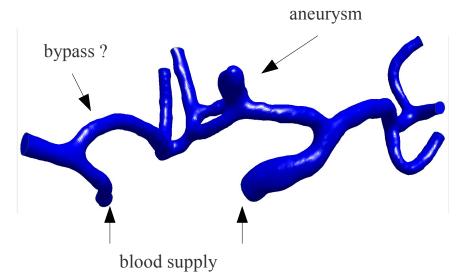
At the same time a growing aneurysm was discovered.

Problem that is to be evaluated

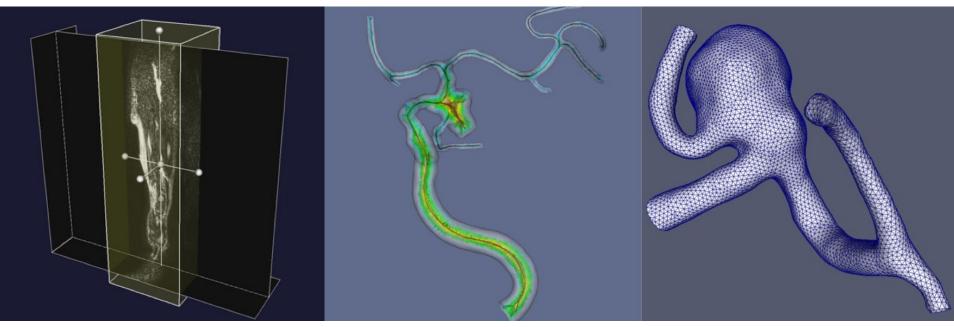
Can we compute a flow that is similar to the measured flow?

Would a bypass be beneficial?





Software tools: VMTK – the vascular modeling toolkit



VMTK is a tool for 3D reconstruction, geometric analysis, mesh generation and surface data analysis for image-based modelling of blood vessels

Main developer: Luca Antiga, Bergamo, Italy

Development by Tangui Morvan (Kalkulo/Simula)

Generation of Dolfin mesh, boundary indicators, material types for e.g. FSI mesh, resolution steering etc.

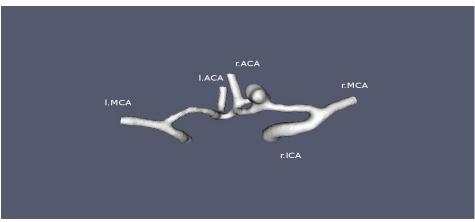
FEniCS: Chorin solver for Navier-Stokes equations

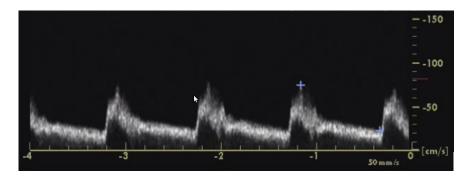
```
# Tentative velocity step
a0 = dot(v, u)*dx + k*nu*dot(grad(v), grad(u))*dx
L0 = dot(v, u0)*dx + k*dot(v, f)*dx - k*dot(v, mult(grad(u0), u0))*dx
# Poisson problem for the pressure
a1 = 1.0e-6*p*q*dx + dot(grad(q), grad(p))*dx
L1 = -(1.0/k)*q*div(us)*dx
                                                                    Form
                                                                                                    Global matrix
                                                   Mathematical
                                                                                         UFC
# Velocity update
                                                                                         interface
                                                   problem
                                                                    implementation
                                                                                                   assembly
a2 = dot(v, u)*dx
L2 = dot(v, us)*dx - k*dot(v, grad(p1))*dx
                                                                                                     DOLFIN
# Assemble matrices
A0 = assemble(a0, mesh)
A1 = assemble(a1, mesh)
A2 = assemble(a2, mesh)
                                                     Weak form
while t < problem.T:
    # Propagate values to next time step
    t += dt
    u0.assign(u1)
    # Compute tentative velocity
    b = assemble(L0, mesh)
    [bc.apply(A0, b, a0) for bc in problem.bcv]
    solve(A0, us.vector(), b, gmres, ilu)
    # Compute p1
    b = assemble(L1, mesh)
    print len(problem.bcp)
    if len(problem.bcp) == 0: normalize(b)
    [bc.apply(A1, b, a1) for bc in problem.bcp]
    solve(A1, pl.vector(), b, gmres, amg)
    if len(problem.bcp) == 0: normalize(pl.vector())
```

Patient specific Simulations

CT-scan, Doppler measurements

Generated a surface mesh
▼(VMTK)
Generated a volume mesh
▼(VMTK)
Computational fluid dynamics
(FENICS)





Intracranial Doppler measurements

Incompressible Navier-Stokes equations with rigid, impermeable walls

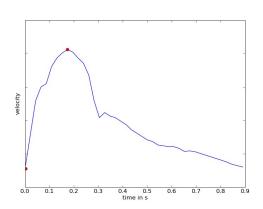
Resistance BC:
$$R = CQ + p_0$$

 ${\cal C}$ - Periferal resistance coefficient

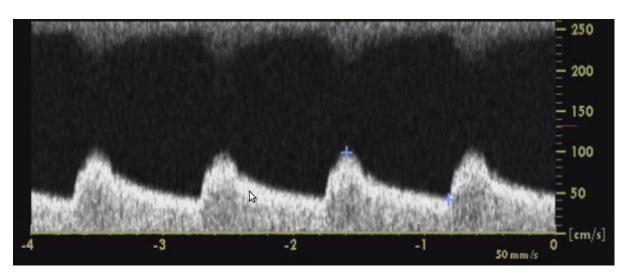
 p_0 - mean arterial pressure

Q - volume flow

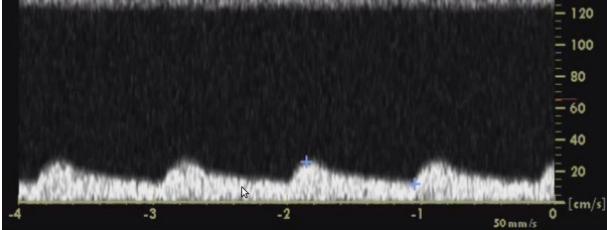
Doppler measurements on the left and right MCA



Used flow curve, adjusted to measurements with min and max flow (red dots)



Right MCA

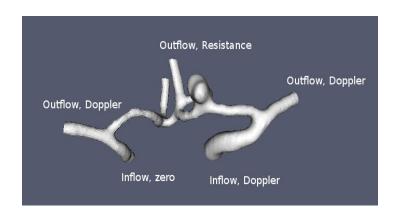


Left MCA

Is resistance boundary condititions sufficients or is patient-specific conditions needed?

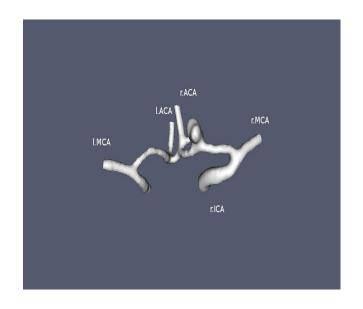


Resistance boundary conditions



Patient specific boundary conditions

The flow is quite different when using patient specific boundary conditions!



place	cross sec area mm^2	vol flux in ml/s	С
r. ICA	12.4	+3.8	
r. MCA	3.6	-1.2	6.0
1. MCA	2.5	-0.9	6.0
r. ACA	2.3	-0.8	8.5
l. ACA	2.6	-0.8	8.5

Table 4: Resistance boundary conditions at all outlets.

place	cross	sec area mm^2	vol flux in ml/s	С
r. ICA		12.4	+3.8	
r. MCA		3.6	-1.7	4.4
l. MCA	3	2.5	-0.3	22.5
r. ACA		2.3	-0.8	8.5
l. ACA		2.6	-0.8	8.5

Table 3: Patient Specific boundary conditions at left and right MCA at Systole.

[Resistance coefficients obtained from Alastrueya, Parker, Peiro, Byrd, Sherwin, J. Biomechanics 2007]

Uncertainties...

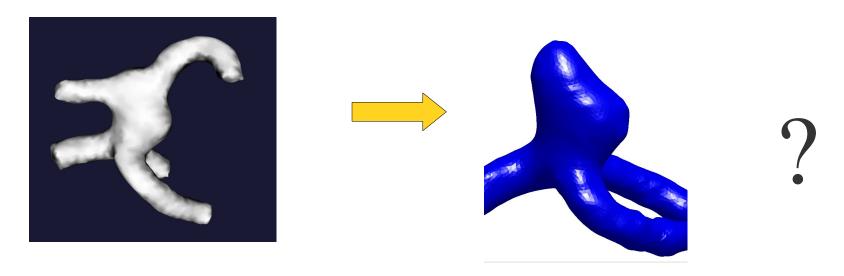


Figure 1. During segmentation.

Figure 2. Removed a blood vein.

The anatomy is uncertain

Velocity measurements and corresponding boundary conditions are even more uncertain!

Conclusions and future work

It seems that patient-specific boundary conditions should be used.

The accuracy in the input data is a major bottleneck, both for intracranial Doppler and MR/CT/DSA.

FeniCS and VMTK, with their scripting capabilities, is an ideal platform for patient studies.