

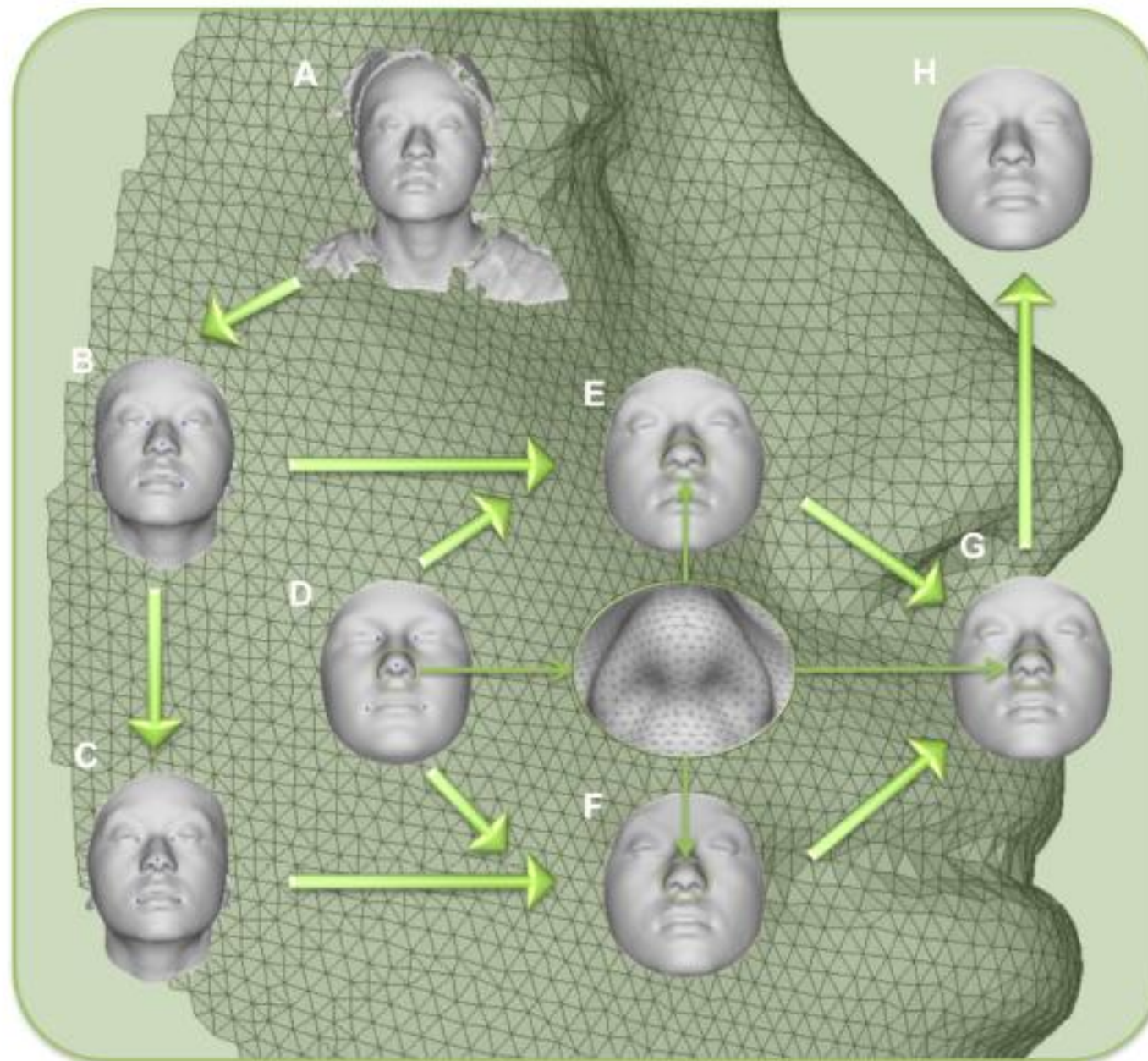
Genetics of MRI phenotypes in acute stroke: potential impact and feasibility

ISGC Stroke Imaging Repository

Vincent Thijs

Current approach

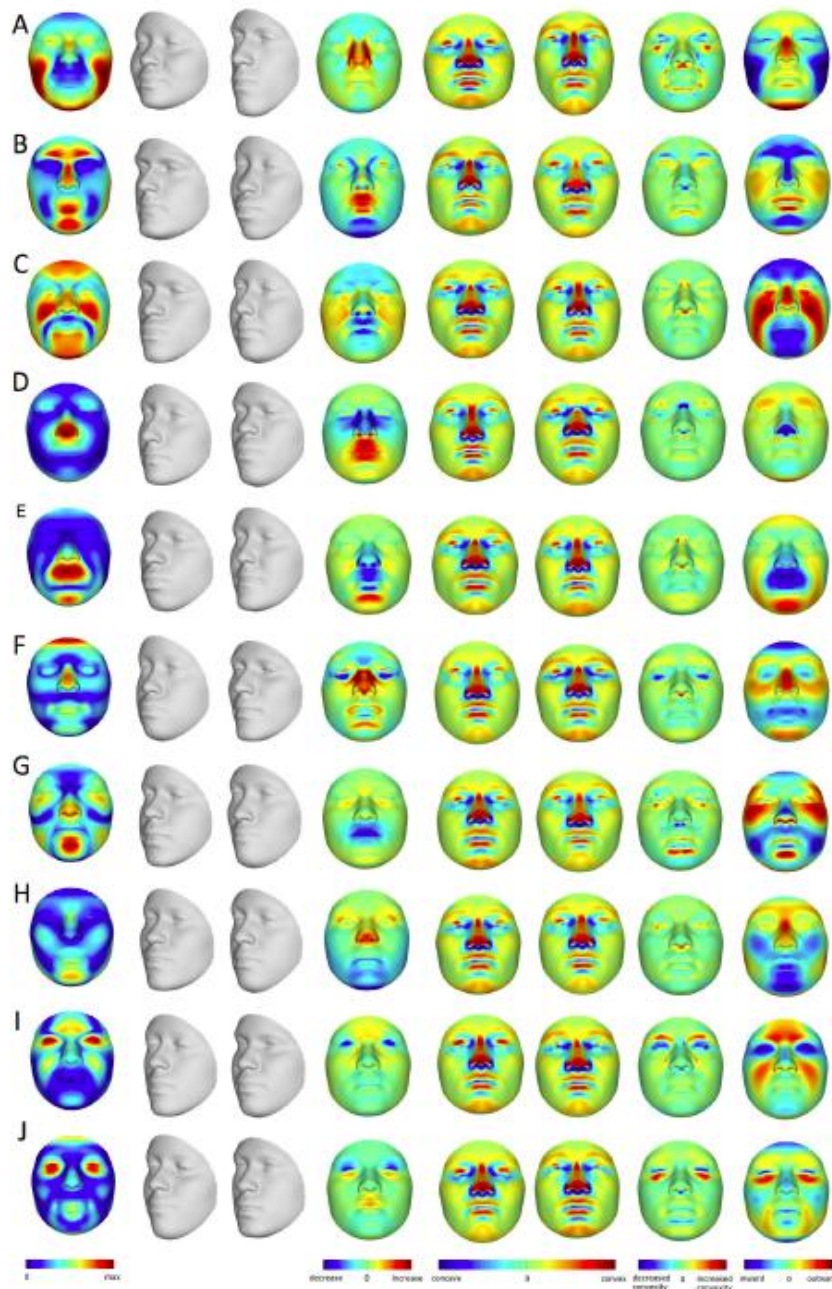
- Complex phenotype (eg ischemic stroke, subtype, aneurysm, univariate/binary)
 - Intermediate phenotype (eg white matter disease, QTL)
 - Gene architecture
- 
- A diagram consisting of three blue curved arrows pointing downwards, indicating a sequential flow from the first bullet point to the second, and then to the third.



Face
projected
on
coordinate
map
With 7150
coordinate
s

Claes P, PLOS GEN

Figure 1. Workflow for 3D face scan processing. A) original surface, B) trimmed to exclude non-face parts, C) reflected to make mirror image, D) anthropometric mask of quasi-landmarks, E) remapped, F) reflected remapped, G) symmetrized, H) reconstructed.
doi:10.1371/journal.pgen.1004224.g001



44 principal components
Explain 98% of human
variation in facial shape



Relationship modeling
To reduce 44 PCA
To one compounding variable



Candidate gene analysis
Influencing compounding variable

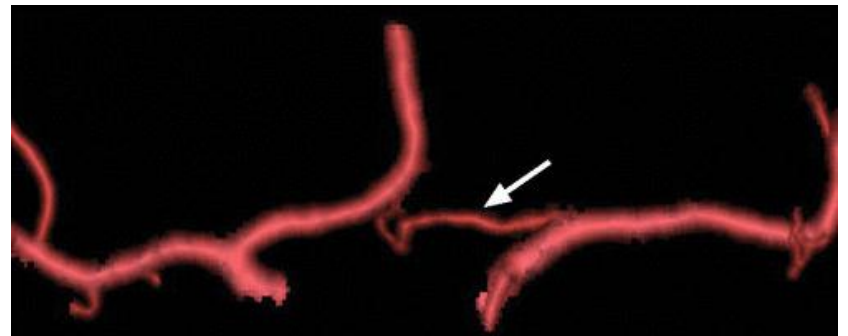
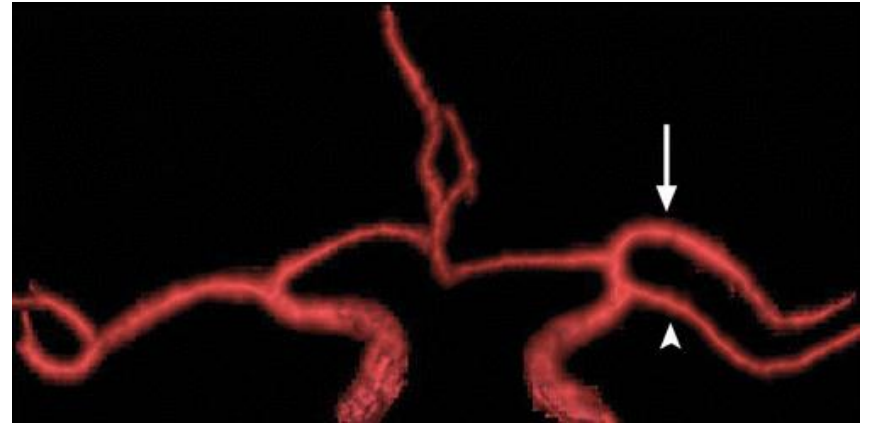
Figure 2. PCA effects on facial morphology. The effects of the first 10 PCs (A–J) on face shape change parameters (FSCPs). The effect as a magnitude of each quasi-landmark displacement is shown first, followed by the alternate transformations (grey faces), the area ratio between both, the curvatures on the transformations, the curvature ratio between both, and finally the normal displacement between both, which is the signed magnitude of the displacement of one quasi-landmark in the direction normal to the surface of the first transformation (left grey faces).
doi:10.1371/journal.pgen.1004224.g002

Different approach

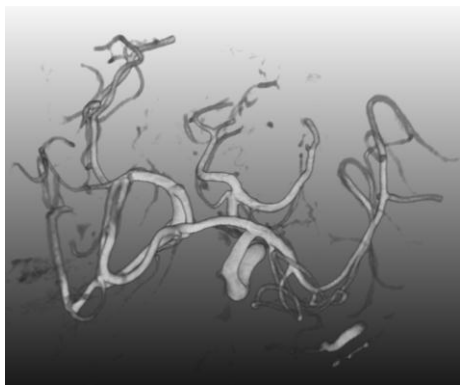
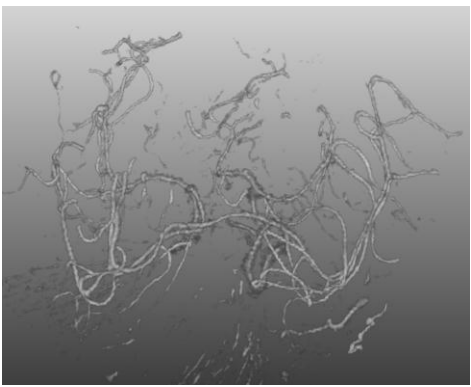
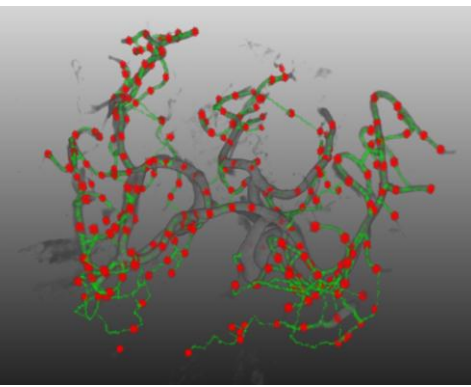
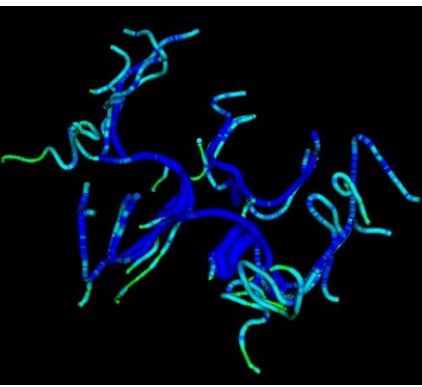
- Complex phenotype (facial features)
- Phenomics using principal component analysis
- Apply statistical modeling (BRIM): one statistical construct using relationship modeling
- Genetic architecture

MRA of circle of Willis

- Large variation
- Biology not understood (DCE1, VEGF potential role)
- Differences in shape relevant for stroke pathophysiology
- Study individual absence or complex trait
- Complex analysis

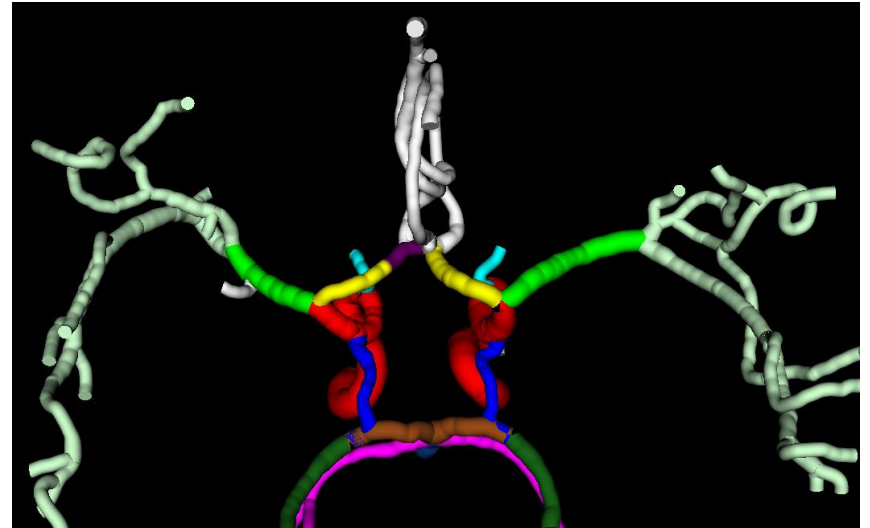


Tools for analyzing MRA data

Image	Tubularity	Overcomplete graph	Result
			

Courtesy D Robben, MICCAI 2013-2014

Results



Courtesy D Robben, MICCAI 2013-2014

Advantages

- The result is a symbolic model representing the vasculature (<> voxel segmentation)
 - No voxels, but a tubular structure
 - Shape, connectivity, diameter,... can be calculated automatically
- Vasculature is anatomically labeled allowing automatic measurement of relevant features (diameter, length, tortuosity) of specific vessels

Phenotypes that could be studied or identifying relevant principal components

- Variants of circle of Willis
- Diameter of vessels
- Stenosis/occlusion
- Aneurysm
-

Further steps

- Validate MRA analysis to detect deviations from normal in pathological situations
- Identify relevant principal components from 'normal' MRA and pathological MRA
- Perform genetic analysis of relevant subgroups

**DATA MAY SOLVE
PROBLEMS**



BUT SPECULATION IS MORE FUN