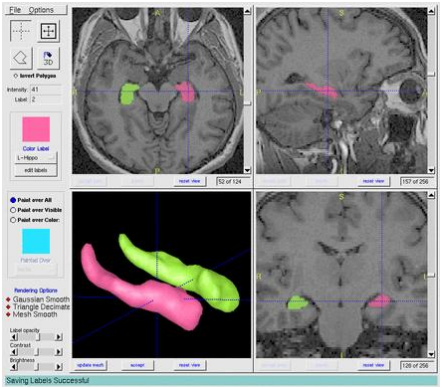
Overview: the project

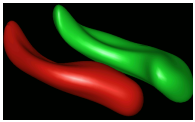
Hippocampus Segmentation (Gerig, Chakos, Schobel, Styner)



1. **Training data:** Expert manual segmentation of 10 images
2. **Shape representation:** Spherical harmonics (more later)
3. **Segmentation:** Image-driven deformation limited by shape model

Overview: the functional data analysis

1. Features are **shape descriptors**: we've done
   - PCA for population understanding
   - a little FLD for schizophrenic/control 2-class discrimination (a separate project)



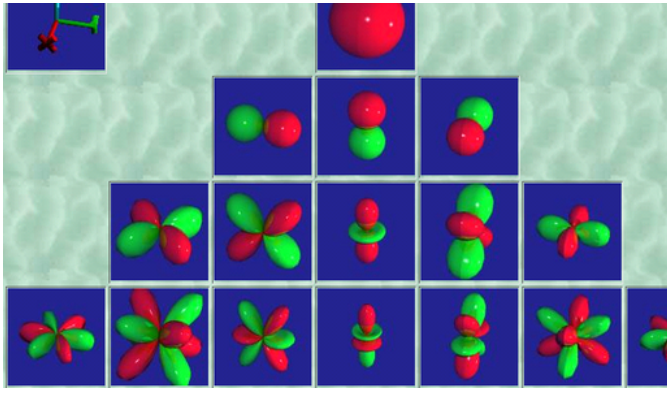
2. Features are **image intensity profiles**: we've done
   - normalization (feature selection)
   - some naive PCA

Modelling shape: PDM

Point Distribution Model

- Classical boundary representation of 3D objects (Cootes, Taylor) as an ordered set of 3D points.
- High dimension feature space – e.g. 1000 points $\Rightarrow$ 3000-dimensional feature space!
- Can capture local deformations (e.g. movement of a single point)

Modelling shape: spharm

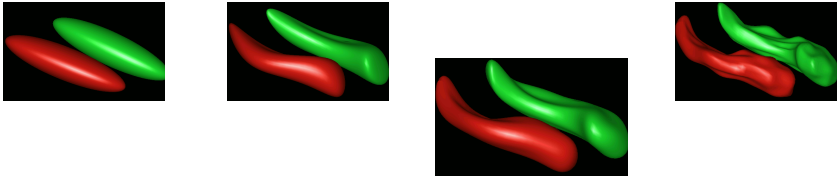


3D analogue to 2D Fourier harmonics (corpus callosum):

- With *Fourier* harmonics, basis functions are combinations of sines and cosines, ellipsoids of increasing frequency
- With *spherical* harmonics, basis functions are combinations of associated Legendre polynomials, with different lobes

Modelling shape: spharm

degree 1 degree 3 degree 6 degree 12



- Quasi *"smoothing"* by limiting degree of expansion to order 12 (feature space is still 507-dimensional)
- *Global* representation – changing a single coefficient affects the entire object
- **Linear** transform from PDM to coefficients of spherical harmonics (orthonormal basis functions)

Modelling shape: PCA

- $n = 10$ patients, $d = 507$-dimensional spharm feature vector
- Note linear transform from PDM to spharm representation: so we expect PCA to be the same for PDMs and spharms.
- [elli-anim1.gif]
- [elli-anim2.gif]
- [elli-anim3.gif]

Modelling image intensity: 1D profiles

- Sample each object uniformly on the boundary
- At each boundary point, sample the MRI along a vector normal to the object boundary
- $n = 10$ patients, $m = 1002$ profiles, each $d = 21$ pixels long
  (so we have 1002 separate populations in 21-D space)

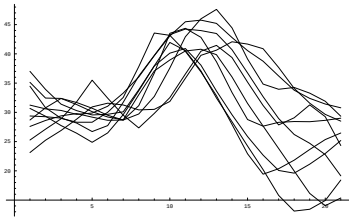
Using the intensity model

- Each profile position is treated independently
- A profile is extracted on-the-fly from the current test image
- A goodness-of-fit is calculated as the Mahalanobis distance in the population for the current profile position
- The goodness-of-fit is used to find an optimal shift for the boundary point in the iterative segmentation algorithm

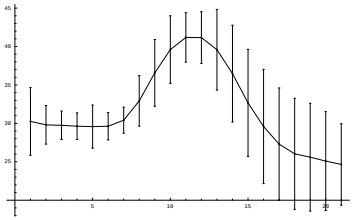
Modelling intensity: statistics

- $n = 10$ patients, $m = 1002$ profiles, each $d = 21$ pixels long
- Profile 1:

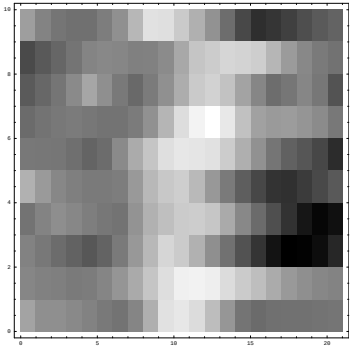
parallel coords overlay



variance at each position



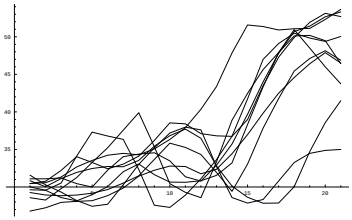
display as image



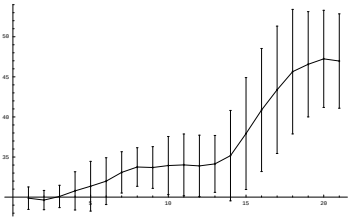
Modelling intensity: statistics

- $n = 10$ patients, $m = 1002$ profiles, each $d = 21$ pixels long
- Profile 99:

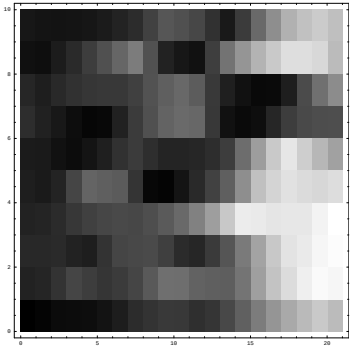
parallel coords overlay



variance at each position



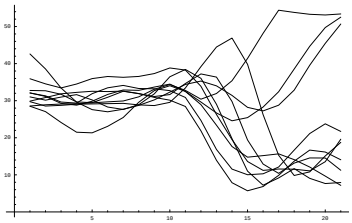
display as image



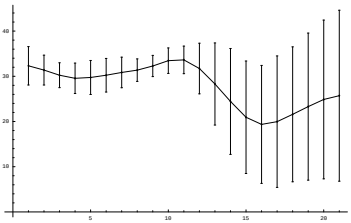
Modelling intensity: statistics

- $n = 10$ patients, $m = 1002$ profiles, each $d = 21$ pixels long
- Profile 900:

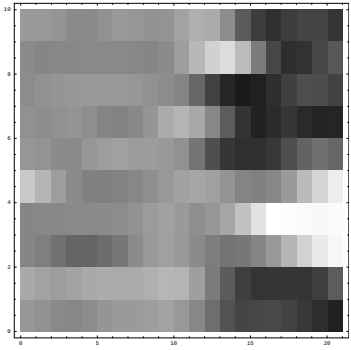
parallel coords overlay



variance at each position

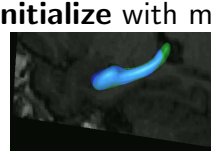


display as image

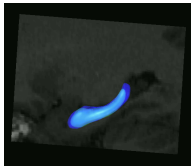


Putting it together: segmentation

- **Initialize** with mean shape



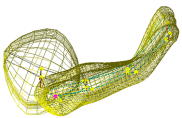
- **Image forces** pull each of the $m = 1002$ boundary points normal to the boundary
- The (noisy) deformation is constrained by a **prior shape model**



Open issues / limitations

Problems with the shape model:

- spharm is **global:** a local deformation affects all coefficients
- spharm is not (very) **intuitive:** difficult to understand the population – e.g. visualization of PCA
- **M-reps** try to resolve these issues (but also introduce much more complexity)



Open issues / limitations

Problems with the image intensity model:

- The statistical models for individual profiles looked pretty bad
- **Normalization** for overall MRI bias, gain
- **Coarse-to-fine** (Markov) approach to profile sample points (region of influence)
- **Multiscale** matching along the profiles