Bayesian ambient space inference for object data

lan Dryden



UNITED KINGDOM · CHINA · MALAYSIA

CIRM, Luminy, September 1st, 2017. Joint work with: Huiling Le, Kwang-Rae Kim, Wen Cheng, Xianzheng Huang, David Hitchcock.

◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの





2 Ambient vs quotient space: functional data

- Molecule matching
- 4 3D ambient regression: faces

5 Discussion

Outline



- 2 Ambient vs quotient space: functional data
- 3 Molecule matching
- 3D ambient regression: faces

5 Discussion

▲□▶▲圖▶▲≣▶▲≣▶ ≣ のQ@

A New Era

"What steam was to the 18th century, electricity to the 19th, and hydrocarbons to the 20th, data will be to the 21st century. That's why I call data a new natural resource."



◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの

Ginni Rometty, Chairman, President and CEO of IBM

New?

Me: "What's new about data?"





Economist.cor

Traditional types of data

What types of data are there?

• Counts, e.g. {0, 1, 2, ...}



Measurements, e.g. 27.52



• Many measurements (Vectors), e.g. (3.2, 1.2, 54.3, 2.1)



◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの

Object Data

- Circlular and spherical data
- Functions
- Dynamical systems
- Shapes and manifold data
- Images
- Trees



Left: FLAT manifold Right NON-FLAT manifold



- Shortest distance between two points may not be a straight line.
- Need to adapt conventional FLAT space data analysis for analysis on manifolds

Shape analysis

KEY ASPECTS:

- SHAPE: remove REGISTRATION information (e.g. Rotation, Translation, Scale - D.G. Kendall)
- Shape data usually lie on a non-flat manifold
- Approximation using a flat tangent space
- Carry out PCA and further statistical inference



・ コット (雪) (小田) (コット 日)

Outline



2 Ambient vs quotient space: functional data

- 3 Molecule matching
- 3D ambient regression: faces

5 Discussion

▲□▶ ▲□▶ ▲□▶ ▲□▶ ▲□ ● ● ●

Functional Data Analysis

Example 1: Berkeley Girls growth-rate data (54 curves - age 1-18)



Functional Data Analysis

Two curves (before and after registration)





・ロト・西ト・ヨト・ヨー シック

Warp

Time-warp (in Diff[0, 1]) - posterior mean and 95% credibility interval



◆□ > ◆□ > ◆豆 > ◆豆 > ~豆 > ◆○ ◆

Ambient versus Quotient Spaces

• The **Ambient Space** *M*, contains standardized functions.

(日) (日) (日) (日) (日) (日) (日)

• Usually a simple metric space, e.g. \mathbb{R}^{p} , \mathbb{L}^{2} , S^{p-1} .

Ambient versus Quotient Spaces

- The **Ambient Space** *M* , contains standardized functions.
- Usually a simple metric space, e.g. \mathbb{R}^{p} , \mathbb{L}^{2} , S^{p-1} .
- The **Quotient Space** Q = M/G, contains the equivalence classes where the group *G* of transformations has been removed.

(日) (日) (日) (日) (日) (日) (日)

• Q is usually non-Euclidean: the geometry can be complicated.

Ambient versus Quotient Spaces

- The **Ambient Space** *M* , contains standardized functions.
- Usually a simple metric space, e.g. \mathbb{R}^{p} , \mathbb{L}^{2} , S^{p-1} .
- The **Quotient Space** Q = M/G, contains the equivalence classes where the group *G* of transformations has been removed.

- Q is usually non-Euclidean: the geometry can be complicated.
- In which space should we work M or Q?

Comparing two objects

- Data in ambient space: X₁ and X₂
- Distance in quotient space:

$$d([X_1], [X_2]) = \inf_{\gamma \in G} d(X_1, X_2 \circ \gamma)$$

- where γ is an isometric transformation, e.g. a time warp: Diff[0, 1]
- Invariance property
 d([X₁ ∘ γ₀], [X₂ ∘ γ₀]) = *d*([X₁], [X₂]).



◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの

Comparing two objects

- Data in ambient space: X₁ and X₂
- Distance in quotient space:

$$d([X_1], [X_2]) = \inf_{\gamma \in G} d(X_1, X_2 \circ \gamma)$$

- where γ is an isometric transformation, e.g. a time warp: Diff[0, 1]
- Invariance property
 d([X₁ ∘ γ₀], [X₂ ∘ γ₀]) = *d*([X₁], [X₂]).
- Geometry/models are usually simpler in the ambient space



◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの

Square Root Velocity Function (SRVF)

- Let *f* be a real valued differentiable curve function $f(t) : [0, 1] \rightarrow \mathbb{R}^{m}$.
- The SRVF is defined as $q: [0, 1] \rightarrow \mathbb{R}^m$, where

$$q(t) = \frac{\dot{f}(t)}{\sqrt{||\dot{f}(t)||}}$$

and ||f|| denotes the standard \mathbb{L}^2 -norm (Srivastava et al., 2011; cf. Younes, 1998).

 Why use the SRVF? The Fisher-Rao (Elastic) metric is reduced to a standard L² metric under SRVF representation.

$$d_{FR}(f_1, f_2) = \|q_1 - q_2\|.$$

Ambient space curves

Berkeley Girls q-functions of growth-rates - need to align them using a time warps



◆□ > ◆□ > ◆豆 > ◆豆 > ̄豆 − のへの

Likelihood Model for *q* function

• A Gaussian process for $q_1(t) - q_2^*(t)$, where

 $q_2^*(t) = \sqrt{\dot{\gamma}(t)}q_2(\gamma(t))$, given a fixed $\gamma(t)$.

- Let q₁([t]) and q₂^{*}([t]) denote the finite M points of q₁(t) and q₂^{*}(t)
- The joint distribution is multivariate normal,

 $q_1([t]) - q_2^*([t]) \sim N(0_M, \Sigma_{M \times M})$ given a fixed $\gamma(t)$.

Prior Model for the Warp

- Discretize the time warp
- Let γ([t]) denote {γ([t_i]), i = 0, 1, 2, ..., M}, the collection of discretized points on the warping function.
- Define $p_i = \gamma([t_i]) \gamma([t_{i-1}])$.
- Note $\sum_{i=1}^{M} p_i = 1$ and $0 < p_i < 1$.
- Denote $P_M = (p_1, p_2, ..., p_M)$ and treat P_M as a random vector, a Dirichlet prior is assigned to $\{P_M | \gamma([t])\}$, i.e. $\pi(P_M) \sim Dirichlet(a)$.

(日) (日) (日) (日) (日) (日) (日)

• Large *a* encourages unit slope $\dot{\gamma}(t) = 1$.

Functional Data Analysis

Two curves (before and after registration)





・ロト・西ト・ヨト・ヨー シック

Warp

Time-warp (in Diff[0, 1]) posterior mean and 95% credibility interval (a = 1 here)



◆□> ◆□> ◆豆> ◆豆> ・豆 ・ 釣べ⊙

Multiple curves

- q-functions: $q_i \sim N(\mu, \kappa^{-1}I), i = 1, \dots, n$.
- Ambient space mean $\mu = E[X]$ (Gaussian prior).
- warps $\gamma_i(t), i = 1, ..., n$ independent Dirichlet prior
- $\kappa \sim \Gamma(\alpha, \beta)$ independent prior
- Simulate from the posterior distribution

$$(\mu, \kappa, \gamma_1, \ldots, \gamma_n)|q_1, \ldots, q_n.$$

(日) (日) (日) (日) (日) (日) (日)

using Markov chain Monte Carlo simulation.

Bayesian analysis - posterior mean

Berkeley Girls growth-rates - q-functions (a = 50)



time

◆□▶ ◆□▶ ◆□▶ ◆□▶ ◆□ ● ● ● ●

Bayesian analysis

Berkeley Girls growth-rates - icons (a = 50)

$$f(t) = \int_0^t q(s) |q(s)| ds$$



. J 🕨 🕨

ъ

Ambient space asymptotic normality and consistency

Subject to the conditions of the Bernstein-von Mises theorem (van der Vaart (1998, p141), we have

$$\sqrt{n}(\hat{\mu}([t]) - \mu([t])) \to N(\frac{1}{\sqrt{n}} \sum_{i=1}^{n} I_{\mu}^{-1} \dot{\ell}_{\mu([t])}(X_i) , I_{\mu([t])}^{-1})$$

in total variation norm as $n \to \infty$, where $\ell_{\mu([t])}(X_i)$ is the derivative of the log-likelihood corresponding to observation *i*. We can state that $\hat{\mu} \to \mu$ in probability as $n \to \infty$, and hence the ambient space mean is consistent. (cf. Allassonnière et al., 2007, 2010)

Quotient space registration

- Let f_1 , f_2 be two functions with SRVFs q_1 , q_2 .
- Warp f₂ to f₁ to minimize the Fisher-Rao distance using the optimal warp

$$\hat{\gamma} = \inf_{\gamma \in \Gamma} || \boldsymbol{q}_1 - \sqrt{\dot{\gamma}} (\boldsymbol{q}_2 \circ \gamma) ||^2.$$



3

• The solution can be obtained by Dynamic Programming (Srivastava et al., 2011).

Ambient space model (e.g. Gaussian with mean μ, variance σ² I) easier to understand and interpret. (+)

◆□ ▶ ◆□ ▶ ◆ □ ▶ ◆ □ ▶ ● ● ● ● ●

- Ambient space model (e.g. Gaussian with mean μ, variance σ² I) easier to understand and interpret. (+)
- Ambient space marginal likelihood very complicated in general. (-)

- Ambient space model (e.g. Gaussian with mean μ, variance σ² I) easier to understand and interpret. (+)
- Ambient space marginal likelihood very complicated in general. (-)
- Ambient space posterior mode/MLE consistent for mean μ in ambient space. (++) (Allassonnière et al., 2007).

- Ambient space model (e.g. Gaussian with mean μ, variance σ² I) easier to understand and interpret. (+)
- Ambient space marginal likelihood very complicated in general. (-)
- Ambient space posterior mode/MLE consistent for mean μ in ambient space. (++) (Allassonnière et al., 2007).
- Quotient space (least squares) estimator biased in general for μ (-) (Miolane et al., 2017)

- Ambient space model (e.g. Gaussian with mean μ, variance σ² I) easier to understand and interpret. (+)
- Ambient space marginal likelihood very complicated in general. (-)
- Ambient space posterior mode/MLE consistent for mean μ in ambient space. (++) (Allassonnière et al., 2007).
- Quotient space (least squares) estimator biased in general for μ (-) (Miolane et al., 2017)
- Quotient space estimator consistent for population Fréchet mean (+) (Bhattacharya and Patrangenaru, 2003)

- Ambient space model (e.g. Gaussian with mean μ, variance σ² I) easier to understand and interpret. (+)
- Ambient space marginal likelihood very complicated in general. (-)
- Ambient space posterior mode/MLE consistent for mean μ in ambient space. (++) (Allassonnière et al., 2007).
- Quotient space (least squares) estimator biased in general for μ (-) (Miolane et al., 2017)
- Quotient space estimator consistent for population Fréchet mean (+) (Bhattacharya and Patrangenaru, 2003)
- Quotient space inference faster (dynamic programming for warping) and relatively easy (+).

Simulation study - sample size n, noise σ



Add iid $N(0, \sigma^2)$ noise and apply a Dirichlet(1) warp to each individual in the sample of size *n*.

ъ
Results - log mean square FR distance versus log *n*



Figure 3: The logarithm of the mean square Fisher–Rao distance to the true mean μ_A versus logarithm of sample size n. The full line is the ambient space estimator and the dotted line is the quotient space estimator. The colors are red ($\sigma = 0.1$), green ($\sigma = 0.3$), blue ($\sigma = 0.5$) and cyan ($\sigma = 1$).

log n

log n

Higher dimensions



Outline



2 Ambient vs quotient space: functional data

Molecule matching

4) 3D ambient regression: faces

5 Discussion

▲□▶ ▲□▶ ▲目▶ ▲目▶ ▲目 ● ● ●

Example 2: Bayesian molecule matching

 Common task in cheminformatics and bioinformatics - the alignment and comparison of two or more molecules.



< □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □

Example 2: Bayesian molecule matching

- Common task in cheminformatics and bioinformatics - the alignment and comparison of two or more molecules.
- Geometric similarity ('steric' properties) is a key property.



(日) (日) (日) (日) (日) (日) (日)

Example 2: Bayesian molecule matching

- Common task in cheminformatics and bioinformatics - the alignment and comparison of two or more molecules.
- Geometric similarity ('steric' properties) is a key property.
- Aligning molecules is vital but extremely difficult



◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの

Molecule matching

 When comparing molecules we are interested in similar parts of molecules rather than the whole match. Matching is sensitive to a prior parameter governing extent of overlap.



◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの

proteins: 1bgc [Granulocyte colony-stimulating factor], 1il6 [Interleukin-6] [wikipedia]

Match matrix and registration

We need to estimate a match matrix *M* with 1 in position (j, k) if molecule 1 atom *j* matches to molecule 2 atom *k*, otherwise zeros; a rotation matrix Γ ; and a translation vector γ .



Model: Given *M*, molecule 2 is a Gaussian perturbation of the matching atoms in molecule 1, independent with common variance $\sigma^2 = 1/\kappa$.

Example Match Matrix

Molecule 1: $n_1 = 4$ points (red) and Molecule 2: $n_2 = 5$ points (blue).



Matching points: $1 \rightarrow 3$; $2 \rightarrow 5$; $3 \rightarrow$ no match; $4 \rightarrow 1$ Match matrix

◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの

Here p = 3 matching points.

Which approach is better - ambient versus quotient?

- Bayesian inference using Markov chain Monte Carlo (MCMC) simulation.
- Kenobi and ILD (2012) compare an ambient space model of Green and Mardia (2006) with a quotient space model (ILD et al., 2007; Schmidler, 2007).
- In a range of settings: performance similar but not the same. Invesigated protein matching and simulation studies.
- Ambient space MCMC algorithms less 'sticky'
- Quotient space MCMC algorithms gave higher posterior probabilities of true matches.
- But Ambient space MCMC algorithms gave lower posterior probabilities of false matches.

Quotient above, ambient below



◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの

Simulations: quotient left, ambient right



Estimated probability of correct match (black) and unmatch (red). Mean and variance from 100 simulations, of length 100,000 after burn-in.

ъ

Reason for general similarity of approaches?

Marginal posterior density (Ambient Space inference).

$$\pi_{\mathcal{A}}(\Theta|X) = \int_{\gamma} \pi(\Theta, \gamma|X) d\gamma.$$
 (1)

Quotient space posterior density

$$\pi_{Q}(\Theta|X) \propto \sup_{\gamma} \pi(\Theta, \gamma|X).$$
⁽²⁾

(日) (日) (日) (日) (日) (日) (日)

 We can consider (2) to be an approximation to the marginal density (1) where the integral is approximated using Laplace's method.

Laplace's method

Laplace's method:

$$\int b(t) \exp\{-Mr(t)\} dt \approx b(\hat{t}) \left(\frac{2\pi}{M}\right)^{p/2} |\Sigma_{\hat{t}}|^{1/2} \exp\{-Mr(\hat{t})\}.$$

where the gradient of r(t) is zero at \hat{t} , and $\Sigma_{\hat{t}}$ is the inverse of the Hessian matrix at \hat{t} (postive definite).

(日) (日) (日) (日) (日) (日) (日)

 The approximation is exact when (γ|Θ) is multivariate Gaussian.

◆□▶ ◆□▶ ▲□▶ ▲□▶ ■ ののの

Outline



- 2 Ambient vs quotient space: functional data
- 3 Molecule matching
- 4 3D ambient regression: faces

5 Discussion

Example 3: 3D face landmarks



ъ

Procrustes (least squares) registered data



◆□▶ ◆□▶ ◆臣▶ ◆臣▶ ─臣 ─のへ⊙

Principal components analysis



▲□▶ ▲□▶ ▲三▶ ▲三▶ 三三 のへで

Ambient space regression model

$$\begin{aligned} Y_i &= \mu(x_i)\Gamma_i + \varepsilon_i, \\ &= \left(\beta_0 + \sum_{j=1}^p \beta_j x_{ij}\right)\Gamma_i + \varepsilon_i \end{aligned}$$

where β_0 lower triangular (for identifiability) $\Gamma_i \in SO(m)$ (rotations),

$$\operatorname{vec}(\varepsilon_i) \overset{i.i.d.}{\sim} N_{km}(\operatorname{vec}(\mathbf{0}), \sigma^2 I_m \otimes I_k).$$

(日) (日) (日) (日) (日) (日) (日)

Likelihood and prior

$$f(Y_1, \dots, Y_n, | \beta, \Gamma_1, \dots, \Gamma_n, \sigma^2) = \frac{1}{(2\pi)^{nkm/2} (\sigma^2)^{nkm/2}} \exp\left(-\frac{1}{2\sigma^2} \sum_{i=1}^n \operatorname{tr}\left[(Y_i - X_i\beta\Gamma_i)^\top (Y_i - X_i\beta\Gamma_i)\right]\right)$$

$$\kappa = 1/\sigma^2 \sim \text{Gamma}(a, b);$$

 $\Gamma_i \sim \text{matrix Fisher}(F_0), \quad i = 1, \dots, n;$
 $p(\beta \mid \Gamma_1, \dots, \Gamma_n, \kappa) \propto 1,$

▲□▶ ▲□▶ ▲ 三▶ ▲ 三▶ - 三 - のへぐ

Posterior

The joint posterior for $(\beta, \Gamma_1, \ldots, \Gamma_n, \kappa)$ is given by

$$p(\beta, \Gamma_1, \dots, \Gamma_n, \kappa \mid Y_1, \dots, Y_n)$$

$$\propto \exp\left(\sum_{i=1}^n \operatorname{tr}(F_0^{\top} \Gamma_i)\right) \left[\prod_{i=1}^n \sin \theta_{i2}\right] \kappa^{a+nkm/2-1} \exp\left(-\frac{\kappa}{b}\right)$$

$$\times \exp\left(-\frac{1}{2}\kappa \sum_{i=1}^n \operatorname{tr}\left[(Y_i - X_i\beta\Gamma_i)^{\top}(Y_i - X_i\beta\Gamma_i)\right]\right).$$

▲□▶ ▲□▶ ▲ 三▶ ▲ 三▶ - 三 - のへぐ

Regression models

$$\begin{array}{lll} \mathsf{M1}: & \mathbf{Y}_{i}^{H} &=& \left\{\beta_{0}+\beta_{1} \mathrm{age}_{i}\right\} \Gamma_{i}+\varepsilon_{i}, \\ \mathsf{M2}: & \mathbf{Y}_{i}^{H} &=& \left\{\beta_{0}+\beta_{1} \mathrm{age}_{i}+\beta_{2} \mathrm{age}_{i}^{2}\right\} \Gamma_{i}+\varepsilon_{i} \\ \mathsf{M3}: & \mathbf{Y}_{i}^{H} &=& \left\{\beta_{0}+\beta_{1} \mathrm{age}_{i}+\beta_{2} \mathrm{age}_{i}^{3}\right\} \Gamma_{i}+\varepsilon_{i}, \end{array}$$

where $Y_i^H = HY_i$. Then we define the predicted model as pre-multiplying each \hat{Y}_i by *C*, for example for M1,

$$C\widehat{Y}_{i} = \left\{ H^{\top}\widehat{eta}_{0} + H^{\top}\widehat{eta}_{1} \operatorname{age}_{i}
ight\}\widehat{\Gamma}_{i},$$

where $C = I_k - \frac{1}{k} \mathbf{1}_k \mathbf{1}_k^{\top}$, I_k is the $k \times k$ identity matrix, $\mathbf{1}_k$ is the column vector of k ones, and $\widehat{\beta}_j = \frac{1}{N_B} \sum_{t \in \mathcal{B}} \beta_j^{(t)}$ is the arithmetic mean of MCMC sample (100k) for β_j after burn-in (100k).

Predicted faces using M1 and M2



ъ

M2 chosen using AIC



< □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □



(ロ)、(国)、(E)、(E)、(E)、(O)へ(C)



(e) Female: ear, bottom left. (f) Female: ear, bottom (g) Male: ear, bottom left. (h) Male: ear, bottom right. right.



Figure 4: Ears and lip (M2).

◆□▶ ◆□▶ ◆ □▶ ◆ □▶ ─ □ ─ の < @



・ロト・(四ト・(日下・(日下・))への)

Outline



- 2 Ambient vs quotient space: functional data
- 3 Molecule matching
- 4 3D ambient regression: faces

5 Discussion

▲□▶▲圖▶▲≣▶▲≣▶ ≣ のQ@

Many other applications. Function and Shape: Arteries



(a)

ъ

Mean differences



・ロト ・ 理 ト ・ ヨ ト ・ ヨ ト … ヨ

Shape and Time: Enzymes

Enzyme data k = 88 landmarks in 3D, time series n = 4216. Some snapshots at 10 equally spaced time points.



Four PNS clusters



Figure 41: PNS plot with clustering color scheme.



Figure 42: Centroid size vs. PNS plot.

▲□▶ ▲□▶ ▲ 三▶ ▲ 三▶ - 三 - のへぐ

Enzyme clusters



Clustering using Princpal Nested Spheres: difficult but useful.

イロト 不良 とくほ とくほう 二日

Needed: more on methods, models and uncertainty

- Circlular and spherical data
- Functions
- Dynamical systems
- Shapes and manifold data
- Images
- Trees





SELECTED REFERENCES

- Allassonnière, S., Amit, Y. and Trouvé, A. (2007). Towards a coherent statistical framework for dense deformable template estimation, *JRSS B*, 69, 3–29.
- Cheng, W., Dryden, I. L., Hitchcock, D. B., and Le, H. (2014). Analysis of proteomics data: Bayesian alignment of functions. *Electronic Journal of Statistics*, 8, 1734–1741.
- Cheng, W., Dryden, I. L., and Huang, X. (2016). Bayesian registration of functions and curves. *Bayesian Analysis*, **11**, 447–475.
- Dryden, I.L. and Mardia, K.V. (2016). Statistical shape analysis, with applications in R. 2nd Edition. Wiley, Chichester.

REFERENCES (CONT.)

- Green, P.J. and Mardia, K.V. (2006). Bayesian alignment using hierarchical models, with applications in protein bioinformatics, *Biometrika*, **93**, 235-254,
- Jung, S., Dryden, I.L. and Marron, J.S. (2012). Analysis of principal nested spheres. *Biometrika*, 99, 551-568.
- Kenobi, K. and Dryden, I.L. (2012). Bayesian matching of unlabelled point sets using Procrustes and configuration models. *Bayesian Analysis*. 7, 547-566.
- Miolane, N., Holmes, S., Pennec, X. (2017). Template shape estimation in Computational Anatomy: Correcting an asymptotic bias. SIAM Journal of Imaging Science.
- Srivastava, A., Klassen, E., Joshi, S.H., and Jermyn, I.H. (2011). Shape Analysis of Elastic Curves in Euclidean Spaces. IEEE Transactions on Pattern Analysis and Machine Intelligence 33 (7), 1415-1428.
Thanks!

EPSRC grant and Royal Society Wolfson Research Merit Award.



http://www.maths.nottingham.ac.uk/~ild

◆□▶ ◆□▶ ◆□▶ ◆□▶ ● ● ● ●