

# Cell-Well Data Objects & Fisher Rao Curve Warping

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# Outline

Two topics in cell culture biology

## (1) Object Oriented Data Analysis (OODA)

- Motivation: Analysis of cell images
- How the choice of data objects orient further analyses

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Two topics in cell culture biology

## (1) Object Oriented Data Analysis (OODA)

- Motivation: Analysis of cell images
- How the choice of data objects orient further analyses

## (2) Functional Data Analysis

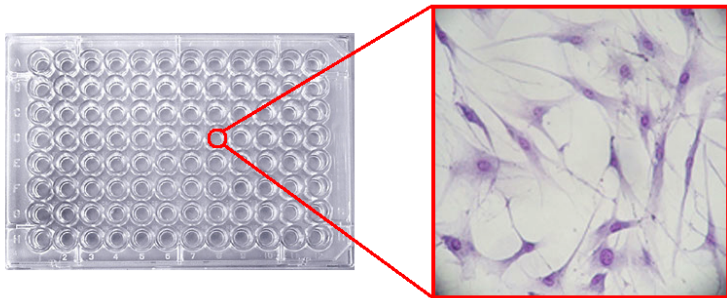
- Motivation: Analysis of cell growth curves
- Decompose horizontal and vertical variabilities

# Object Oriented Data Analysis

- Proposed by Wang & Marron, 2007
- Data objects: Atoms of statistical analysis
  - Numbers
  - Vectors (Multivariate analysis)
  - Curves (Functional data analysis)
- More complex objects
  - Trees
  - Images
  - Shapes

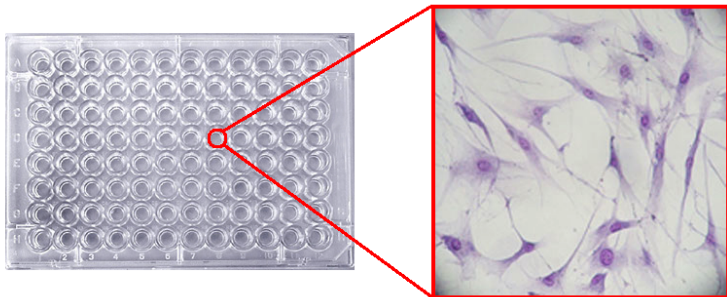
# Background

Goal: Media development for cell culture



# Data Objects

- Wells?
- Cells?

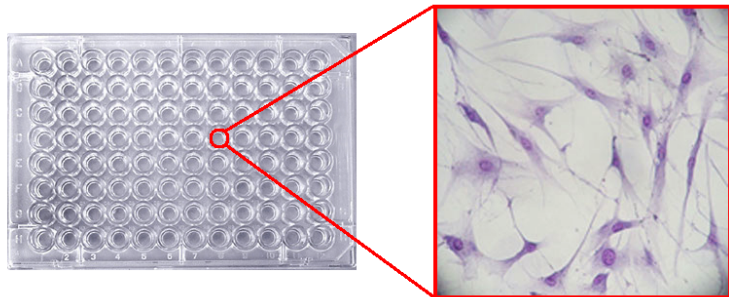


# How OODA works

- (1) Fully understand data structure
- (2) Choose appropriate data objects
- (3) Come up with an “appropriate” analysis

## Motivation

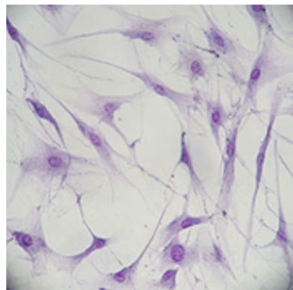
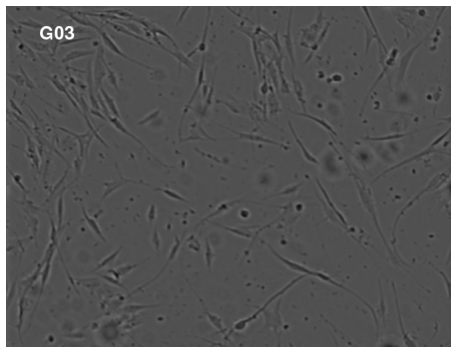
- Confluence: Percent of environment used by cells
- Passage cell culture based on confluence level
- Image a well  $\rightarrow$  Estimate confluence level  $\rightarrow$  Passage





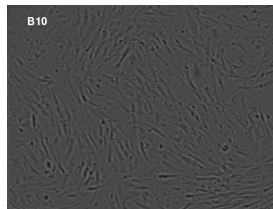
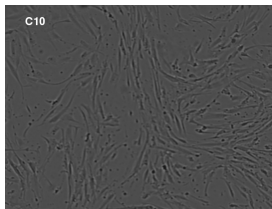
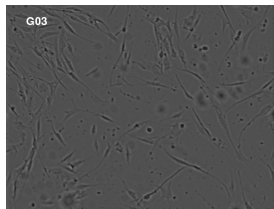
# The Challenge: Bright Field Imaging

- Defocused image of cell shadows
- Difficult to estimate confluence using BF images

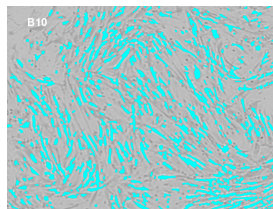
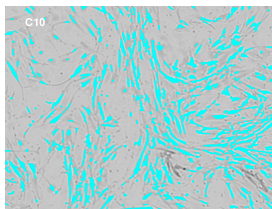
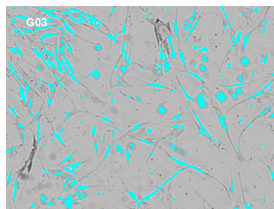


# The Challenge: Bright Field Imaging

## Cell shadows



## IPLab cell identification



## How to Estimate Confluence

- (1) Counting the cells (cyan objects)
- (2) Biologists' manual estimation
  
- (3) Objective statistical estimation
  - Improves over the counting approach
  - Support automated passaging

## How to Estimate Confluence

(1) Counting the cells (cyan objects)

(2) Biologists' manual estimation

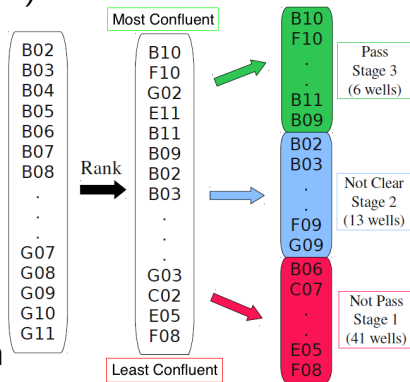
- Varies among people
- Consensus estimation

*bio-rank*

*bio-classification*

(3) Objective statistical estimation

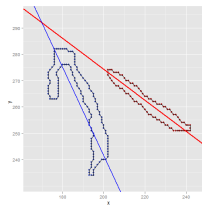
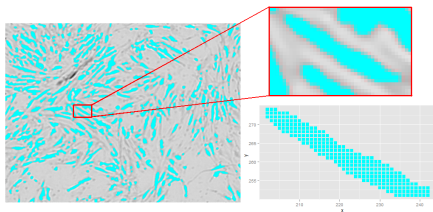
- Improves over the counting approach
- Support automated passaging



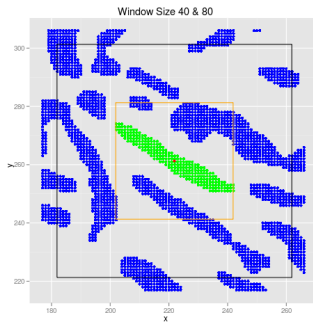
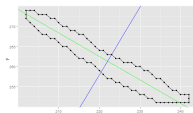
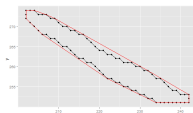
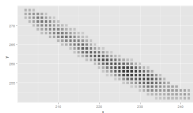
# Image Feature Extraction

- Image preprocessing
  - Remove uneven background shading
  - Remove granular noise
  - Intensity normalization
- Two types of confluence-related features
  - Features of An Individual Cell (32)
  - Additional Entire-Well Features (13)

# Features of An Individual Cell

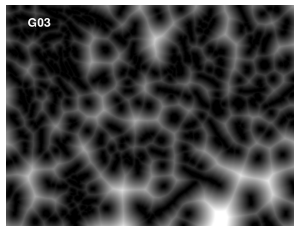
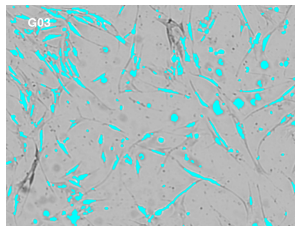
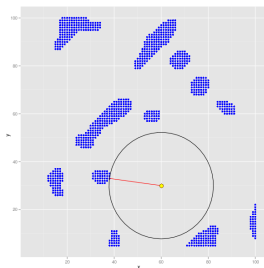


- Intensity
- Shape & size
- Local density
- Cell orientation



## Additional Entire-Well Features

- Cell number
- Cell gap size/intensity

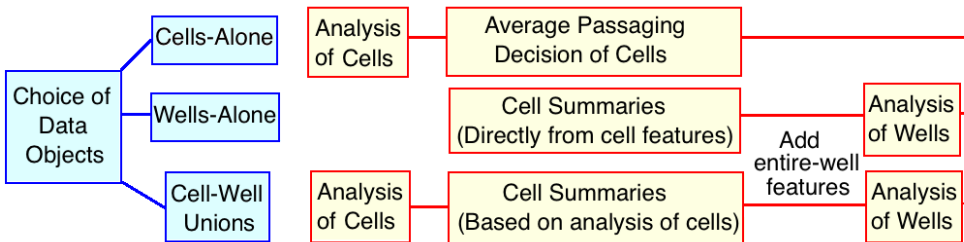


# The Choice of Data Objects

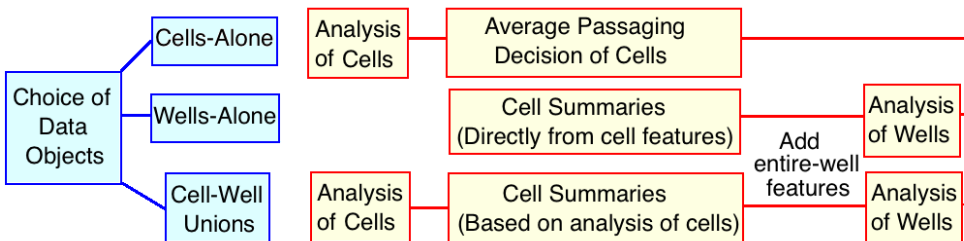
- Two data sets
  - Cell data (features of each individual cell);
  - Well data (additional entire-well features)
- Different choices of data objects
  - Cells-alone
  - Wells-alone
  - A new type of data objects: Wells  $\cup$  Cells



# The Choice of Data Objects



# The Choice of Data Objects



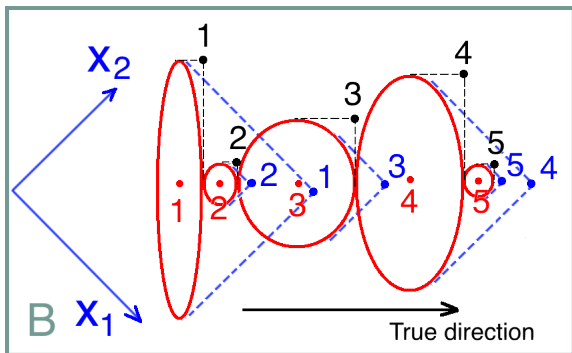
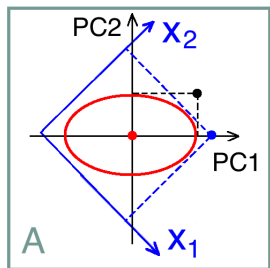
- Cells-Alone: Ignore additional well data
- Wells-Alone vs. C-W Unions  
How to summarize the cells?  
E.g. feature-wise summaries, PC summaries

## Compare Data Objects

- DWD of passaging groups
- % of false passaging decision
  - Cells-Alone: 25%
  - Wells-Alone: 8.6%
  - Cell-Well Unions: 5.2%
- Cells-alone are not a good choice
- Further study of the wells-alone and the unions...

# Cell Summarization

Can either impair or preserve the bio-pattern in cell data



# Cell Summarization

- How well the bio-pattern is preserved depends on
  - Choice of statistics
  - Variability of cell distributions across wells
  - Rotation of cell data before summarizing
- OODA is independent of and suggests analysis method
- C-W unions are a good choice for such data structure

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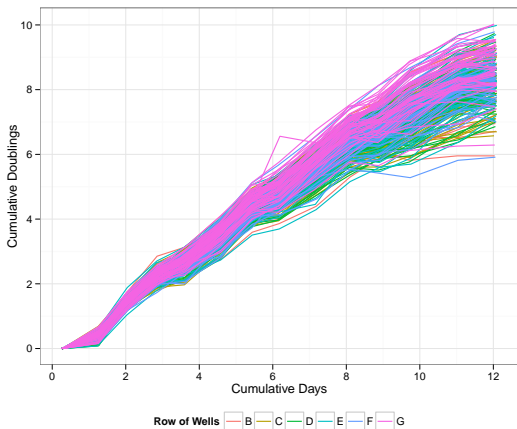
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### (2) Functional Data Analysis

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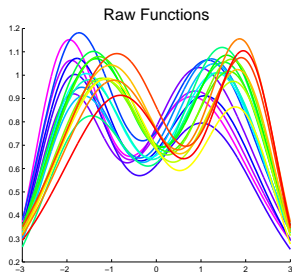
# Motivation

- Cell growth curves: Media effect, Batch effect, etc.
- Analysis of variabilities among curves



# How to Understand the Variability?

- Toy Example to develop appropriate approaches

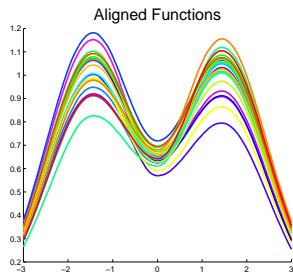
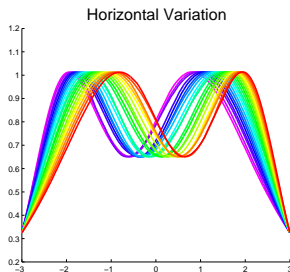
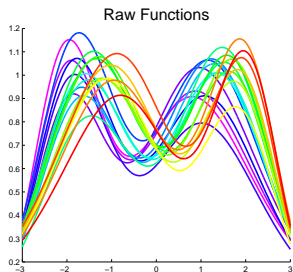




# How to Understand the Variability?

- Toy Example to develop appropriate approaches
- Insightful decomposition

→ Horizontal var + Vertical var



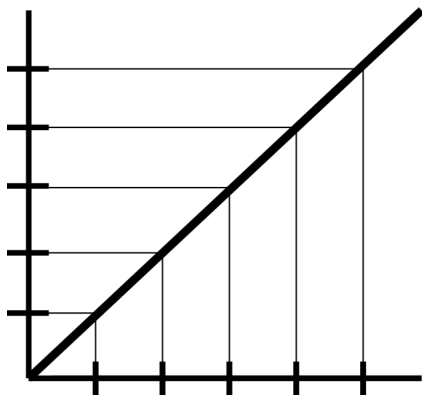
# Curve Registration

- Consider domain warping  $\gamma : [0, 1] \rightarrow [0, 1]$
- $\gamma(x)$  is a diffeomorphism (smooth)



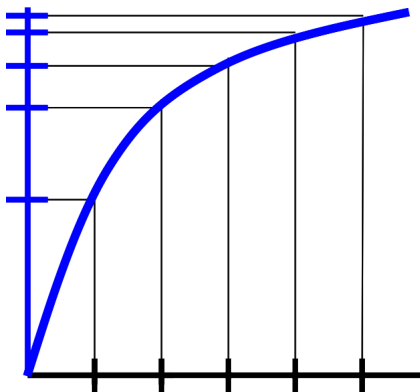
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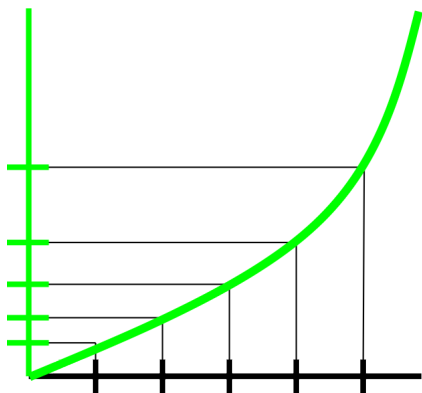
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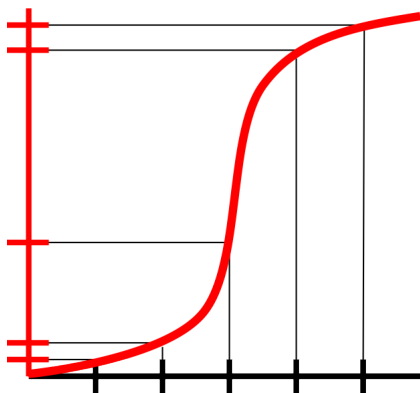
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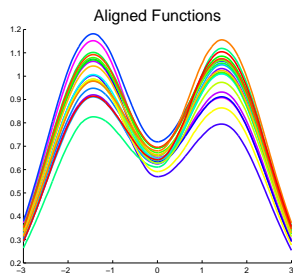
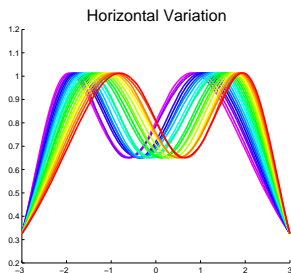
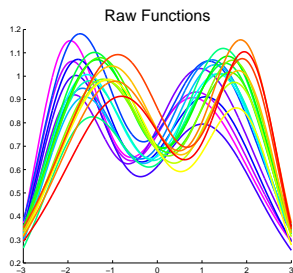
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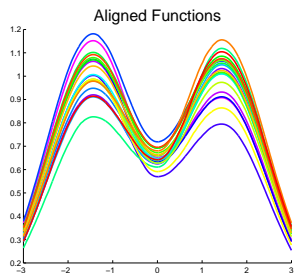
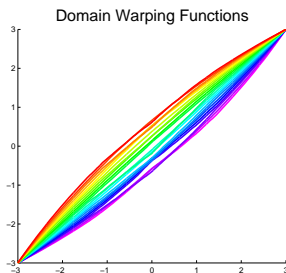
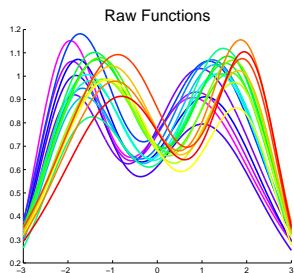
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## How to Understand the Variability?

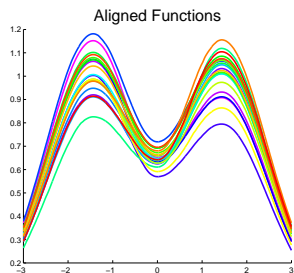
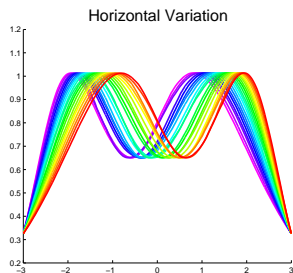
- Toy Example to develop appropriate approaches
- Curve registration:  $f(\gamma(x)) = \tilde{f}(x)$ 
  - Warping functions + Aligned functions
  - Horizontal var + Vertical var





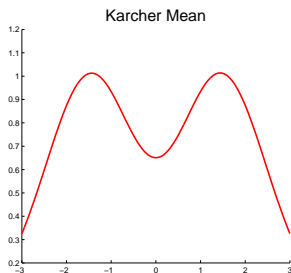
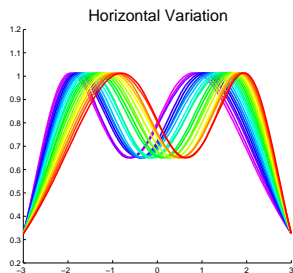
# What Are the Data Objects?

- “Equivalence” of two curves:  $f_1 \sim f_2$
- $\exists \gamma$  so that  $f_1 \circ \gamma = f_2$



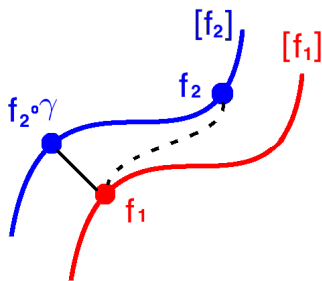
# What Are the Data Objects?

- Data object = Equivalence group of curves
- A representer of the group:  $f$
- Notation of a data object:  $[f]$
- Orbit, Quotient space



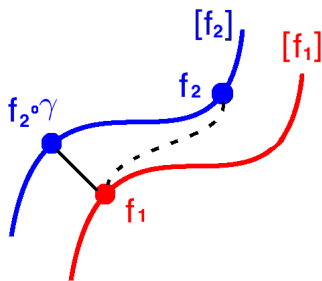
# Curve Registration

- Align  $f_2$  to  $f_1$
- Find a “good” representer of  $[f_2]$ , i.e.  $f_2 \circ \gamma$
- $\inf_{\gamma \in \Gamma} d(f_1 - f_2 \circ \gamma)$



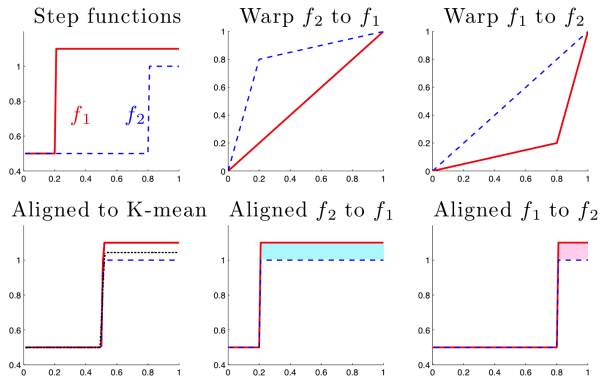
# Metrics in Curve Space

- What is the appropriate metric  $d$ ?
- Traditional choice:  $\|\cdot\|$
- $\inf_{\gamma \in \Gamma} d(f_1 - f_2 \circ \gamma)$



# Metrics in Curve Space

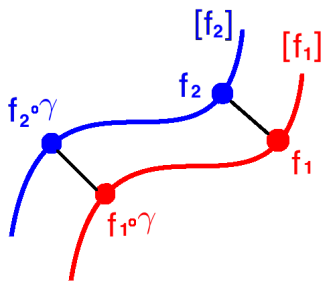
- Issues in  $\mathcal{L}^2$  Metric
- $\inf_{\gamma \in \Gamma} \|f_1 - (f_2 \circ \gamma)\| \neq \inf_{\gamma \in \Gamma} \|(f_1 \circ \gamma) - f_2\|$



# Metrics in Curve Space

- Solution: Warping-invariant metric

$$d(f_1, f_2) = d(f_1 \circ \gamma, f_2 \circ \gamma)$$

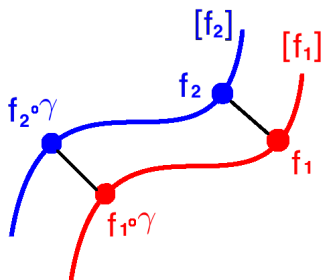


## Metrics in Curve Space

- Fisher Rao Metric (C. R. Rao, 1945)
- It is the unique solution (Cencov, 1982)

$$d_{FR}(f_1, f_2) = d_{FR}(f_1 \circ \gamma, f_2 \circ \gamma)$$

- Challenge: Complicated  
Sample statistics are not clear



## Metrics in Curve Space

- Square Root Velocity Function

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

$$f(t) = f(0) + \int_0^t q_f(s) |q_f(s)| ds$$

- Simplifies FR framework (Srivastava et al, 2010)

$$d_{FR}(f_1, f_2) = \|q_{f_1} - q_{f_2}\|$$

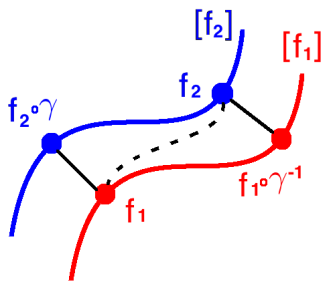


## Metrics in Quotient Space

- Distance between equivalence groups

$$d_Q([f_1], [f_2]) = \inf_{\gamma \in \Gamma} d_{FR}(f_1, f_2 \circ \gamma) = \inf_{\gamma \in \Gamma} \|q_{f_1} - q_{f_2 \circ \gamma}\|$$

- Independent of the choice of  $f_1, f_2$



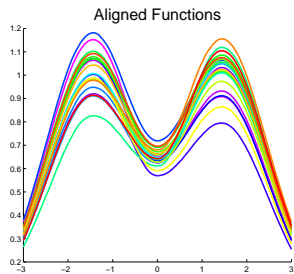
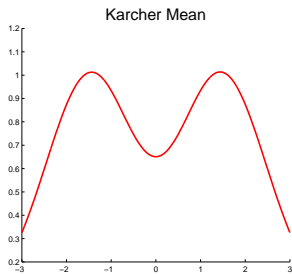
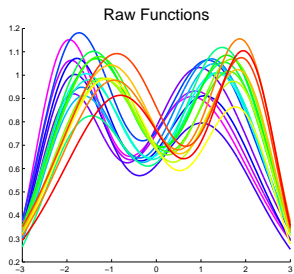
## Mean in Quotient Space

- Consider equivalence groups

$$[f_1], [f_2], \dots, [f_n]$$

- Karcher mean  $[\mu] = \operatorname{argmin}_{[f]} \sum_{i=1}^n d_Q([f], [f_i])^2$
- Choose “best” representer of  $[\mu]$  so that the mean of warping functions = Identity

# Mean in Quotient Space



# Proteomics Data

- Measurements: TIC (Total Ion Count) Chromatograms  
Modern type of chemical spectra

- Intensity as a function of time

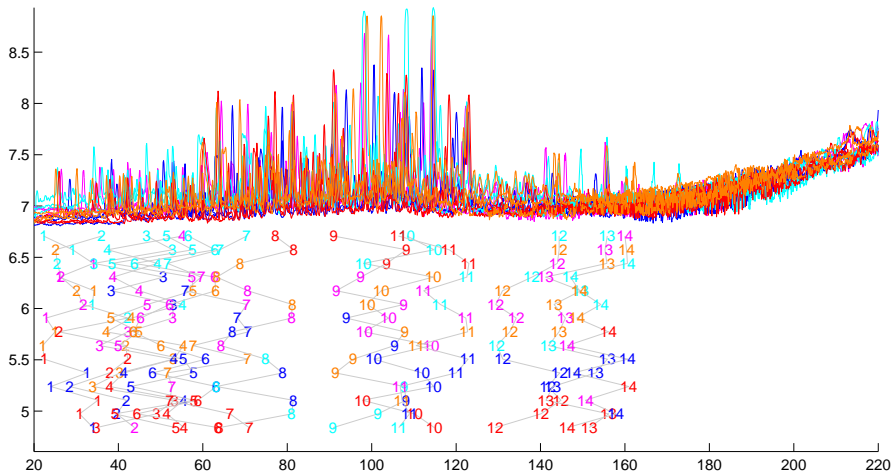
- 15 functions

- Samples: A, B, C, X, Y
- Runs: 1, 2, 3

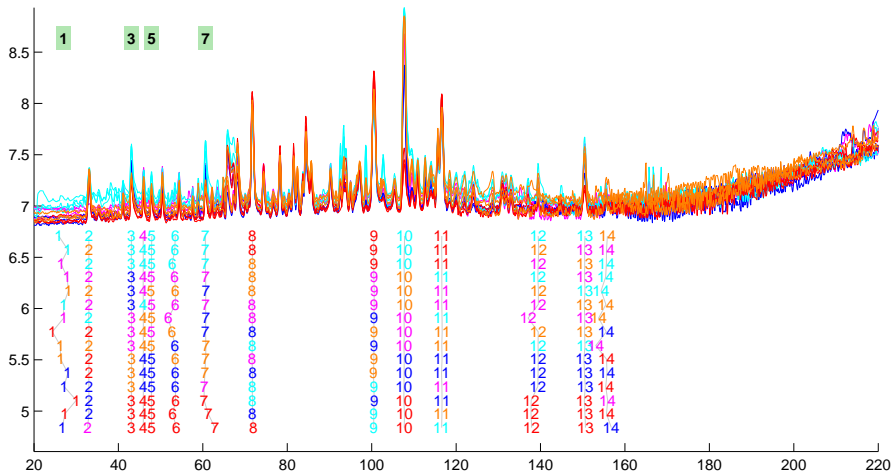
Functions are colored by sample

- 14 features are marked, including “spiked in” features (1, 3, 5, 7)
- Goal: Warp the functions to line up the features

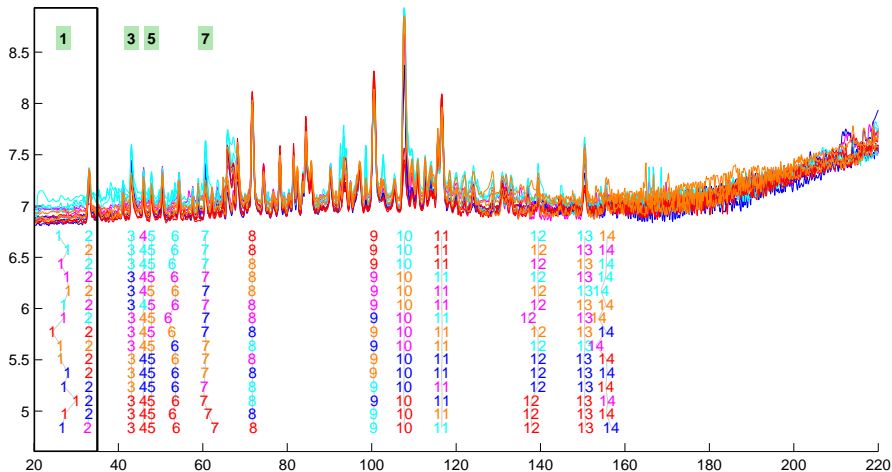
# Unaligned Functions



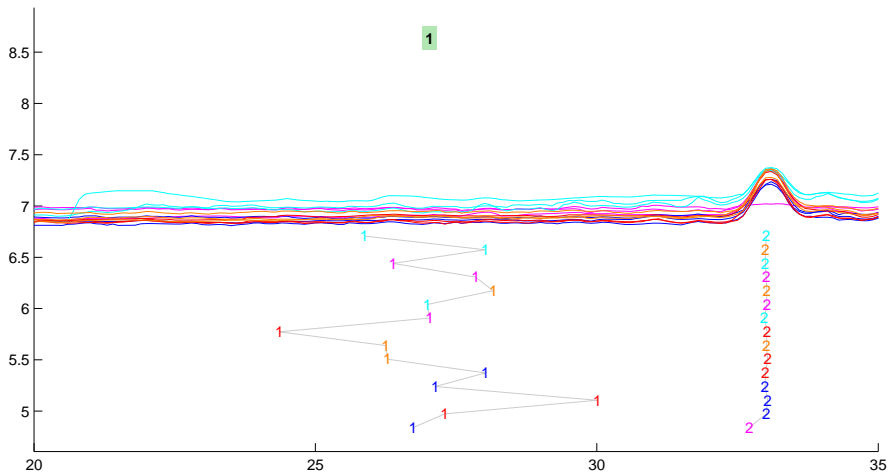
# Aligned Functions



## Zoom-in

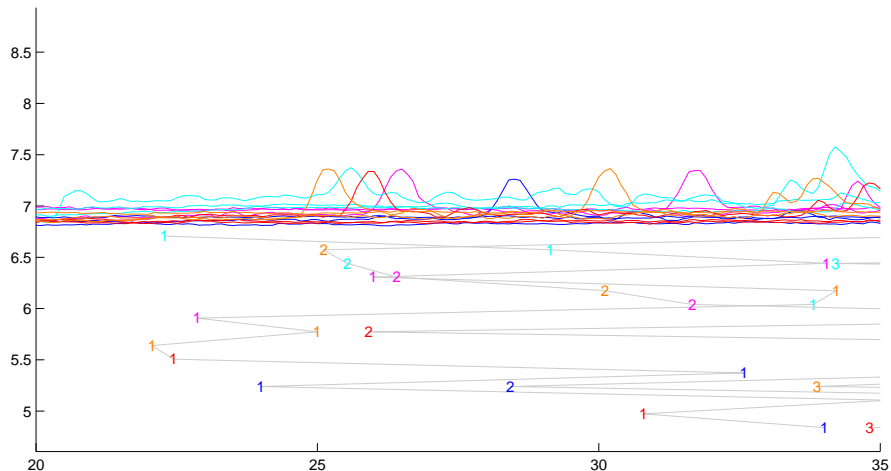


# Zoom-in: Aligned Functions

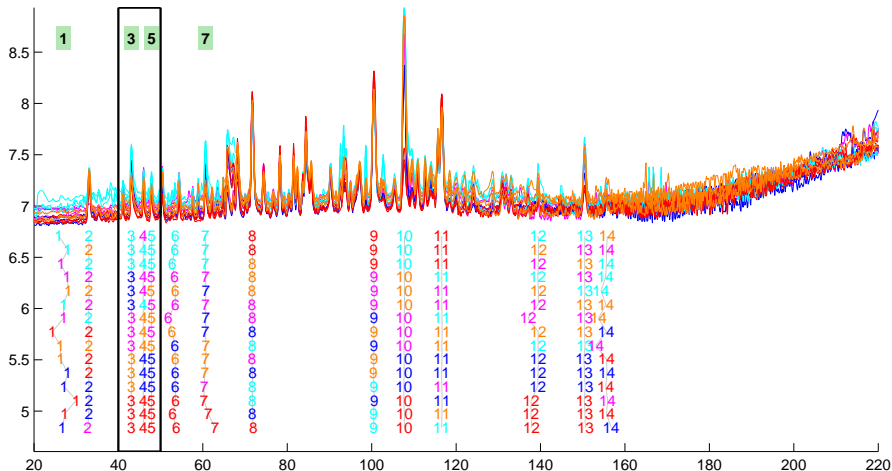




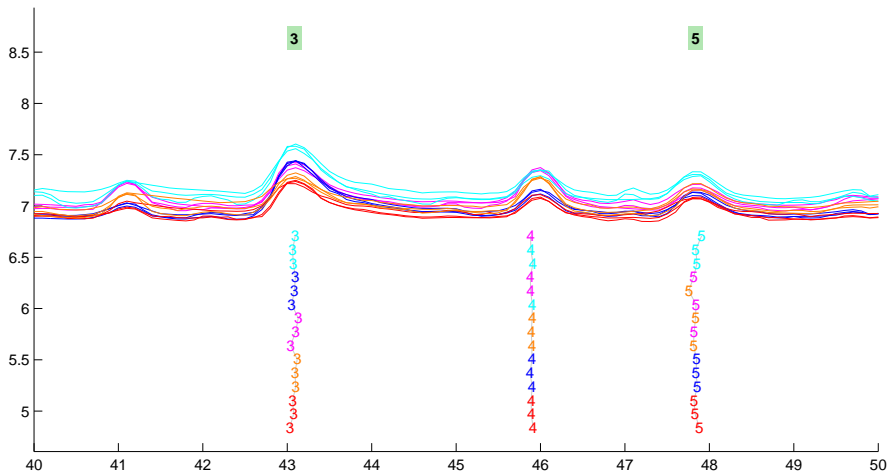
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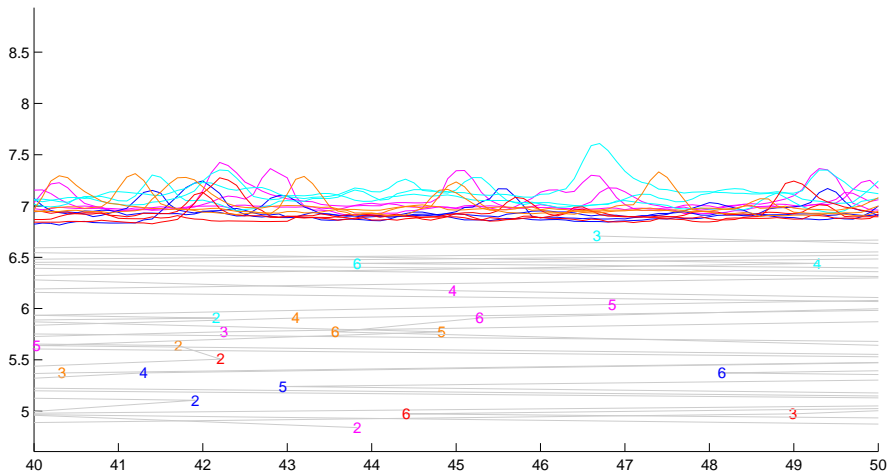
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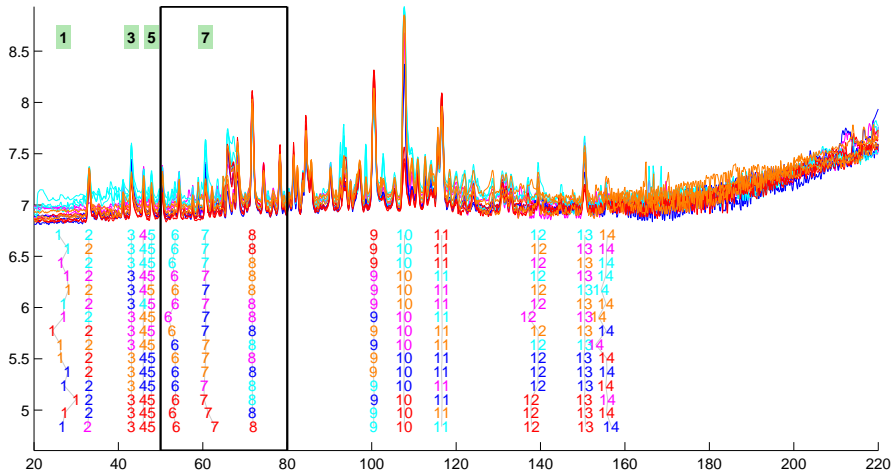
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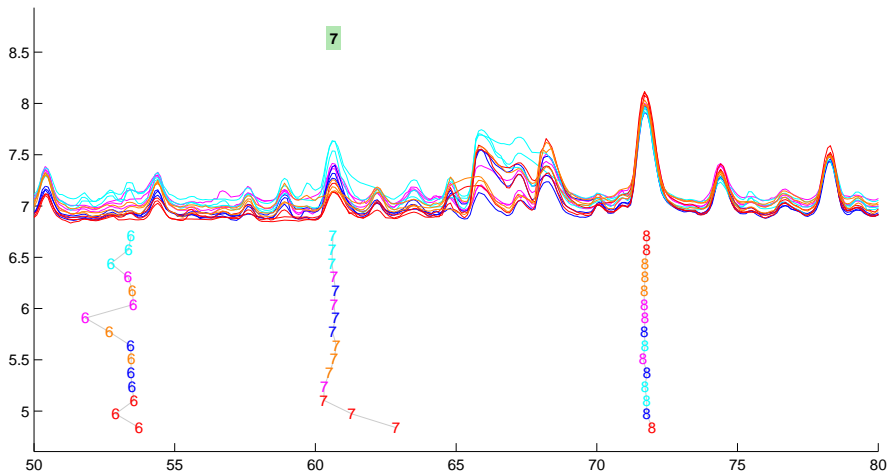
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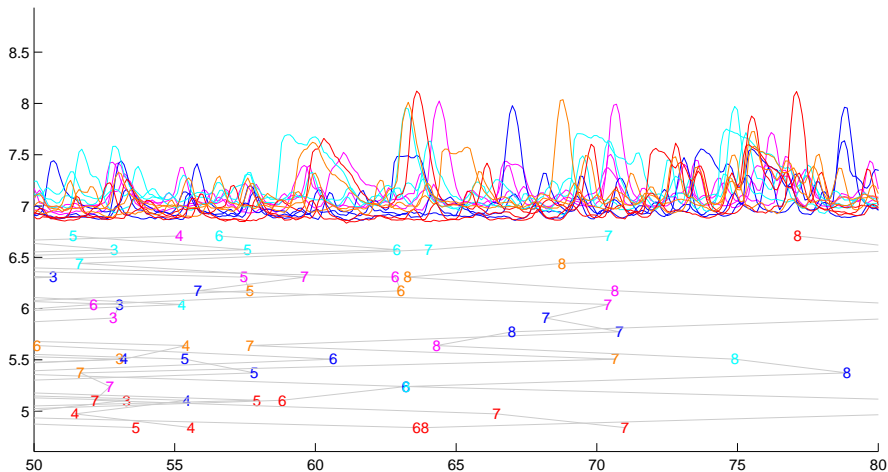
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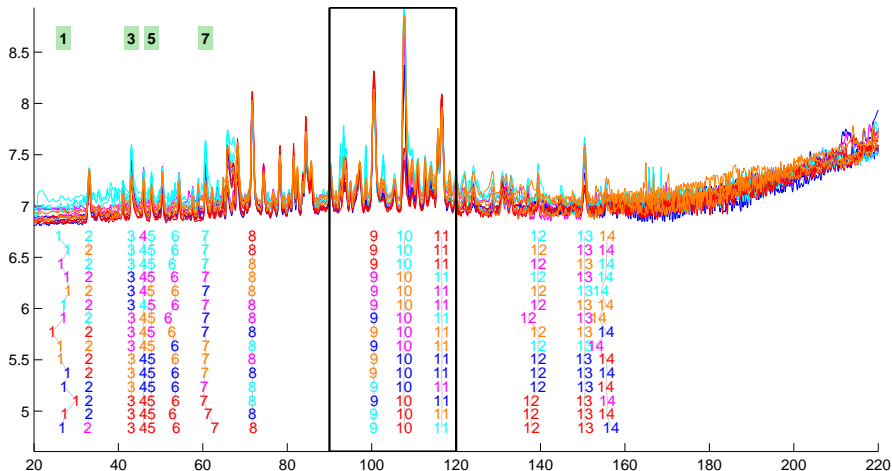
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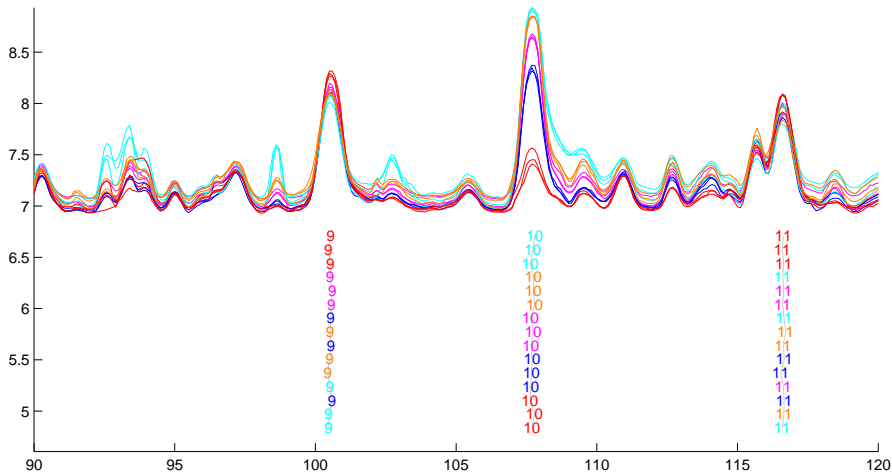


## Zoom-in

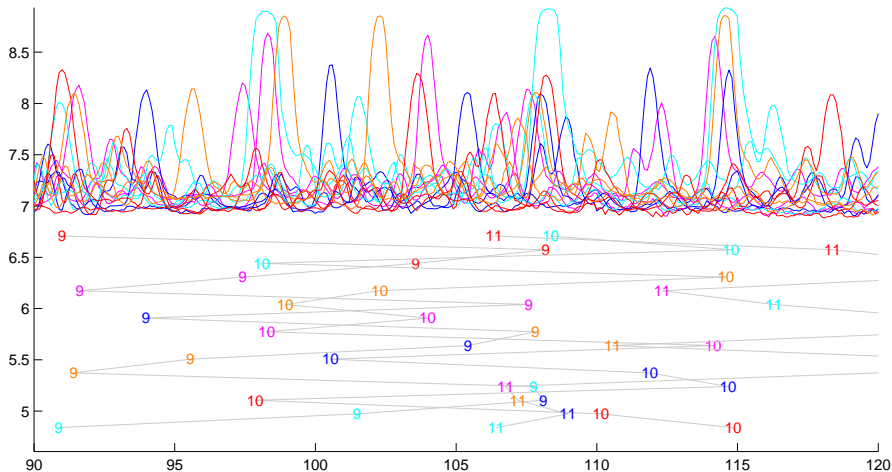




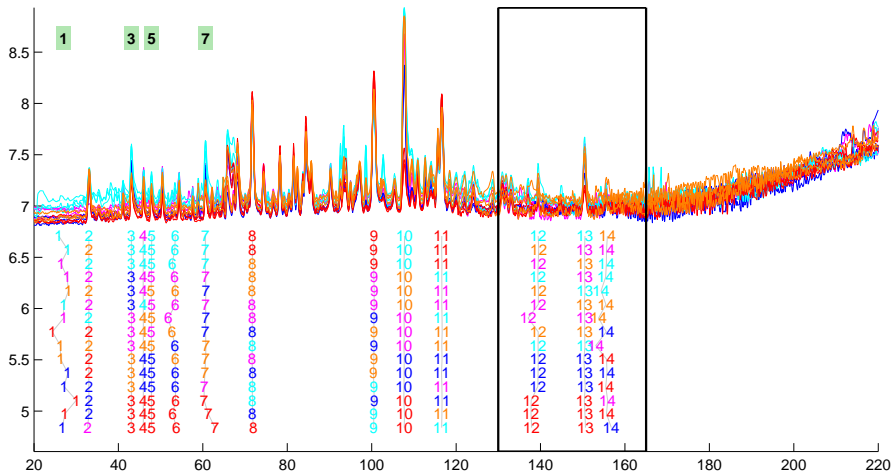
# Zoom-in: Aligned Functions



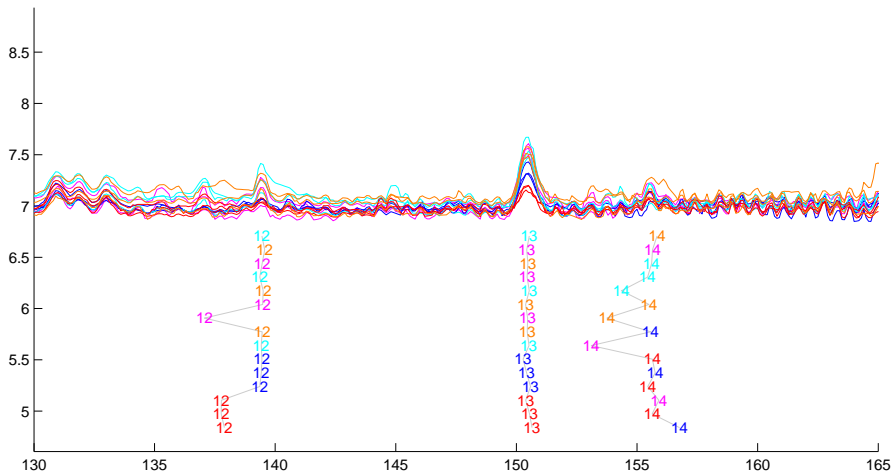
# Zoom-in: Unaligned Functions



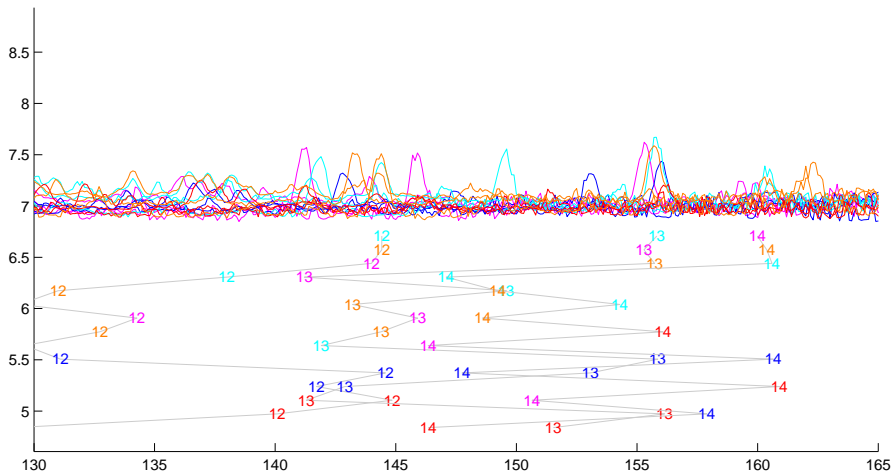
## Zoom-in



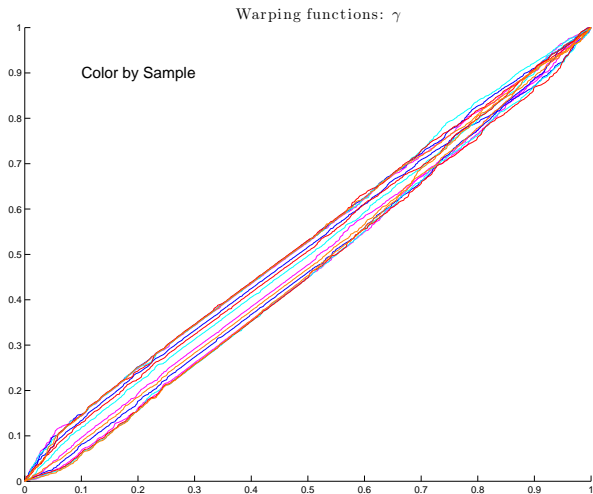
# Zoom-in: Aligned Functions



# Zoom-in: Unaligned Functions



# Warping Functions



## Additional Information

## Appendix: Fisher Rao Metric

- Define Fisher Rao metric as

$$\ll v_1, v_2 \gg_f = \frac{1}{4} \int_0^1 \dot{v}_1(t) \dot{v}_2(t) \frac{1}{|\dot{f}(t)|} dt$$

where  $f \in \mathcal{F}$  and  $v_1, v_2 \in T_f(\mathcal{F})$

- Define Fisher Rao distance as

$$d_{FR}(f_1, f_2) = \inf_{\alpha: [0,1] \rightarrow \mathcal{F}, \alpha(0)=f_1, \alpha(1)=f_2} L[\alpha]$$

where  $\alpha(\tau)$  is a differentiable path connecting  $f_1$  and  $f_2$  in  $\mathcal{F}$

$$L[\alpha] = \int_0^1 (\ll \dot{\alpha}(\tau), \dot{\alpha}(\tau) \gg_{\alpha(\tau)})^{1/2} d\tau$$



# Cell Image Data Visualization

