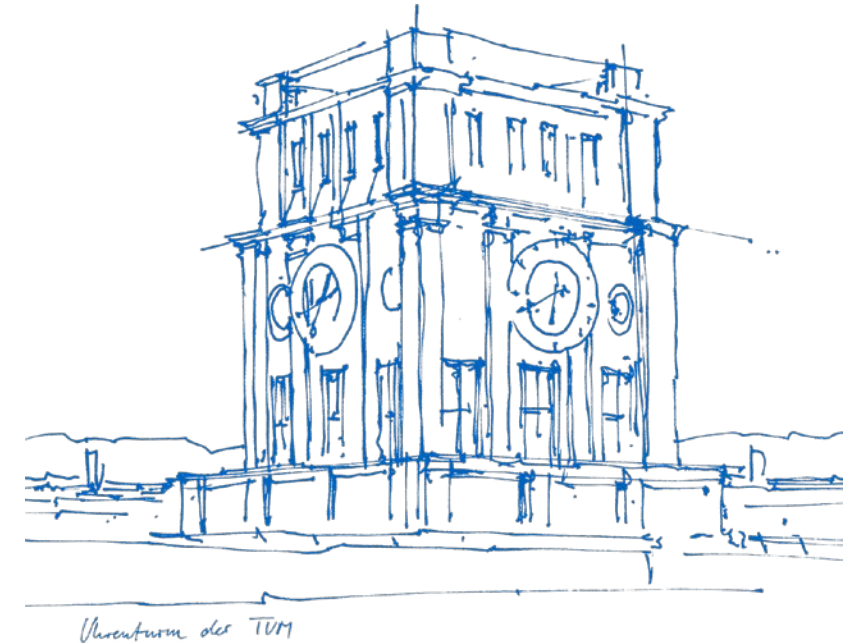


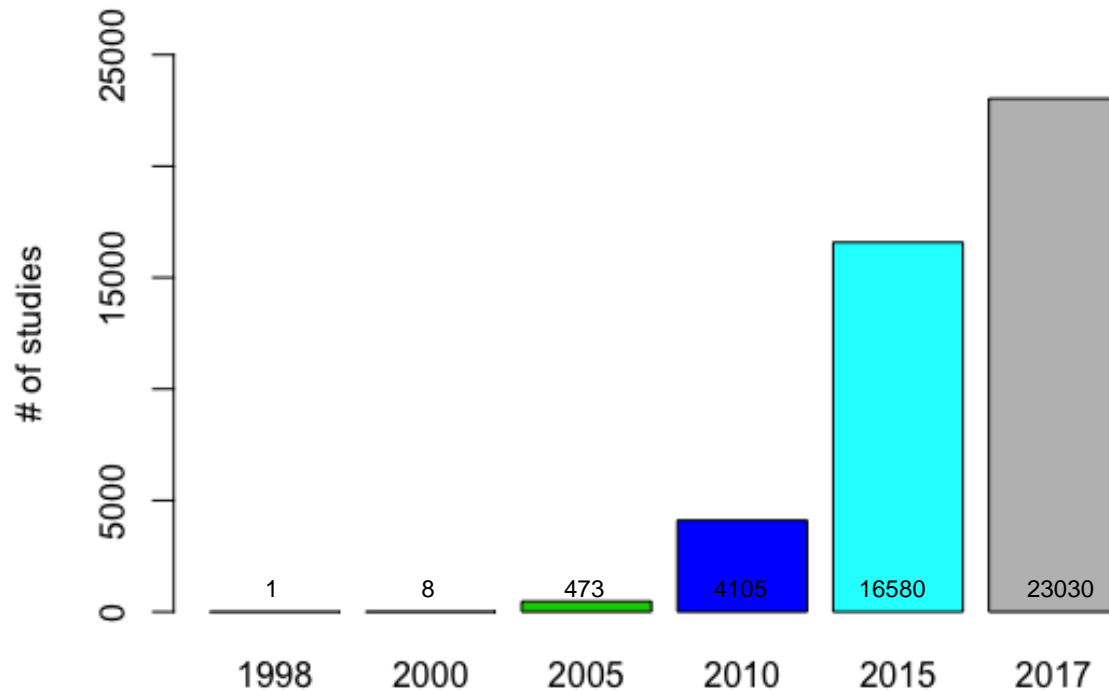
Embracing the Uncorrelated:

*Dynamic Time Warping for the Exploration of
High Dimensional Time-Series Metabolomics
Data from the HuMeT Study*

*Aaron Novikoff
Master student - Technische Universität München*



Growth of Metabolomics Research



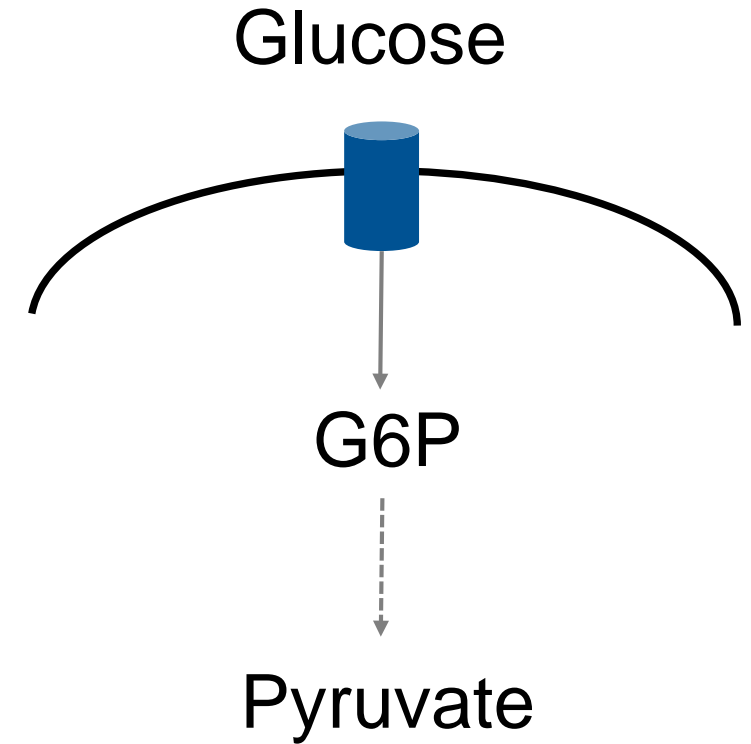
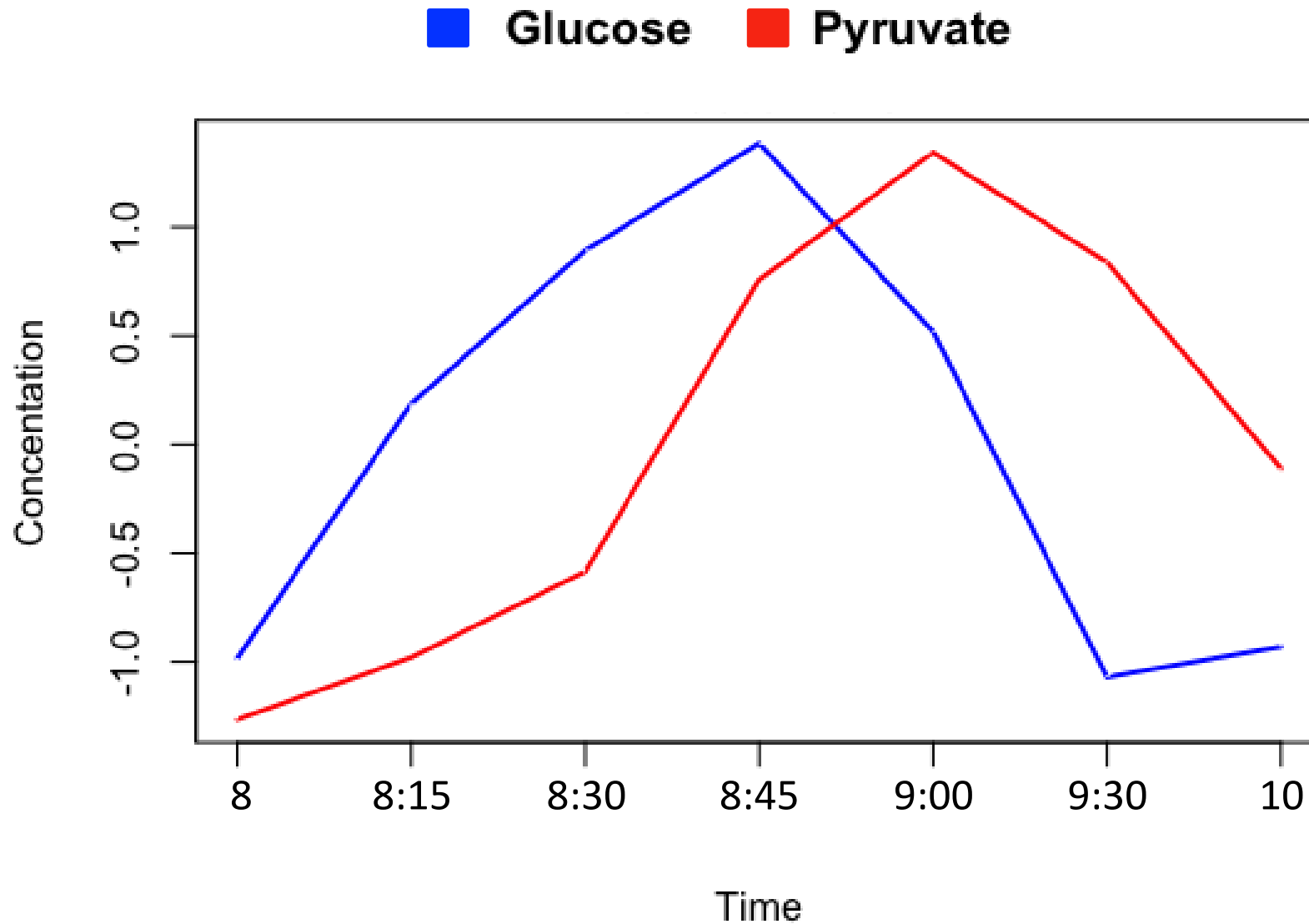
Major Contributors:

- Epidemiology
- Pharmacometabolomics
- Oncology (cancer)
- Lung and Cardiovascular



Time-Series metabolomics

The Fundamental Issue



Correlation: 0.26

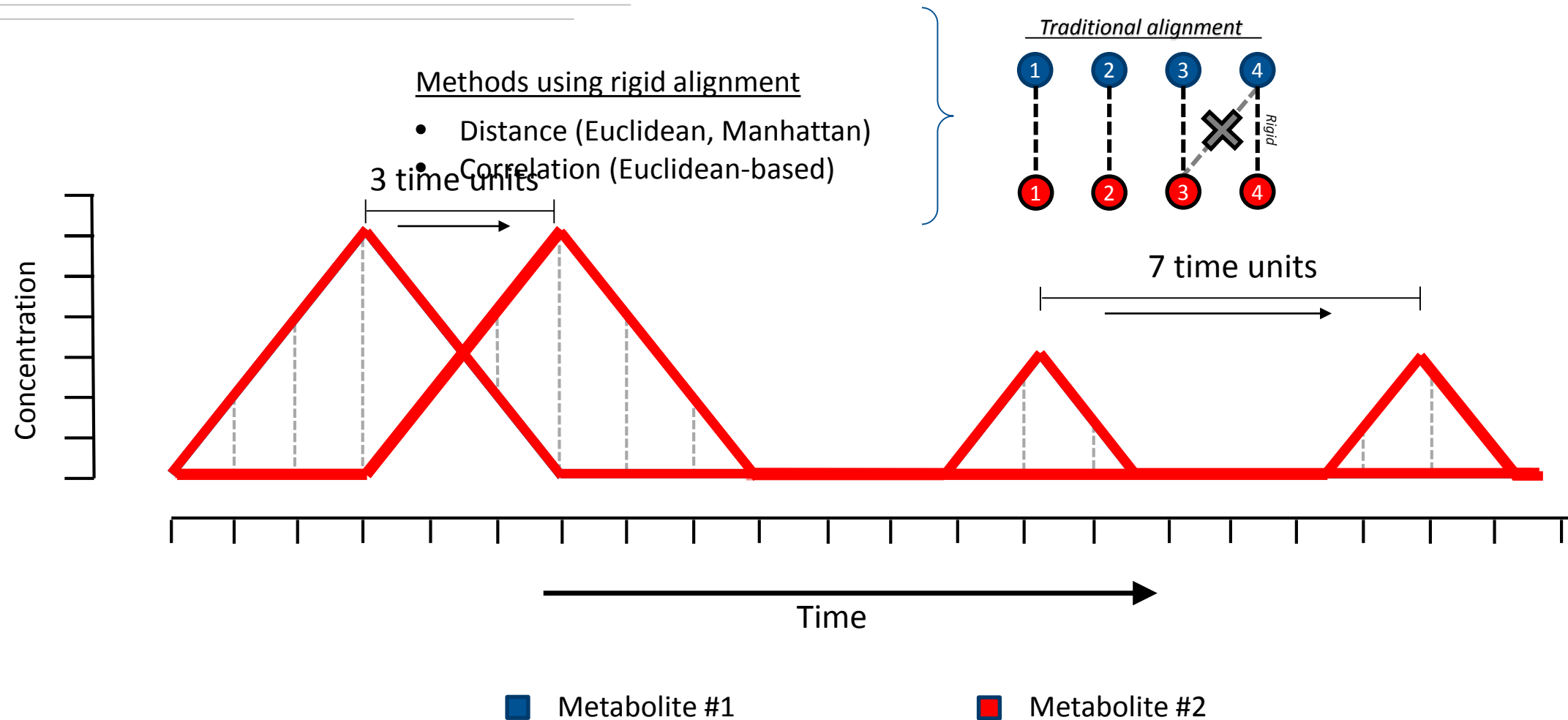
Primary Question

How do we identify latent trend line shape similarities?

By first understanding the fundamentals

Key Points:

- Non-uniform lag
- Traditional distance measures rely on rigid pairwise alignment



Key Points:

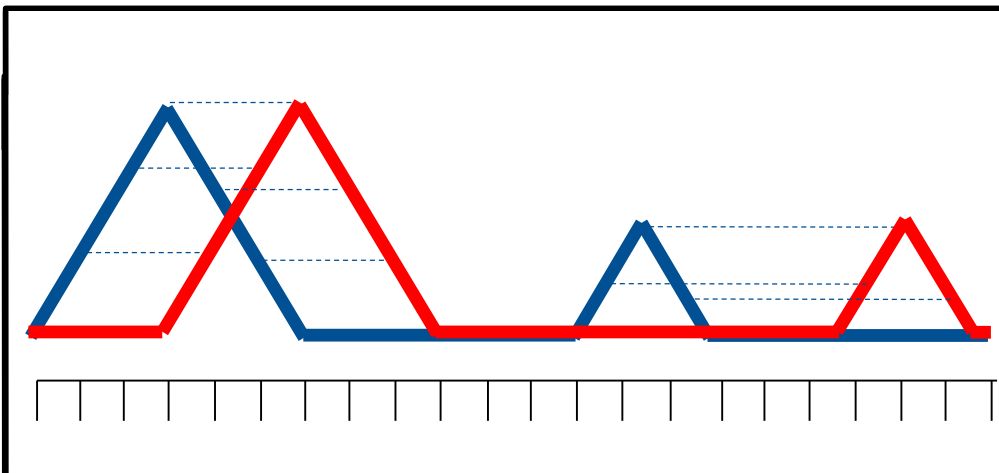
- Non-uniform lag
- Traditional distance measures rely on rigid pairwise alignment

What is Dynamic Time Warping?

- DTW identifies the alignment producing the lowest distance value
- Global and local alignment

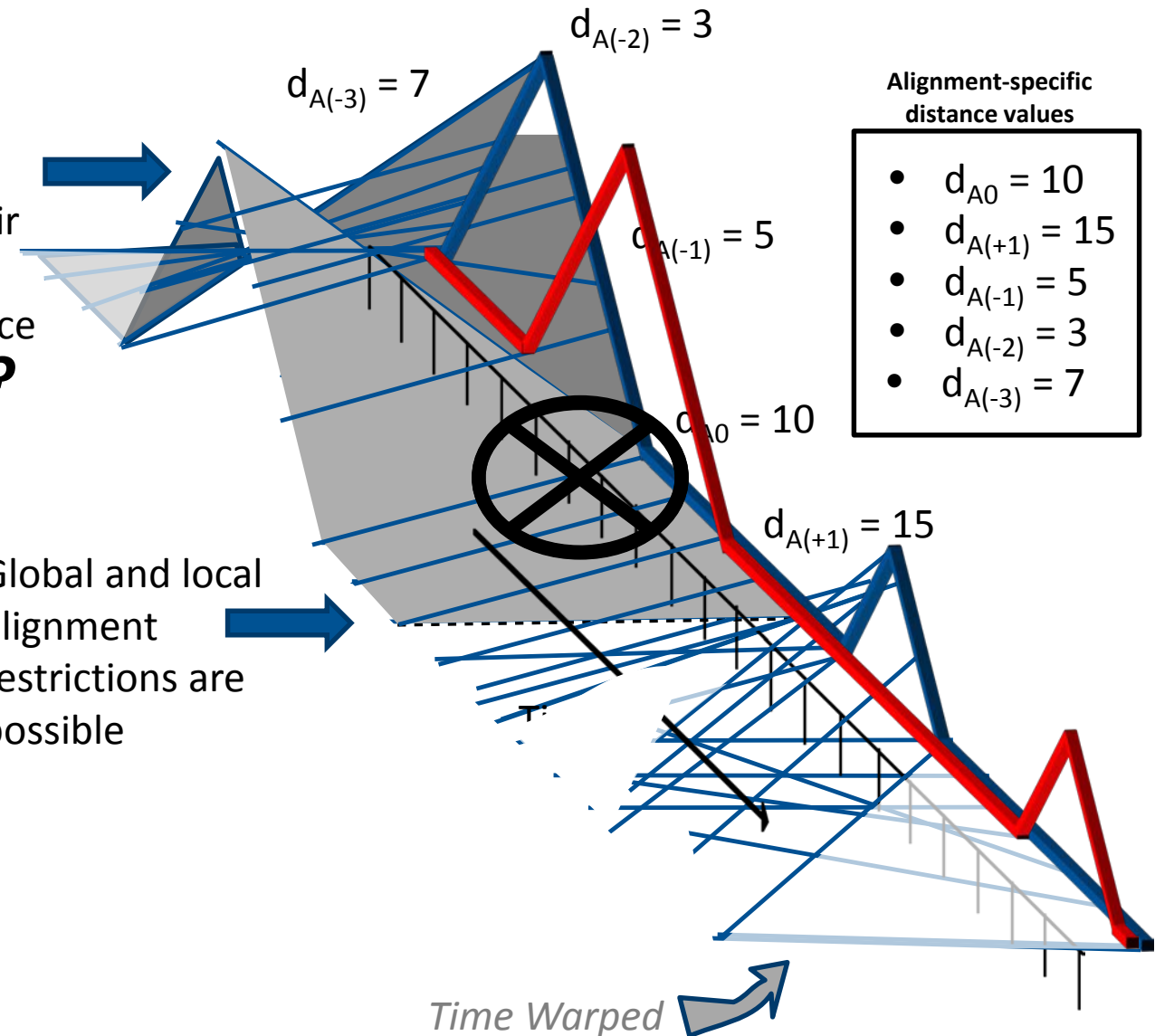
What is Dynamic Time Warping (DTW)?

- Time warp: repeating specific observations on metabolite X until metabolite Y is fitted.



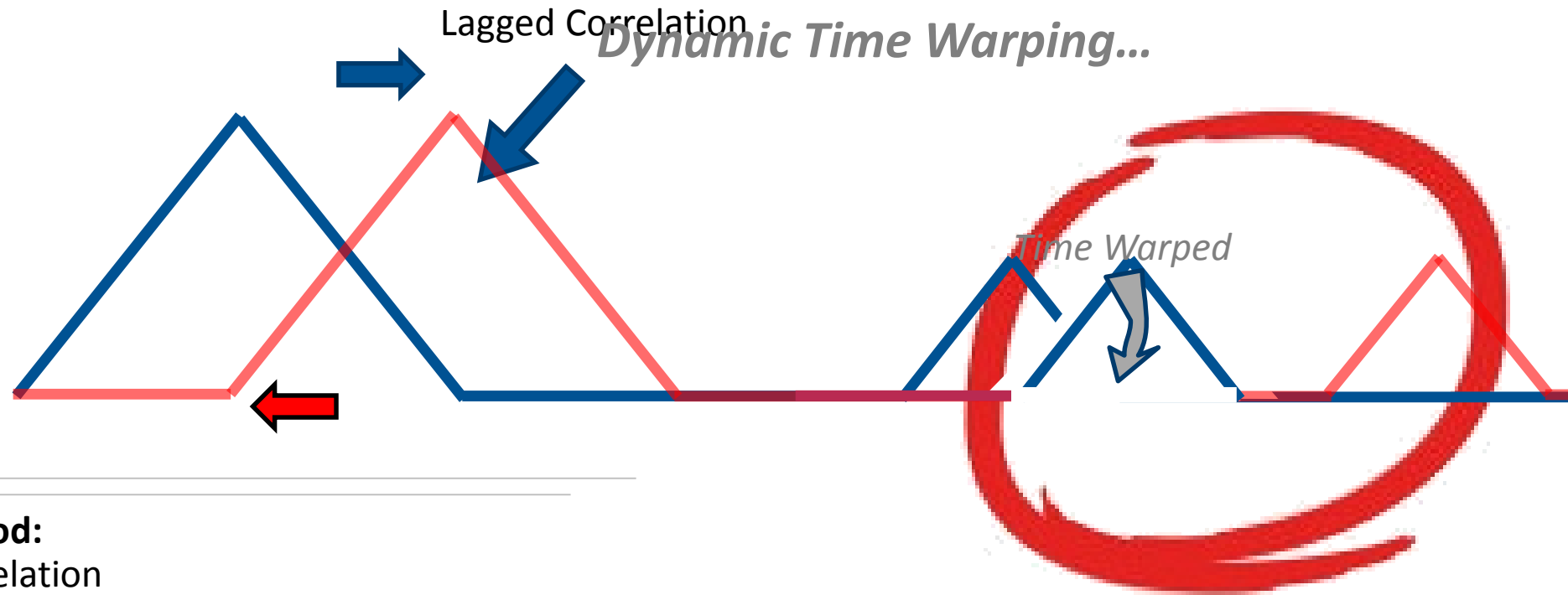
- Identifies the alignment pair producing lowest distance value

- Global and local alignment restrictions are possible



Time-Series Metabolomics Data

- Metabolite #1
- Metabolite #2

**Similar Method:**

- Cross-correlation
 - Uniform shift of variable
 - Non-equidistant alignment similarities are missed

Does not handle irregularity of time series, but lagged correlation does. The optimal alignment distribution linear fashion to align with the nearest pairwise point are often missed

Quick Summary

What is Dynamic Time Warping?

- DTW identifies the alignment producing the lowest distance value

Don't similar methods exist?

- Cross-correlation
 - Uniform shift of alignment

Why would we need Dynamic Time Warping ?

- Non-uniform shifts in alignment allows us to identify correlations not seen in traditional statistics.

So, does it work?

HuMet Study

Oral Glucose Tolerance Test

Data origin: HuMet Study

Method: GC/MS; LC/MS; NMR

Type of samples: Plasma

Measurements by: Metabolon Inc.

of subjects:

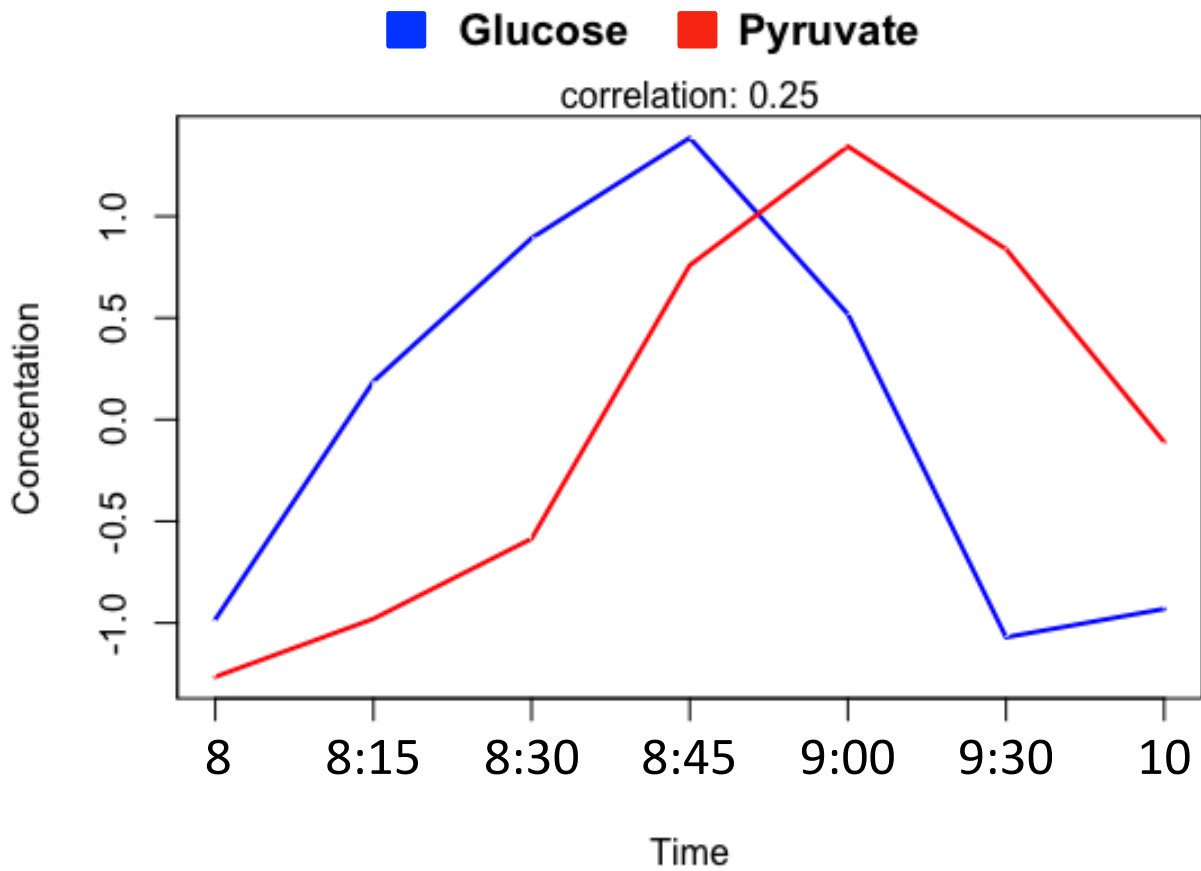
- 15 young men selected to be as homogenous as possible

of variables: 1000+

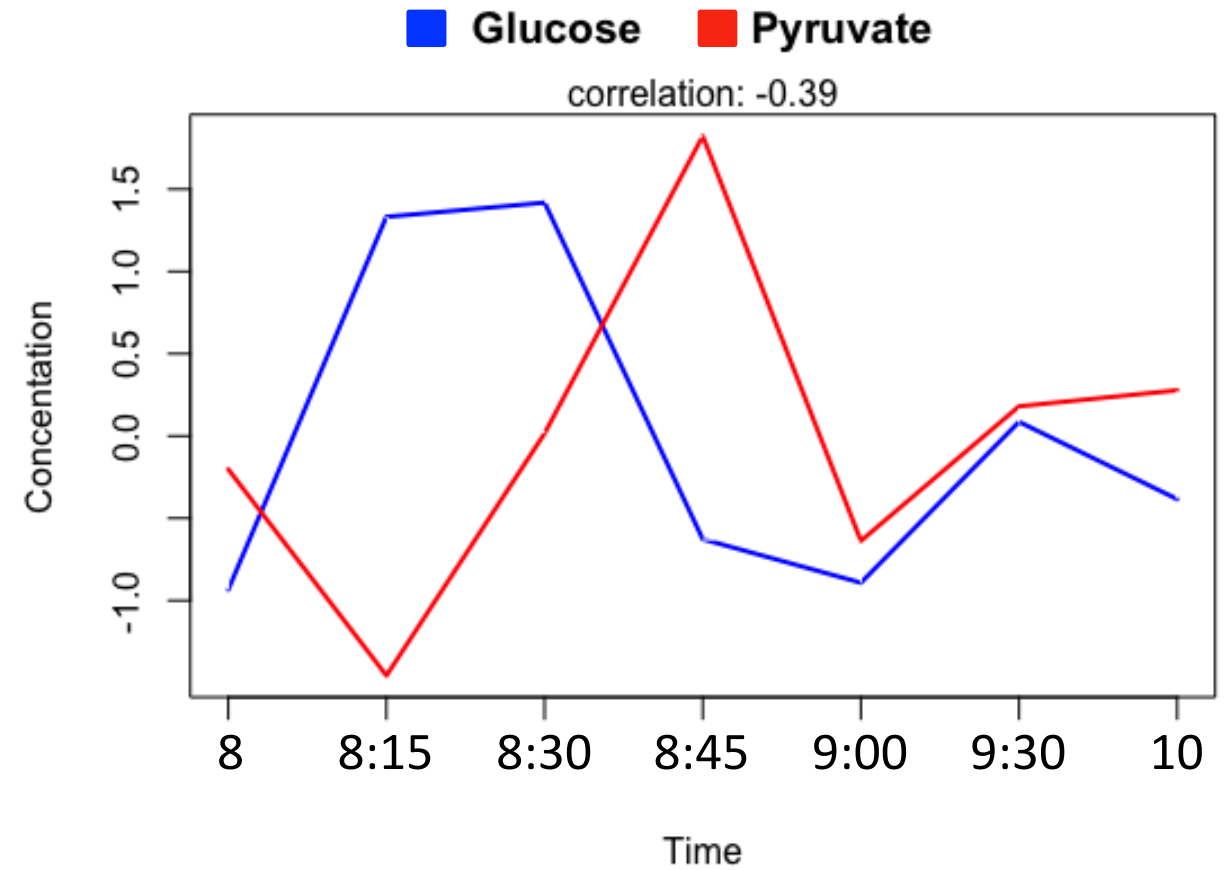
- Amino Acids
- Carbohydrates
- Energy

Time:

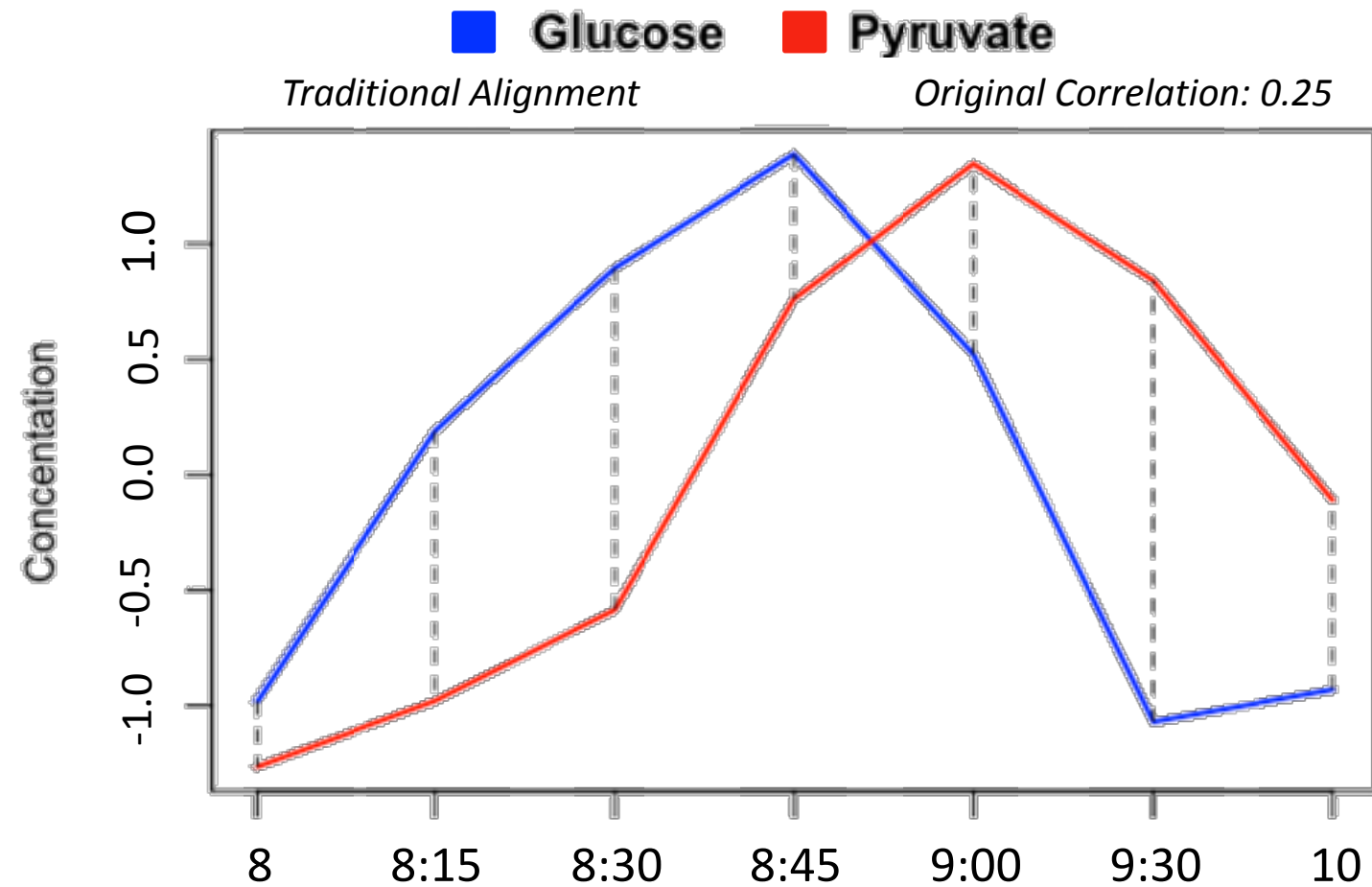




Subject 1



Subject 2



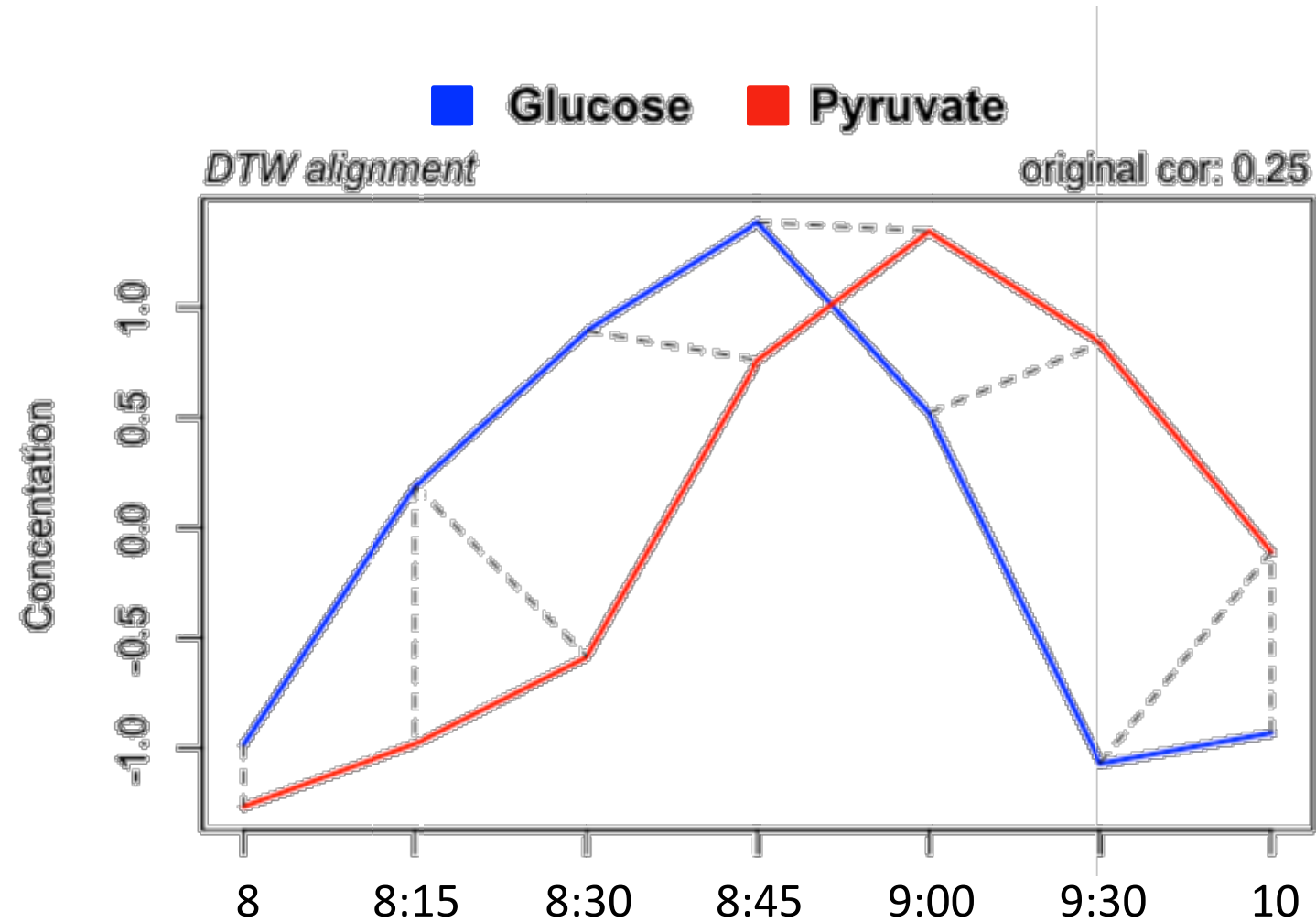
Example: Euclidean Distance

Metabolite 1

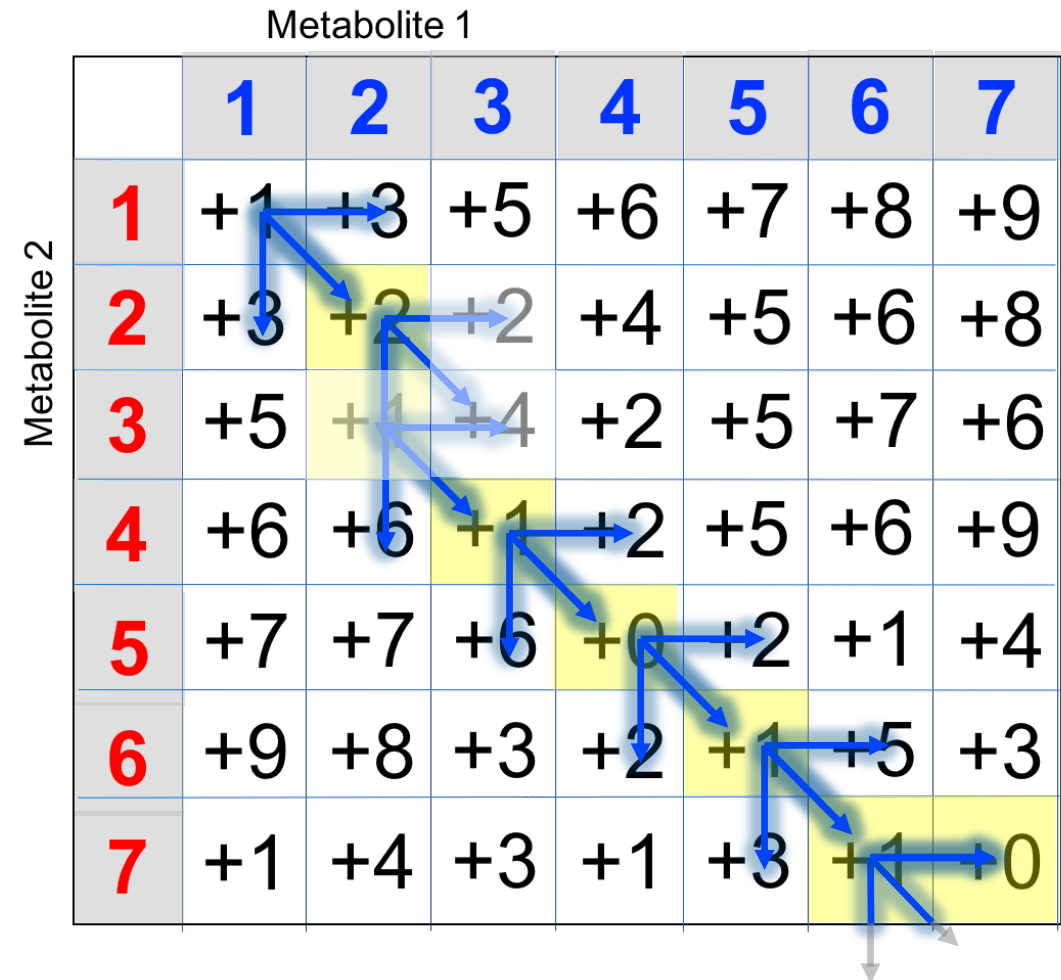
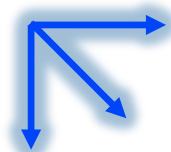
	1	2	3	4	5	6	7
1	+1	+3	+5	+6	+7	+8	+9
2	+3	+2	+2	+4	+5	+6	+8
3	+5	+1	+4	+2	+5	+7	+6
4	+6	+6	+1	+2	+5	+6	+9
5	+7	+7	+6	+0	+2	+1	+4
6	+9	+8	+3	+2	+1	+5	+3
7	+1	+4	+3	+1	+3	+1	+0

Metabolite 2

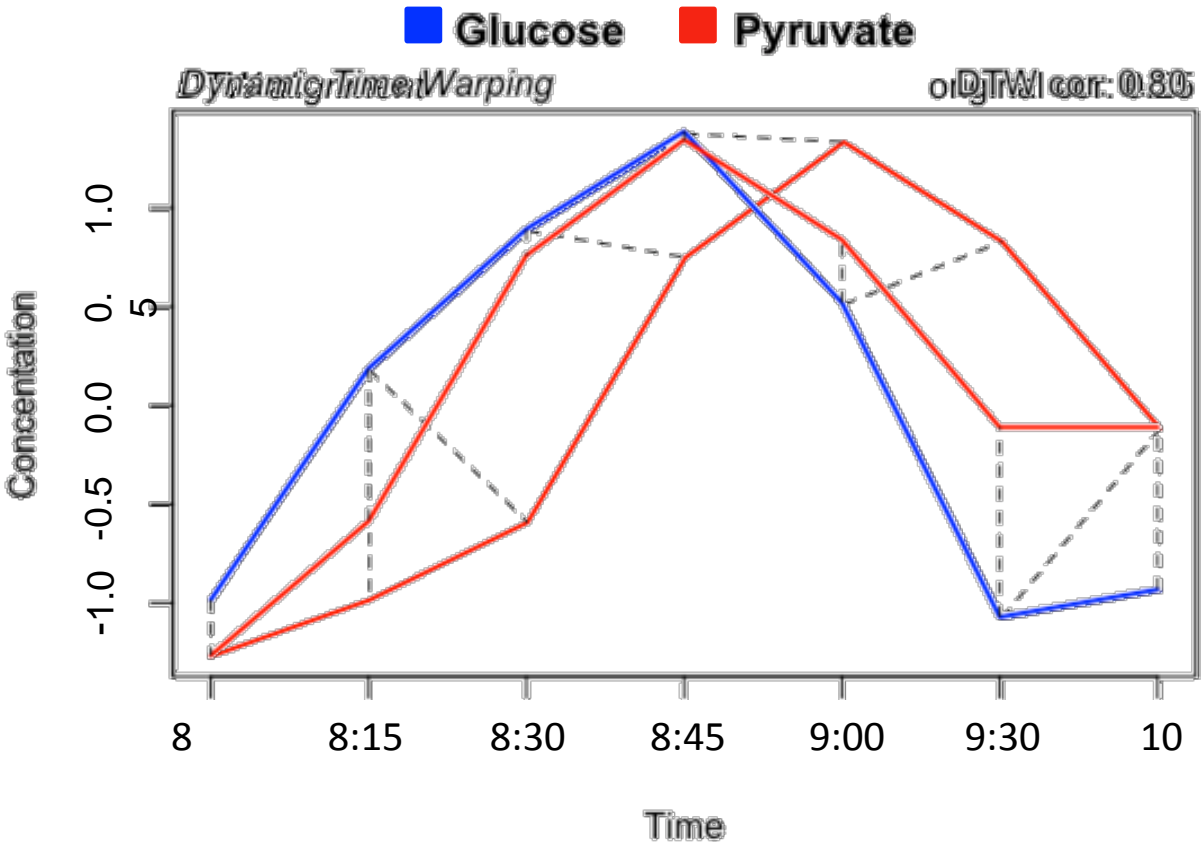
Traditional distance = 16



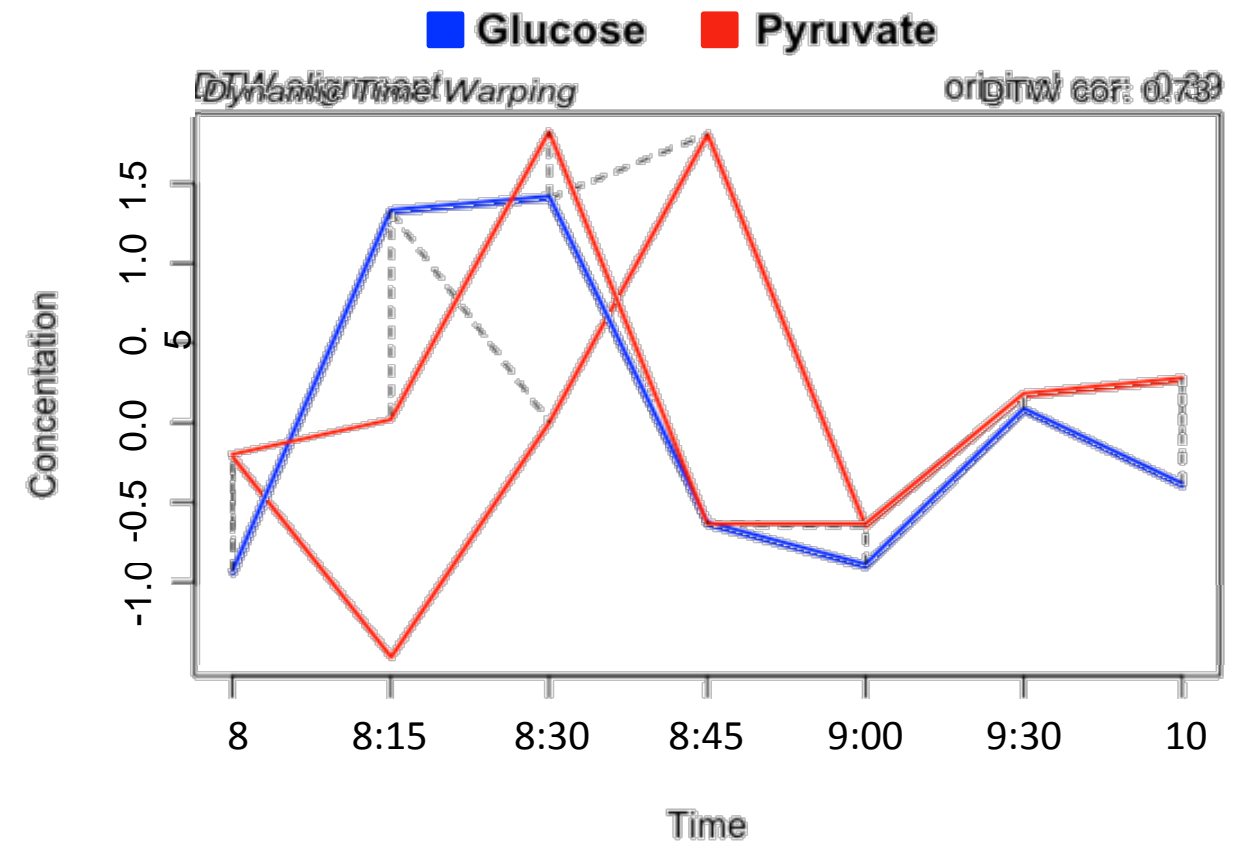
Example: Dynamic Time Warping



DTW distance = 7



Subject 1



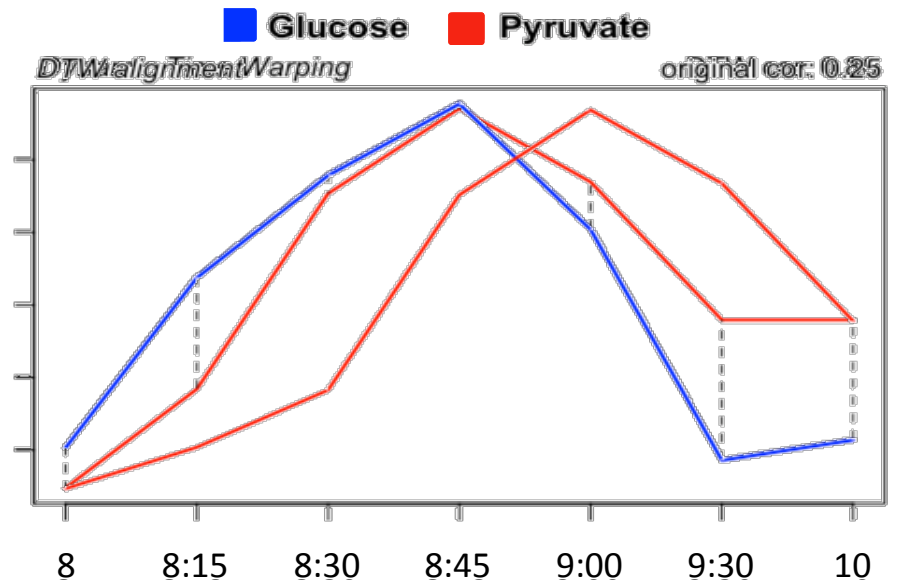
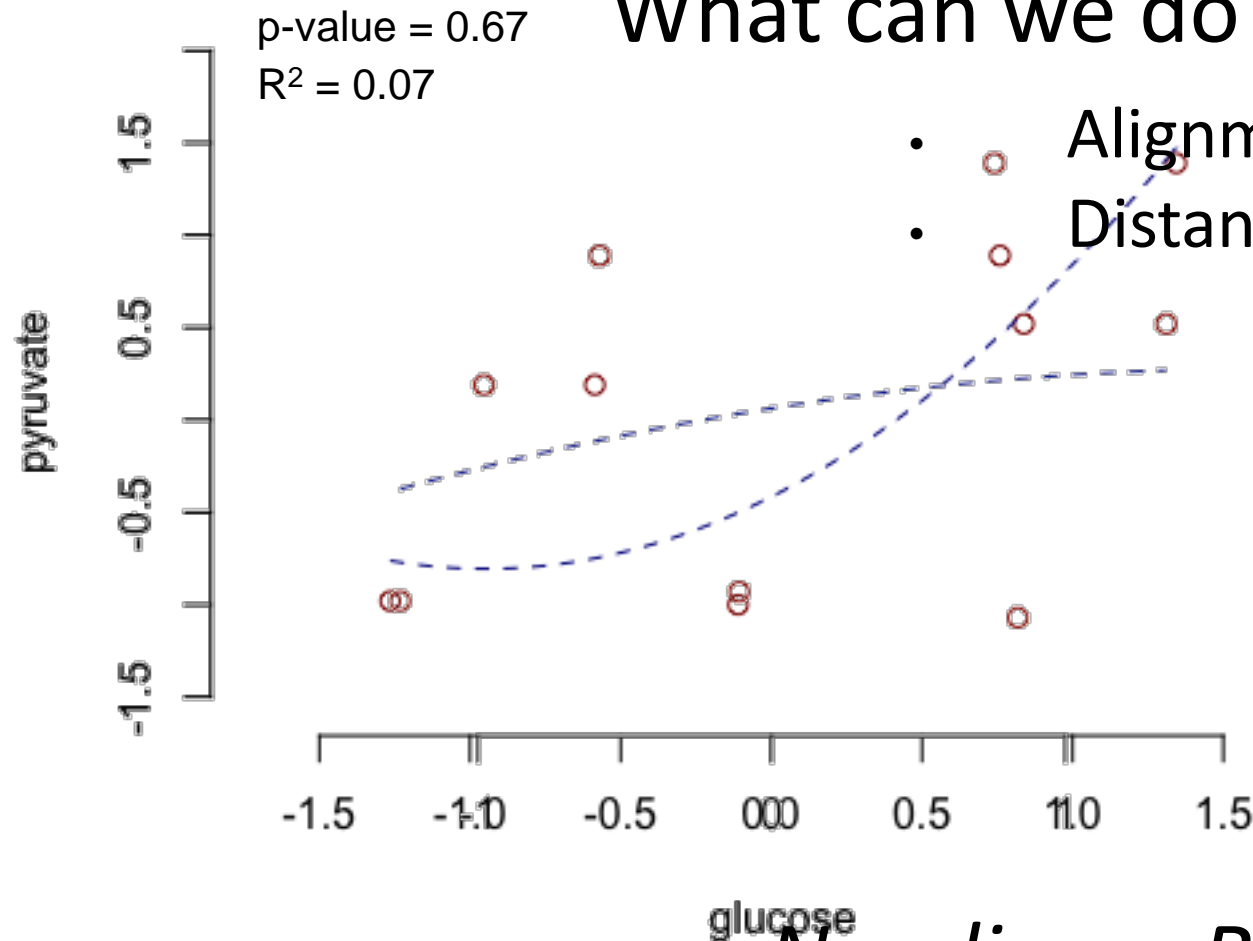
Subject 2

Non-linear Regression

~~Modified Alignment~~

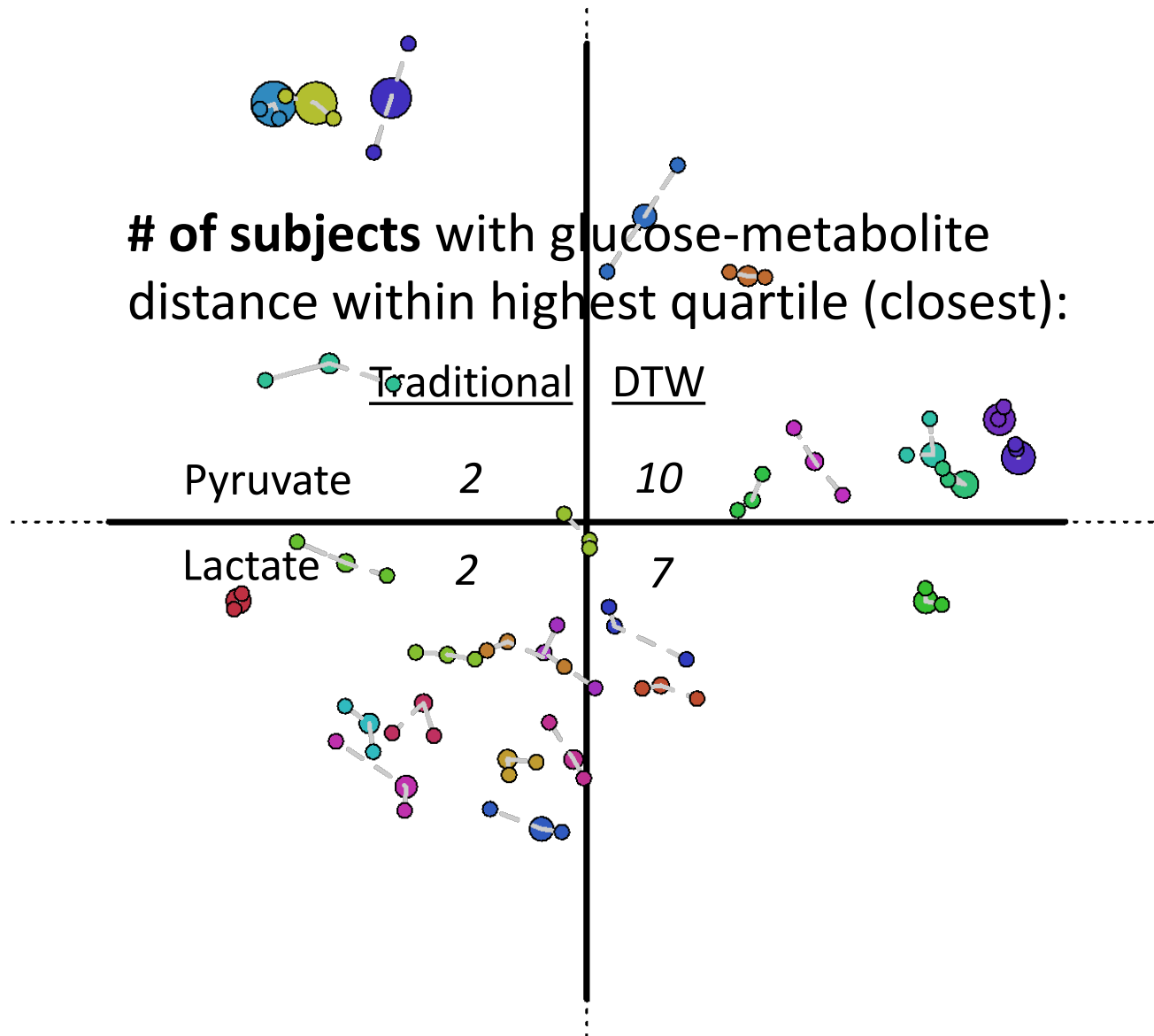
What can we do with our new

- Alignments
- Distance



Non-linear Regression

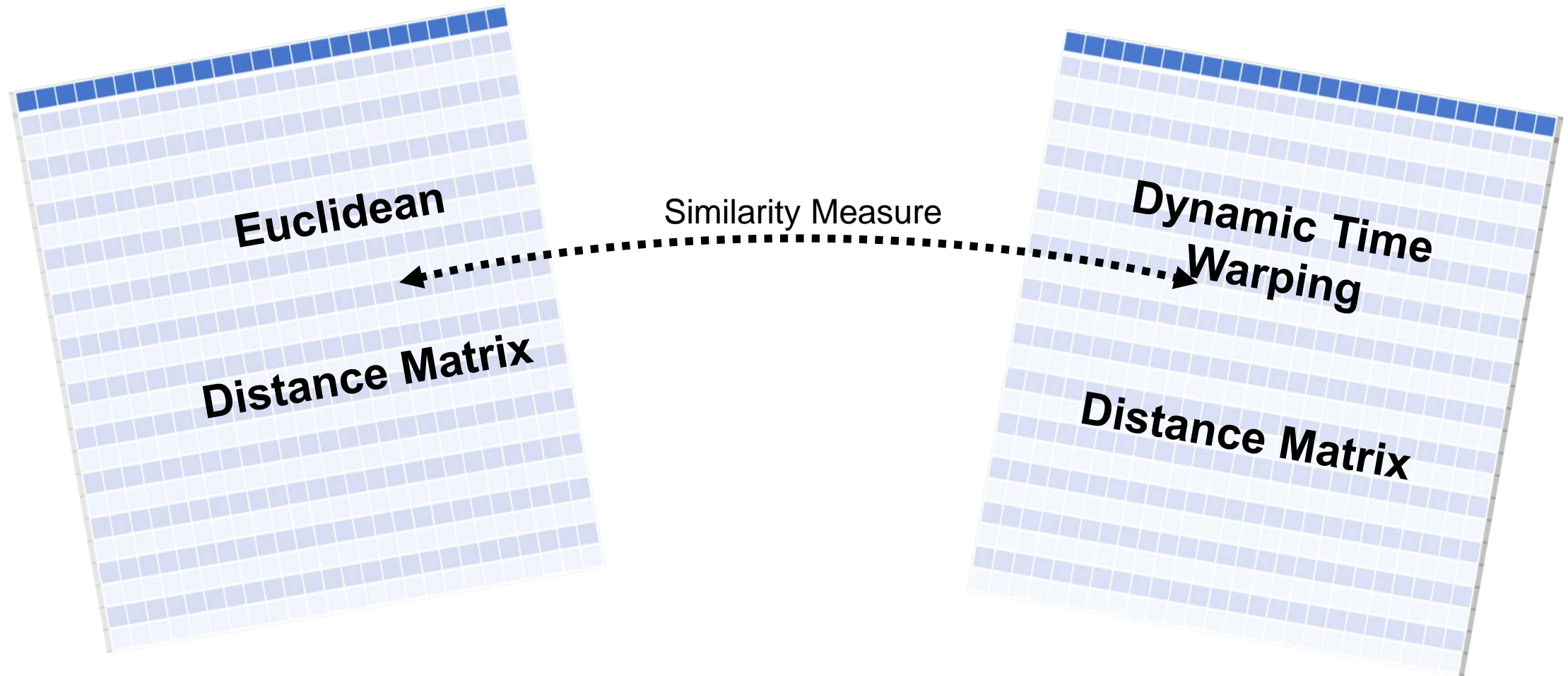
Feature Selection



Ranking of Average Subject Glucose-Metabolite Distance

Metabolite	Metabolite-Glucose Rank (DTW)	Metabolite-Glucose Rank (EUC)
N-acetyltryptophan	4	28
phenyllactate (PLA)	10	84
oxalate (ethanedioate)	17	58
indoleacetate	19	62
alpha-hydroxyisocaproate	23	91
pyruvate	24	74
indolepropionate	26	60
beta-hydroxyisovalerate	28	44
hypotaurine	31	77
3-hydroxyisobutyrate	33	71

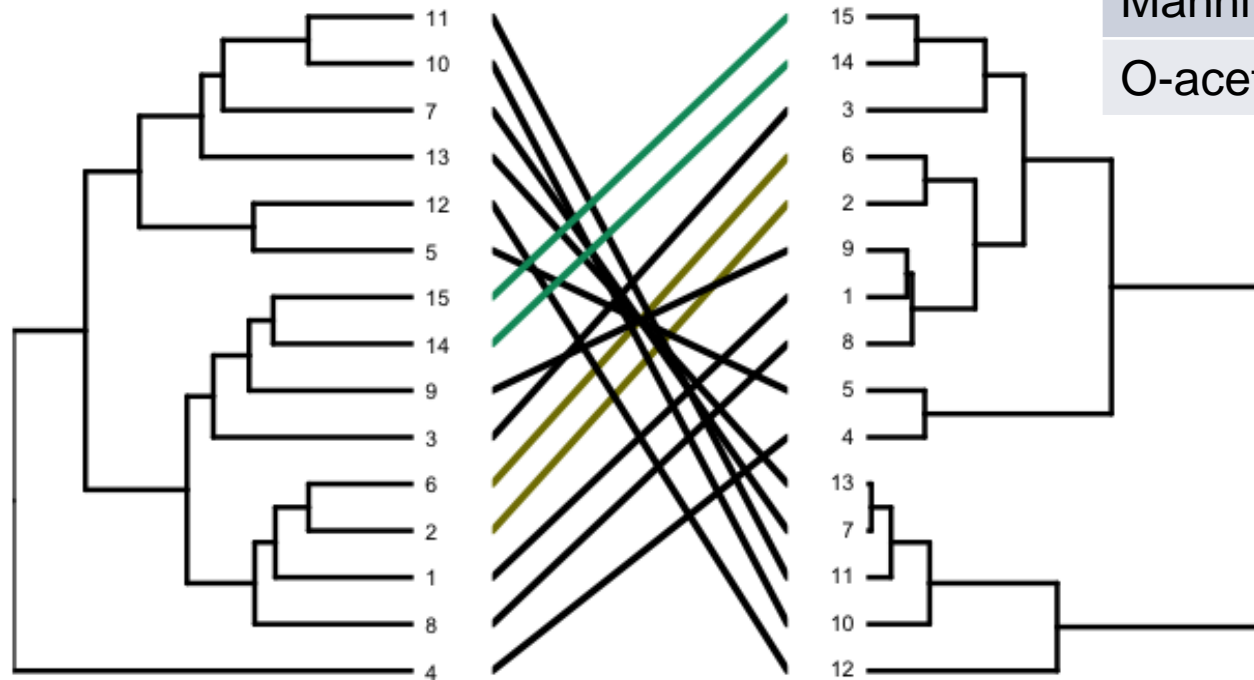
BCAA intermediate



Euclidean-DTW Correlation: 0.85

Subject Cluster compare

Glucose-Only Subject Clustering



Multivariate DTW vs. Glucose-only Subject Clustering Comparison

Metabolite1	Metabolite 2	Cophenetic Correlation
Mannitol	Kynurenate	0.69
O-acetylhomoserine	Kynurenate	0.62



Multivariate - Glucose DTW Clustering

A special thank you to:

- *Prof. Hannelore Daniel*
- *Dr. Jan Krumsiek*
- *Systems Medicine of Diabetes group (ICB-Helmholtz)*
- *Dr. Kurt Gedrich*
- *Dr. Pieter Giesbertz*
- *Alessio Ciurli*