Analyzing Nonlinear Variations in Thermal Performance Curves

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Joint work with

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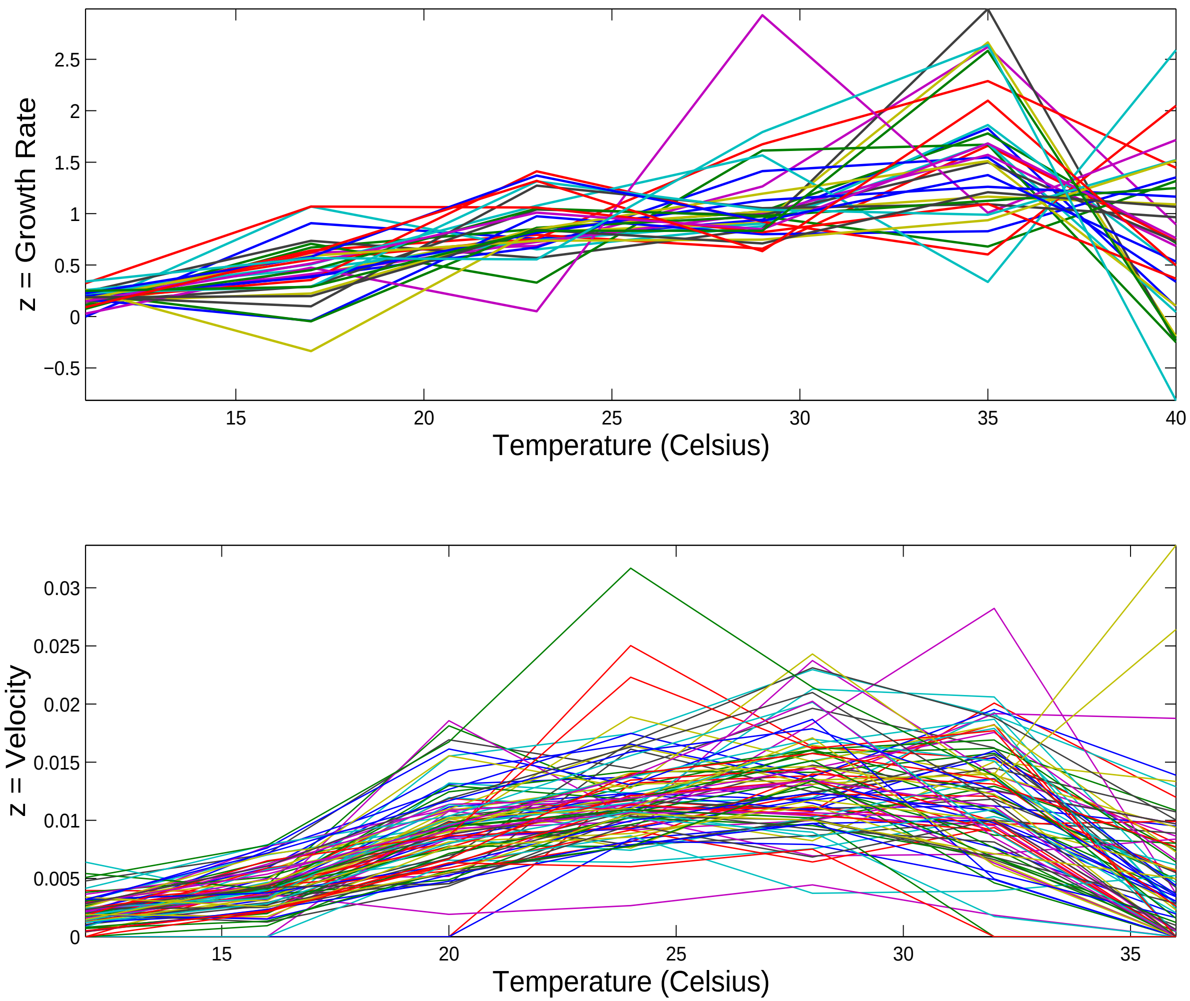
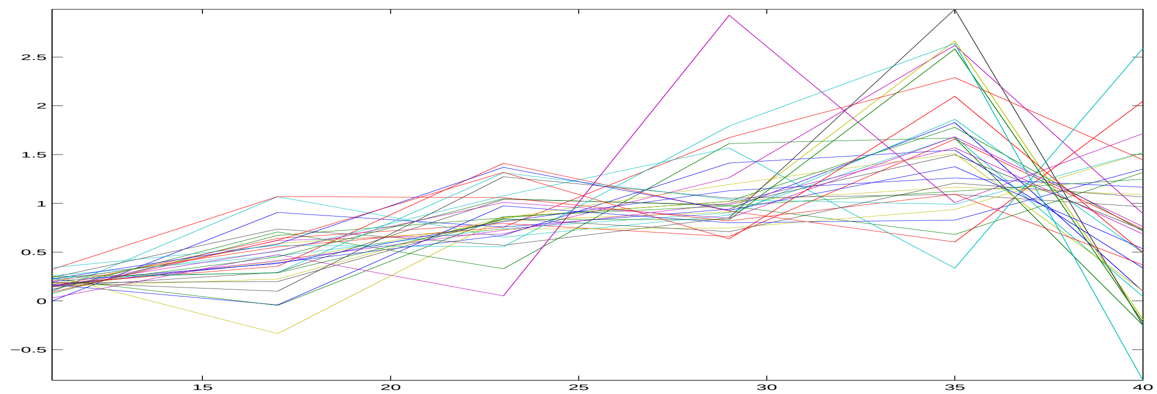

z = Growth Rate
Temperature (Celsius)
z = Velocity
Temperature (Celsius)

Outline

- Data
- Motivation and model
- Results

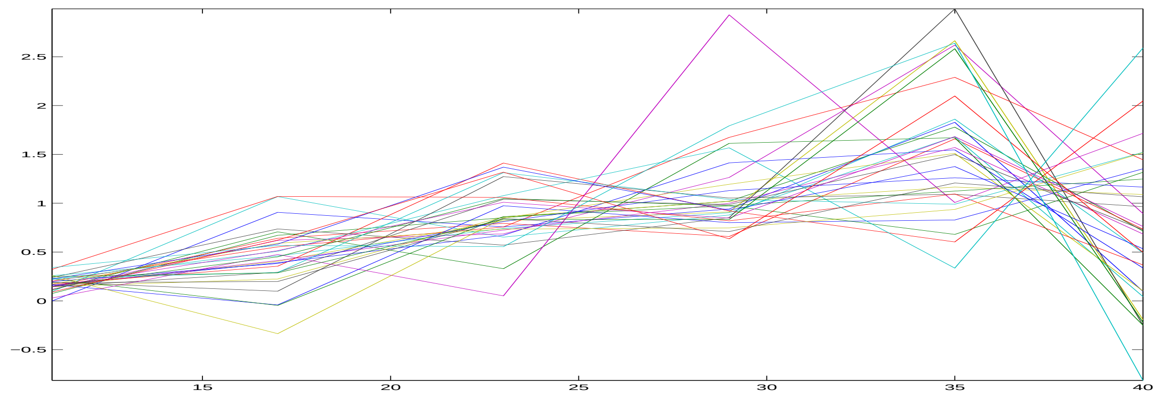
	Caterpillar	*Wasp*
Performance z	growth rate	velocity
Temperature t (Celsius)	$d = 6, t \in [11, 40]$	$d = 7, t \in [12, 36]$

- Thermal performance curve $(\mathbf{TPC})$: $z = f(t)$.
- Continuous Reaction norm: $z = f(e)$



TPC Feature(1): Curves' variation $\equiv$ Genetic variation

- Family = individuals of similar genotype.
  Ex: offsprings of same parents, clones,...
- Population = n families, Ex: $n = 32$ (cater.), $n = 87$ (wasp).



TPC Feature (2), Template shape $f(t)$:

- $\uparrow$, reaches a max and $\downarrow$.
- Rate of $\uparrow$ slower than rate of $\downarrow$.
- Tendency toward a unique max.

Outline

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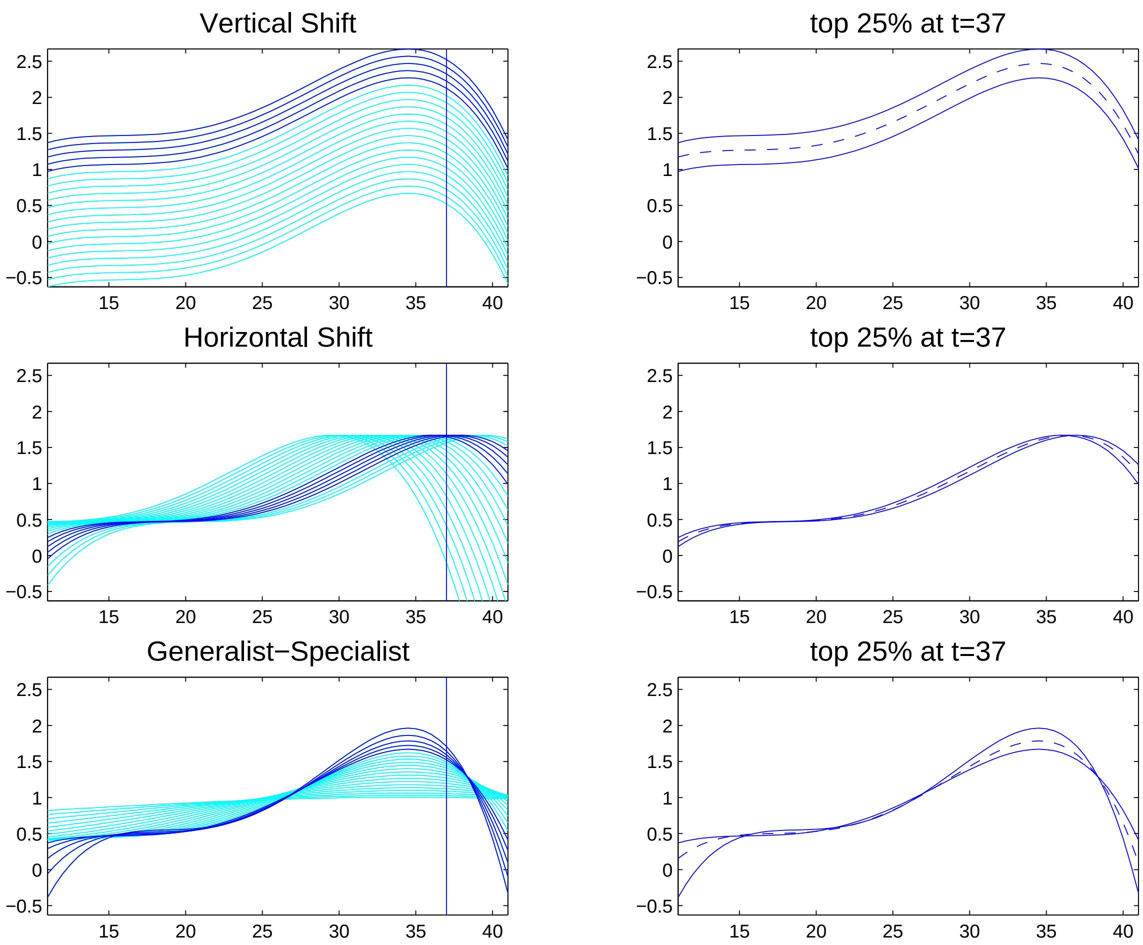
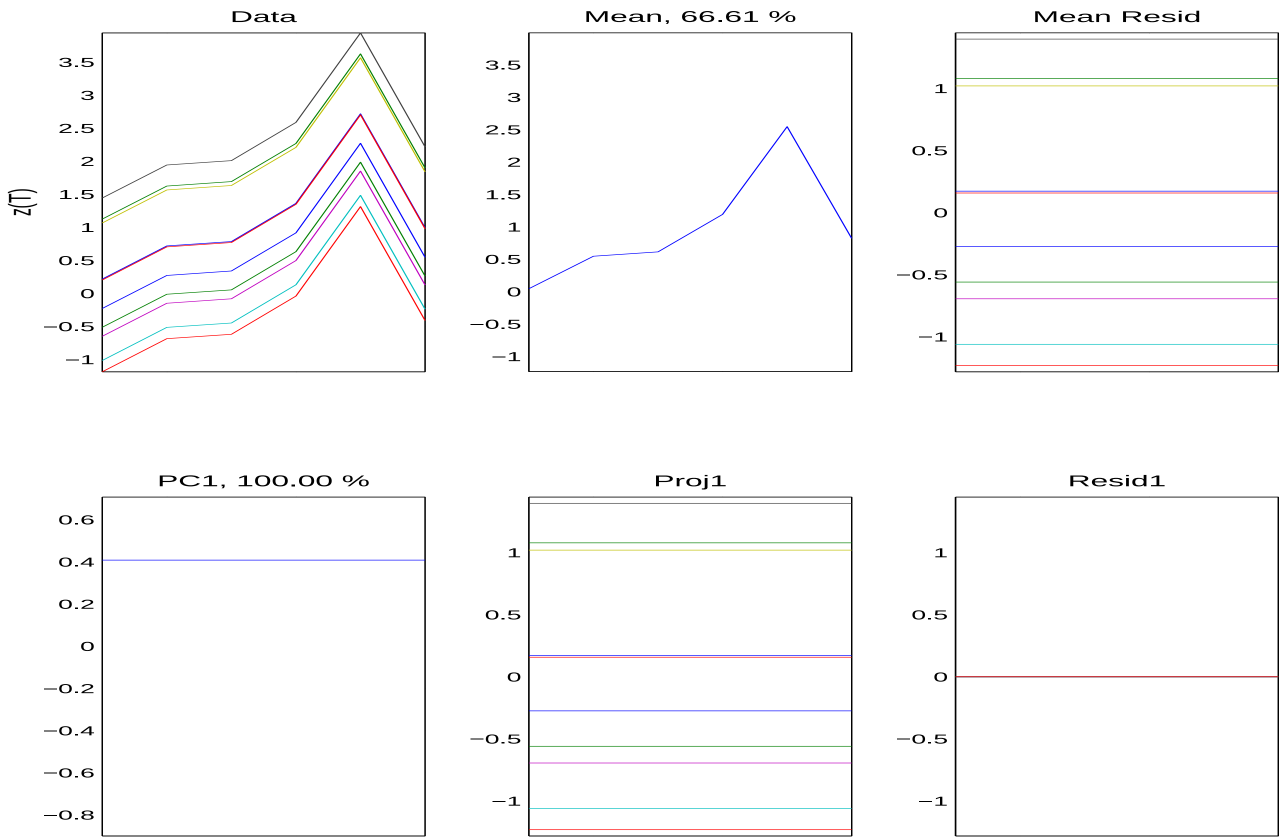
- Goal: Analyze three TPC modes of variation.
- Motivation: **evolution** of gen. variation under **selection**.
- Mode of variation $\equiv$ Constraint to evolution

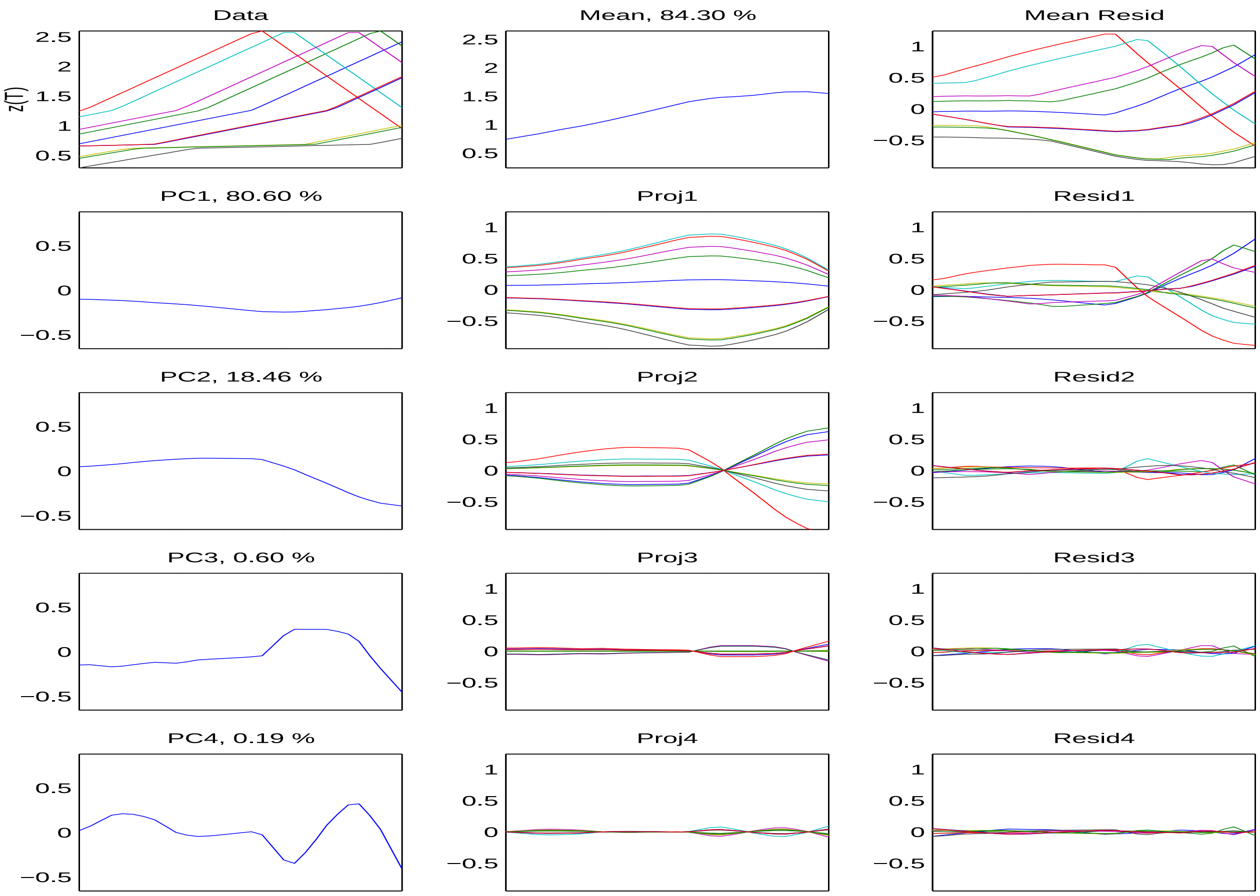


Mode of variation **before** selection – Genetic variation **after** selection

Vertical Shift, Linear mode of variation



Horizontal Shift, Nonlinear mode of variation



Classical PCA	Template Modes of Variations
No assumption on shape	Template shape of TPCs.
Linear PC of G	**Nonlinear** modes of variation of G.
Meaning of each PC?	Biological modes.

Model

$$
\begin{aligned}
Z_i(t_j) &= R_i(t_j) + \epsilon_{i,j}, 1 \leq i \leq n \text{ and } 1 \leq j \leq d. \\
R_i(t) &= w_i f\left(w_i(t - m_i)\right) + h_i
\end{aligned}
$$

	Parameter	Variation
Vertical shift	h_i	linear
Horizontal shift	m_i	nonlinear
Gen-Spec	w_i	nonlinear

Quantification of nonlinear mode (glimpse)

Classical PCA	Template Modes of Variations
Center of variation : $\bar{Z}$	Center of variation: Template shape
RSS quantify a linear PC	$\widetilde{RSS}$ quantify a nonlinear mode.

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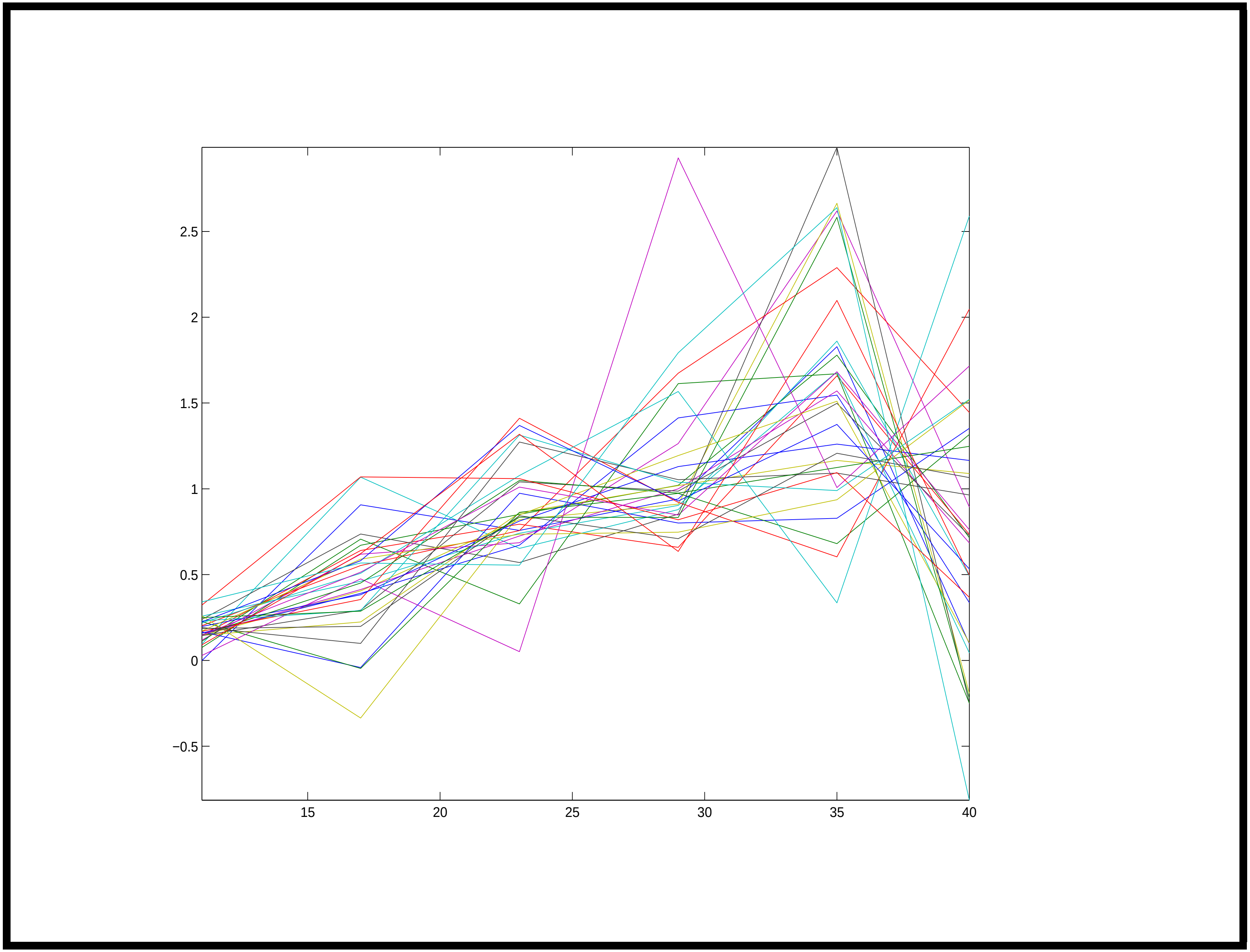
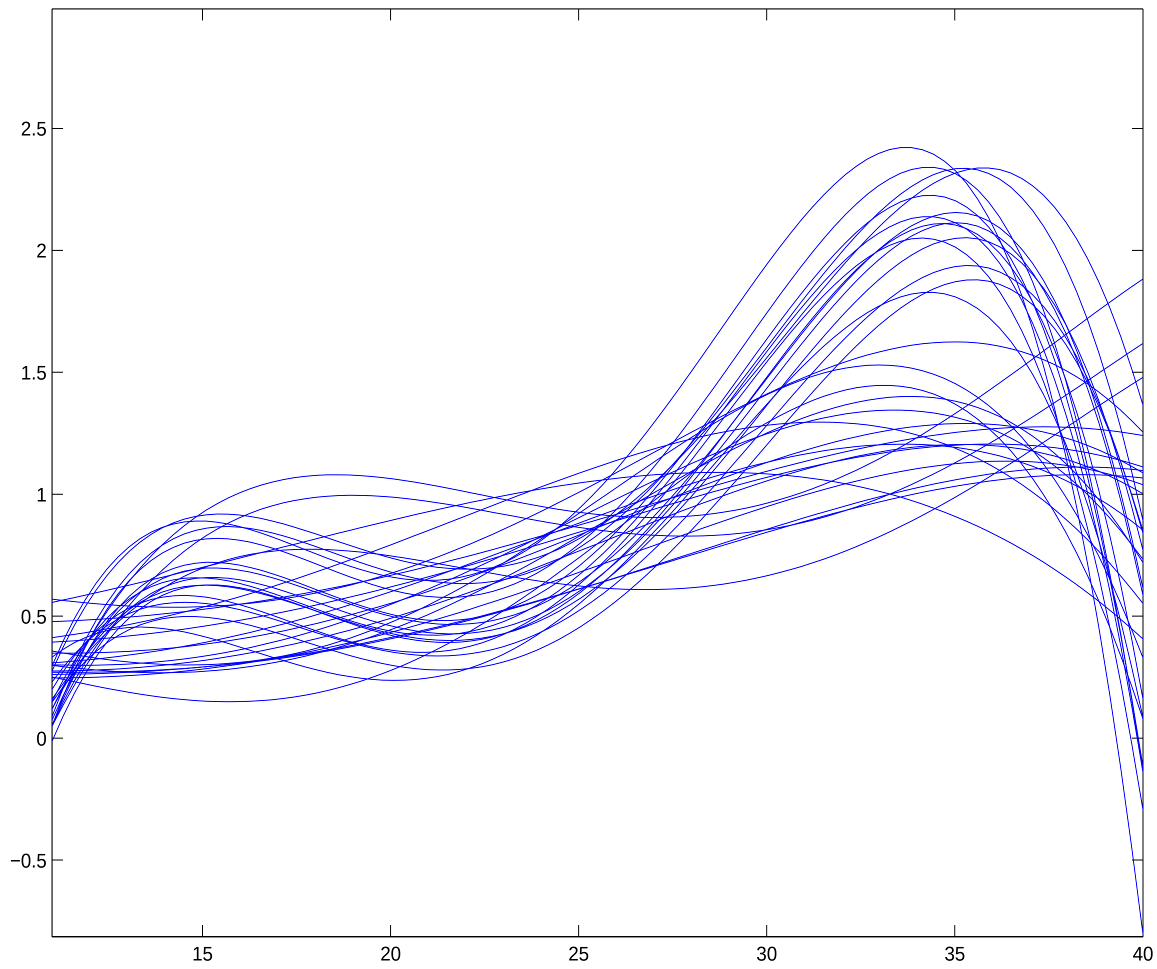

2.5
2
1.5
1
0.5
0
−0.5
15
20
25
30
35
40


2.5
2
1.5
1
0.5
0
−0.5
15
20
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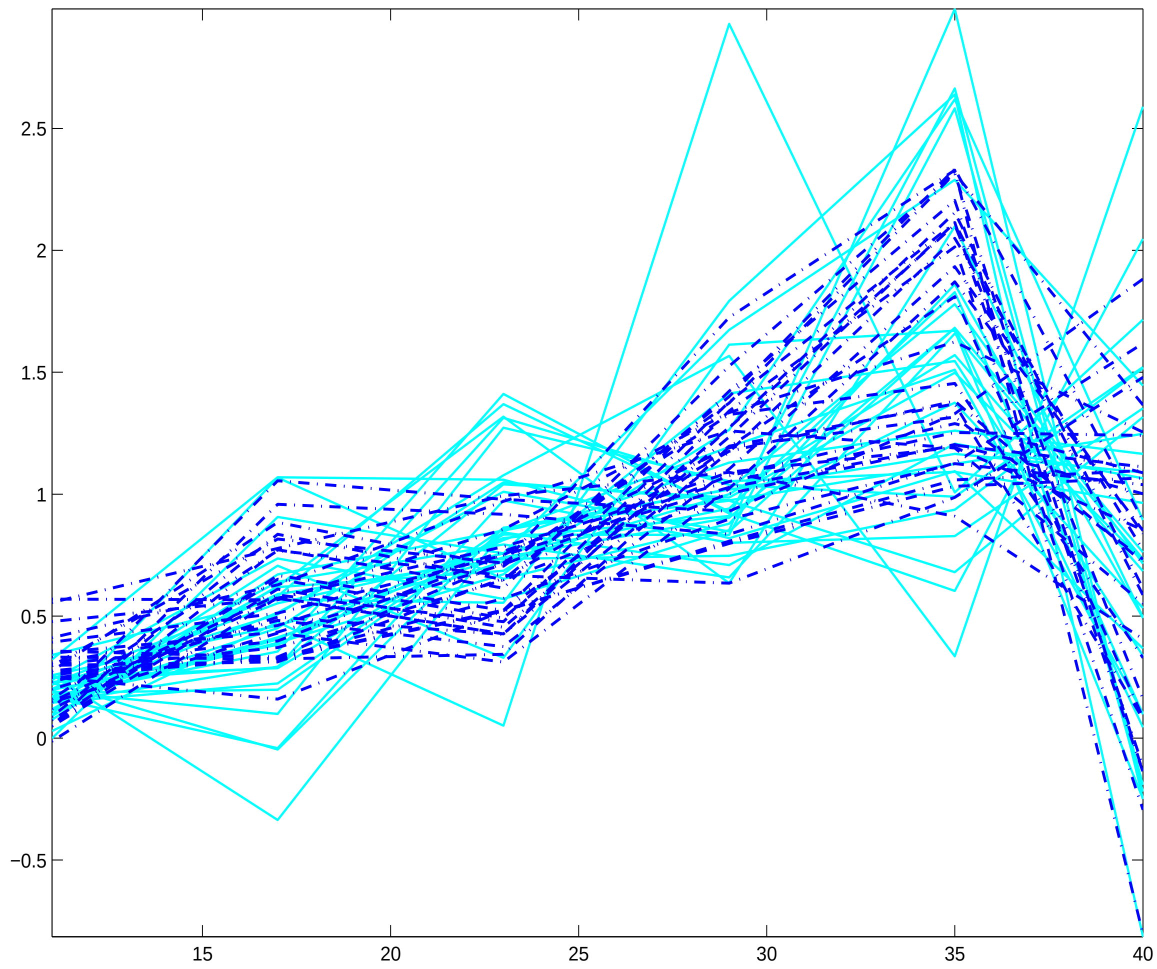
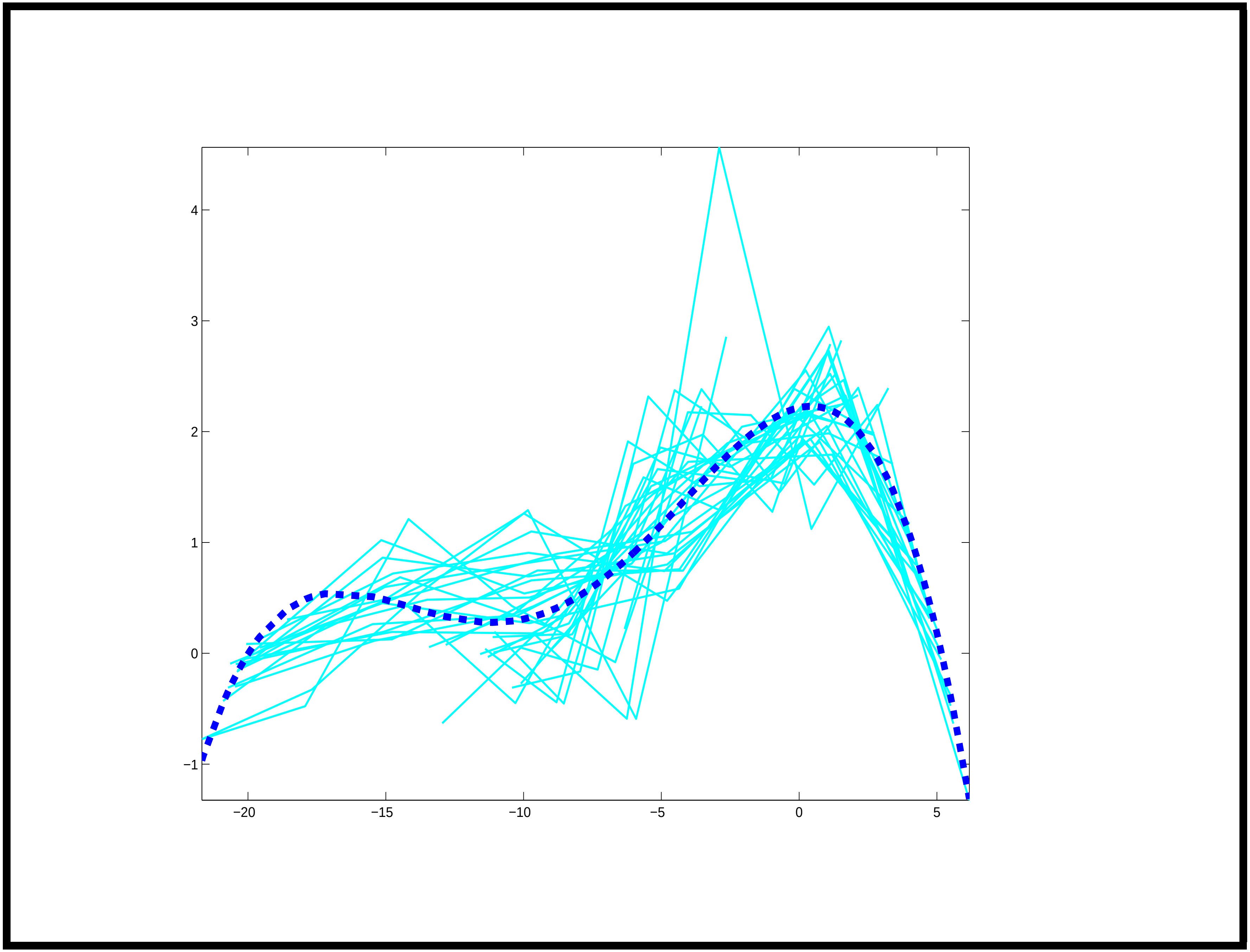
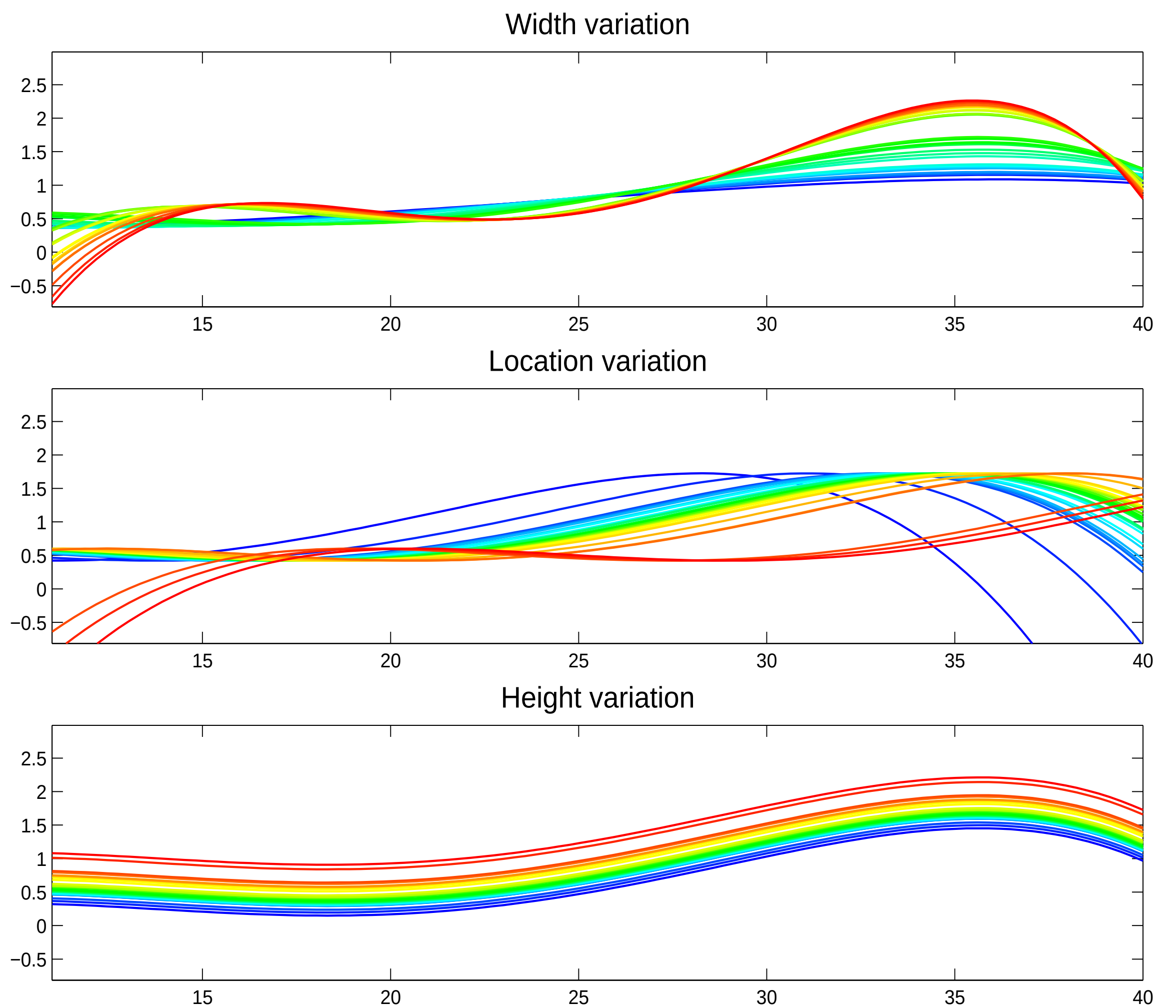
30
35
40

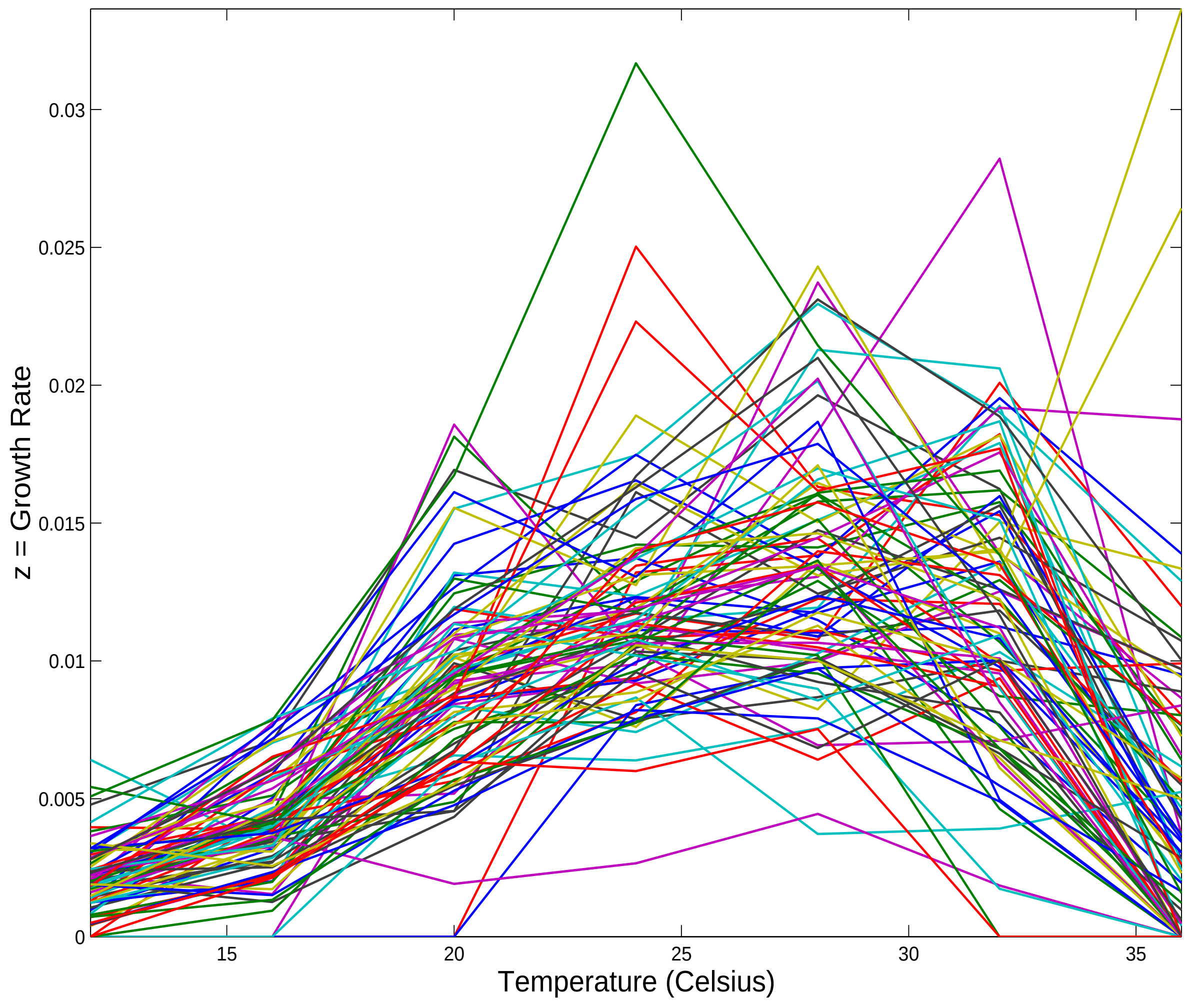

2.5
2
1.5
1
0.5
0
−0.5
15
20
25
30
35
40

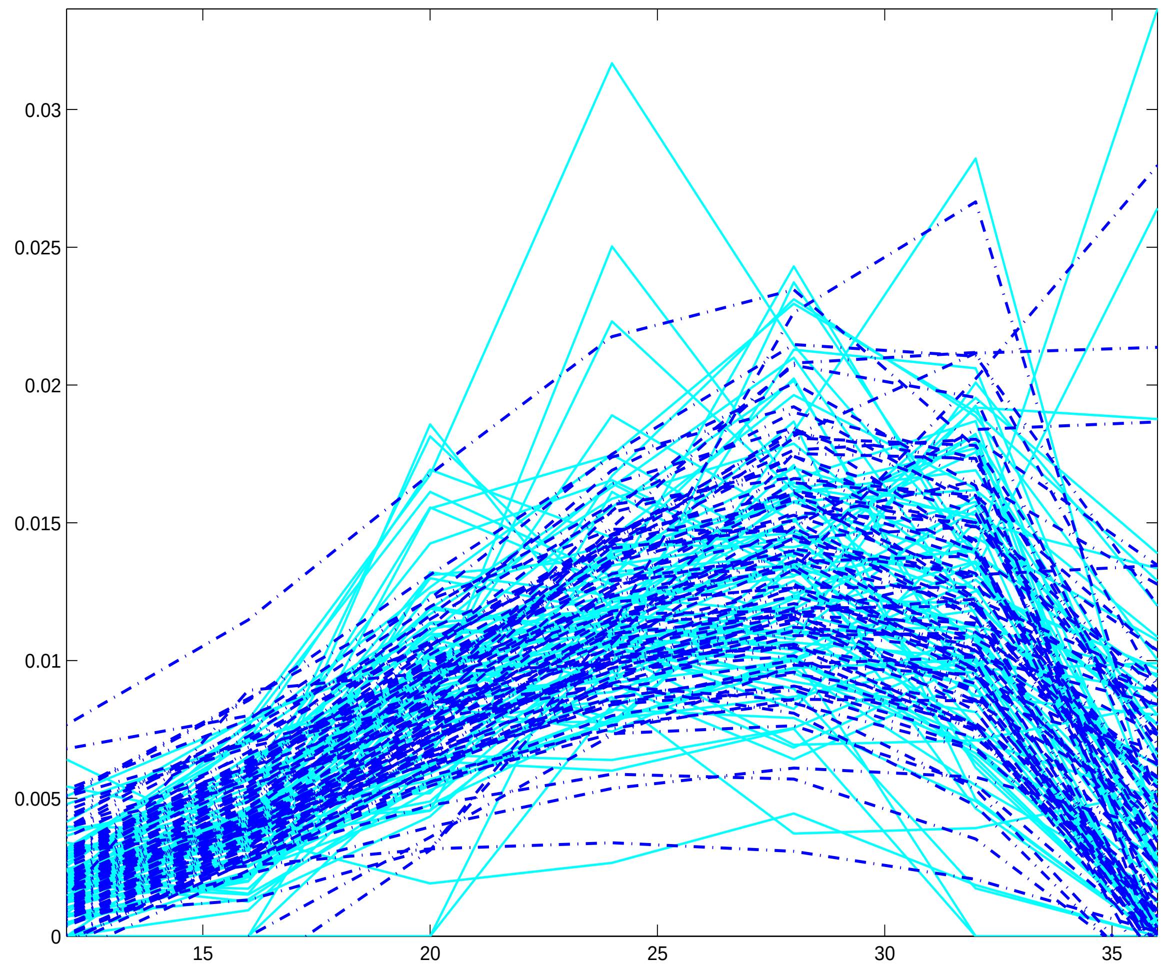


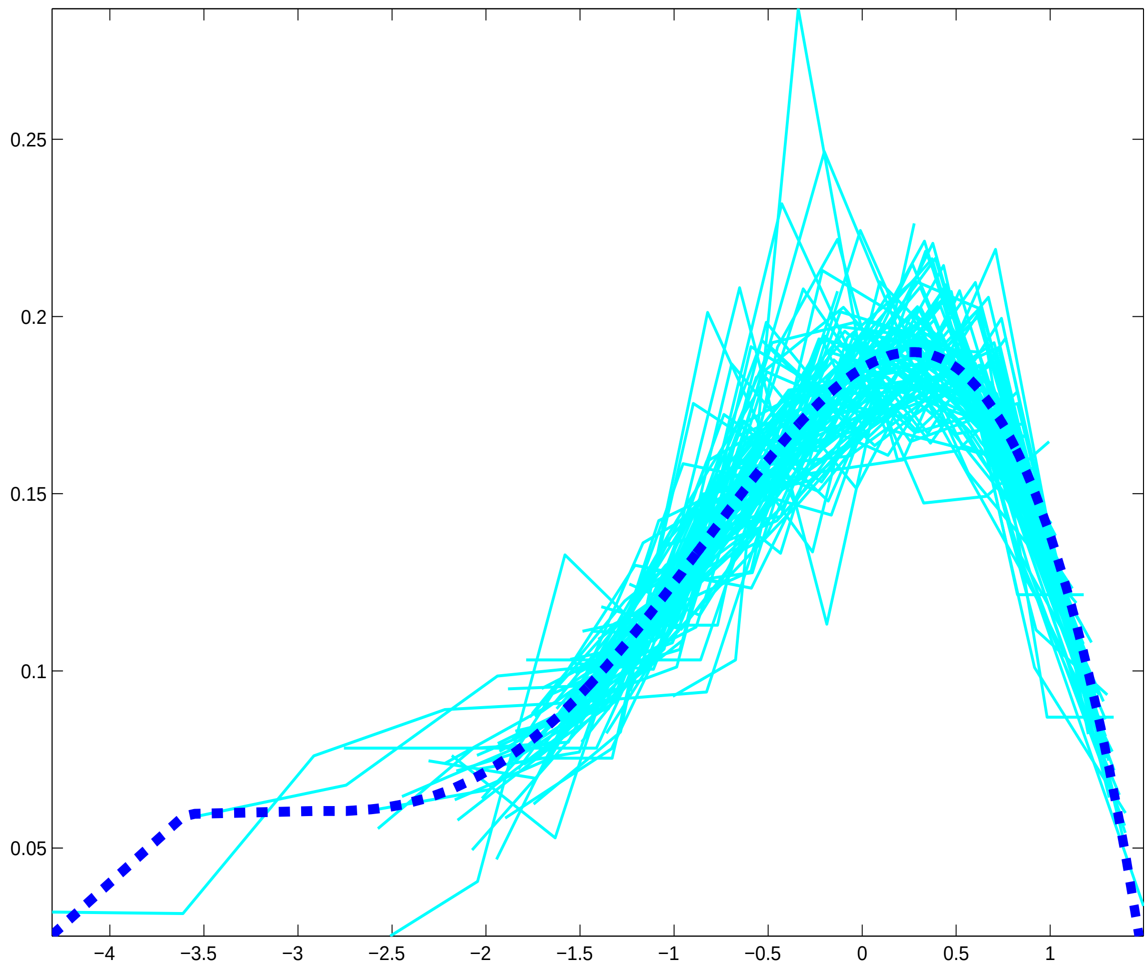
4
3
2
1
0
−1
−20
−15
−10
−5
0
5


Width variation
Location variation
Height variation
2.5
2
1.5
1
0.5
0
−0.5
15
20
25
30
35
40

Mode of variation	$\widetilde{RSS}$(Caterpillar)
Generalist Specialist	43.40%
Horizontal Shift	20.85%
Vertical Shift	7.36%
Horiz-Gen.Spec	3.78%
Model total	75.28%
Error	24.72%


0.03
0.025
0.02
0.015
0.01
0.005
0
15
20
25
30
35
z = Growth Rate
Temperature (Celsius)


0.03
0.025
0.02
0.015
0.01
0.005
0
15
20
25
30
35



0.25
0.2
0.15
0.1
0.05
−4
−3.5
−3
−2.5
−2
−1.5
−1
−0.5
0
0.5
1

Mode of variation	$\widetilde{RSS}$(Wasp)
Generalist Specialist	30.31%
Horizontal Shift	35.50%
Vertical Shift	15.84%
Horiz-Gen.Spec	3.99%
Model total	86.64%
Error	13.36 %

Conclusion for Evolutionary Biology: Selecting individuals with highest performance in a range of temperature will not result in the next generation in a population with highest performance over all ranges of temperatures.

Assuming a common shape of curves, the Template Modes of Variation allows to decompose curves' variance into linear and nonlinear modes and to quantify each mode. Linear modes are a particular case of this method of decomposition.

Current work

- Contribution of VS in total variation.
- Clustering.
- In stat, for $d' \geq 2$.
  - Convergence of the estimates from the data to true "center" and "spread".
  - Sensitivity analysis of the decomposition to common shape.

THANK YOU