

The rpm package: Aligning LC/MS mass spectra with R

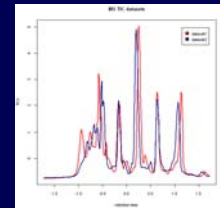
Benjamin Sausen⁽¹⁾
 Marc Kirchner^(1,2)
 Hanno Steen⁽²⁾
 Judith A.J. Steen⁽²⁾
 Fred A. Hamprecht⁽¹⁾



⁽¹⁾Interdisciplinary Center for Scientific Computing, University of Heidelberg, Heidelberg, Germany
⁽²⁾Children's Hospital Boston, Boston, MA, USA

Overview

- LC/MS
 - liquid chromatography
 - mass spectrometry
- total ion current (TIC)
 - non-linear distortions
 - alignment for inter-sample comparability
- challenge
 - landmark-free
 - robustness



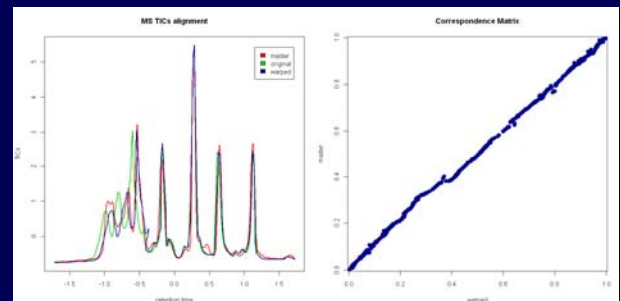
Methods

- Robust Point Matching (RPM) [1]
 - matches two point sets $\{x_i\}$ and $\{v_a\}$
 - alternating approach
 - estimate correspondence matrix
 - estimate transformation $f: \{v_a\} \rightarrow \{x_i\}$
 - annealing steps
- adaption to LC/MS data
 - warping constrained to LC domain
 - new distance metric for correspondence estimation
 - additional slope information

^[1]Chui H, Rangarajan A (2002)



Results



Acknowledgments

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