

Poster Award für Theodore Alexandrov

Die internationale Konferenz zu Intelligenten Systemen und Molekularbiologie (ISMB) ist die weltweit größte Konferenz zu diesem Fachgebiet. Vom 11. bis 13. Juli 2010 fanden sich rund 2000 Teilnehmer in Boston, MA, USA, zu Fachvorträgen, Workshops und einer umfassenden Poster-Session ein.

Die Beiträge dieser Konferenz werden durch eine Kommission bewertet, die anschließend in unterschiedlichen Kategorien Auszeichnungen verleiht. Von den etwa 750 eingereichten Poster wurden drei ausgezeichnet, darunter auch jenes von Theodore Alexandrov, Zentrum für Technomathematik (ZeTeM) und den beiden Co-Autoren Peter Maaß (ZeTeM) und Herbert Thiele (Bruker Daltonik GmbH).

Spatial Segmentation of MALDI-imaging Data

Bruker Daltonics



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Introduction

MALDI-imaging is a mass spectrometry technique for studying thin spatial samples (e.g. a tissue section). MALDI-imaging is modern and fast growing technology with spatial resolution upto 10 μm used to localized proteins and small molecules for many purposes. For a spatial point with coordinates (x,y) a high-dimensional mass spectrum is measured.

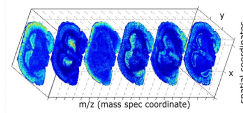
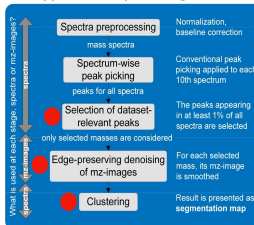


Fig. 1 Schematic representation of a MALDI-imaging data set (data cube).

We propose a new procedure for spatial segmentation of MALDI-imaging data which clusters all spectra into different groups based on their similarity.

The partition is represented by a segmentation map which explains the full data set with one image. The key point of this procedure is the edge-preserving denoising of images corresponding to specific masses (m/z-images).

Our approach to spatial segmentation



Acknowledgments

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Ferdinand von Eggeling (both University Hospital Jena, Jena, Germany)

ISMB'2010, Poster R16

Pipeline steps

- Selection of dataset-relevant peaks
Reduces dimensionality (x100)

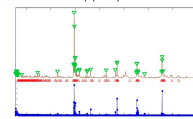


Fig. 2 Mean spectrum (brown), frequencies of peaks (blue) and selected dataset-relevant peaks (green triangles).

- Edge-preserving denoising of m/z-images
Diminishes pixel-to-pixel variation

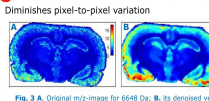


Fig. 3 A. Original m/z-image for 6648 Da. B. Its denoised version.

- Clustering
Splits spectra (pixels) into groups

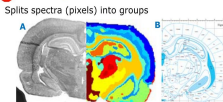


Fig. 4 A. Halves of optical image and the segmentation map. B. Schematic of the anatomical structure of the rat brain atlas (Elsevier). Anatomical structure is highlighted.

Interpretation of a cluster

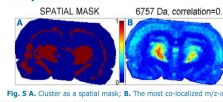


Fig. 5 A. Cluster as a spatial mask. B. The most co-localized m/z-image.

Importance of denoising

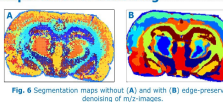


Fig. 6 Segmentation maps without (A) and with (B) edge-preserving denoising of m/z-images.

Applications

Neuroendocrine tumor

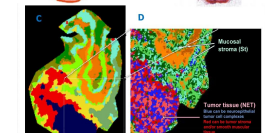
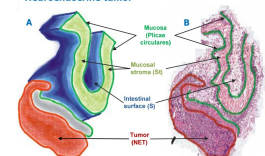


Fig. 7 A. 3D-structure of the tissue. B. optical image of the H&E stained section. C. Segmentation map, strong denoising. Tumor area is found (blue and red clusters). D. A part of the segmentation map, weak denoising. Tumor area shows the heterogeneous composition.

Bacteria Interactions

Study of natural products in zones of interactions of bacteria colonies.

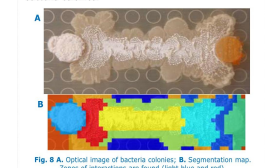


Fig. 8 A. Optical image of bacteria colonies. B. Segmentation map. Zones of interactions are found (light blue and red).

Conclusions

- New pipeline for spatial segmentation of MALDI-imaging data is proposed
- Potential of the approach is proven
- Segmentation maps highlight morphological/histological structures
- University of Bremen-Bruker patent application 20100225/267

Das Poster präsentiert eine neue Pipeline für die räumliche Segmentierung von MALDI-Imaging Daten. Diese Pipeline verwendet Clusterverfahren für aufbereitete Spektren. Die Grundidee ist, räumliche Beziehungen zwischen den Spektren zu benutzen, um die Variabilität zwischen den Pixeln zu reduzieren. Die einzelnen Schritte der Pipeline sind: Vorverarbeitung der Spektren, Auswahl relevanter Massen, Entrauschen der zu diesen Massen korrespondierenden Bilder mit Bildverarbeitungstechniken (lokal beschränktes, kantenerhaltendes Entrauschen) und statistisches Clustering. Die erzeugten Segmentierungsbilder weisen hinsichtlich Glattheit, Detailinformationen und Übereinstimmung mit anatomischen und histologischen Strukturen eine hohe Qualität auf.

Für das Poster siehe www.math.uni-bremen.de/zetem/news.