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**Metabolite-based clustering and visualization of mass spectrometry data using one-dimensional self-organizing maps**  
 Peter Meinicke<sup>1\*</sup>, Thomas Lingner<sup>1</sup>, Alexander Kaefer<sup>1</sup>, Kirstin Feussner<sup>2</sup>, Cornelia Göbel<sup>3</sup>, Ivo Feussner<sup>3</sup>, Petr Karlovsky<sup>4</sup> and Burkhard Morgenstern<sup>1</sup>

Address: <sup>1</sup>Department of Bioinformatics, Institute of Microbiology and Genetics, University of Göttingen, Göttingen, Germany; <sup>2</sup>Department of Developmental Biochemistry, Institute for Biochemistry and Molecular Cell Biology, University of Göttingen, Göttingen, Germany; <sup>3</sup>Department for Plant Biochemistry, Abbe-Weber-Haller Institute for Plant Sciences, University of Göttingen, Göttingen, Germany and <sup>4</sup>Molecular Phytopathology and Insecticide Research Unit, University of Göttingen, Göttingen, Germany

Email: Peter Meinicke\* - [pmeinicke@gwdg.de](mailto:pmeinicke@gwdg.de); Thomas Lingner - [thlingner@gwdg.de](mailto:thlingner@gwdg.de); Alexander Kaefer - [akaefer@gwdg.de](mailto:akaefer@gwdg.de); Kirstin Feussner - [kfeussner@gwdg.de](mailto:kfeussner@gwdg.de); Cornelia Göbel - [cgobel@gwdg.de](mailto:cgobel@gwdg.de); Ivo Feussner - [ifeussner@gwdg.de](mailto:ifeussner@gwdg.de); Petr Karlovsky - [pkarlov@gwdg.de](mailto:pkarlov@gwdg.de); Burkhard Morgenstern - [bmorgen@gwdg.de](mailto:bmorgen@gwdg.de)

\* Corresponding author

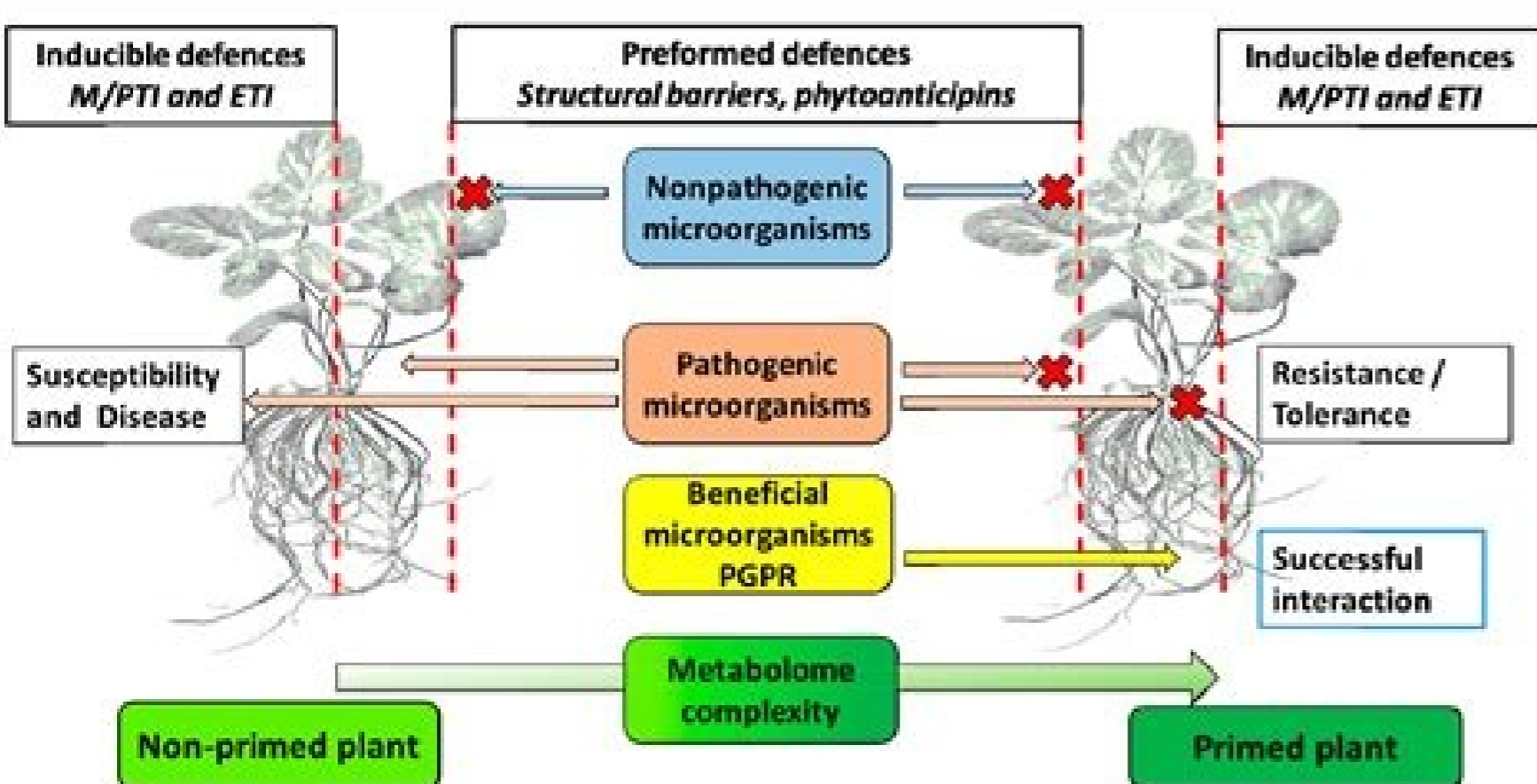
Published: 26 June 2008  
 Algorithm for Molecular Biology 2008, 3:9 doi:10.1186/1745-7188-3-9  
 Received: 24 January 2008  
 Accepted: 26 June 2008

This article is available from <http://www.almob.org/content/3/1/9>  
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**Abstract**  
**Background:** One of the goals of global metabolomic analysis is to identify metabolic markers that are hidden within a large background of data originating from high-throughput analytical measurements. Metabolite-based clustering is an unsupervised approach for marker identification based on grouping similar concentration profiles of putative metabolites. A major problem of this approach is that in general there is no prior information about an adequate number of clusters.  
**Results:** We present an approach for data mining on metabolite intensity profiles as obtained from mass spectrometry measurements. We propose one-dimensional self-organizing maps for metabolite-based clustering and visualization of marker candidates. In a case study on the wound response of Arabidopsis thaliana, based on metabolite profile intensities from eight different experimental conditions, we show how the clustering and visualization capabilities can be used to identify relevant groups of markers.  
**Conclusion:** Our specialized realization of self-organizing maps is well-suited to gain insight into complex pattern variation in a large set of metabolite profiles. In comparison to other methods our visualization approach facilitates the identification of interesting groups of metabolites by means of a convenient overview on relevant intensity patterns. In particular, the visualization effectively supports researchers in analyzing many putative clusters when the true number of biologically meaningful groups is unknown.

**Background**  
 Metabolomics is a fundamental approach in basic research to detect and quantify the low molecular weight molecules (metabolites) in a biological sample. Besides the other so-called "omics" technologies (genomics, transcriptomics, proteomics), metabolomics is becoming a key technology that facilitates the measurement of the ultimate phenotype of an organism [1]. In particular, metabolomics allows untargeted global screening approaches based on the measurements of signal intensities.

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Review  
**Metabolomics in Plant Priming Research: The Way Forward?**

Fidele Tugizimana , Msizi I. Mhlongo, Lizelle A. Pieter and Ian A. Dubery 

Department of Biochemistry, Research Centre for Plant Metabolomics, University of Johannesburg, Auckland Park 2006, South Africa; [Fideletu@gmail.com](mailto:Fideletu@gmail.com) (F.T.); [msizi.mhlongo17@gmail.com](mailto:msizi.mhlongo17@gmail.com) (M.I.M.); [lpeter@uj.ac.za](mailto:lpeter@uj.ac.za) (L.A.P.)  
 \* Correspondence: [idubery@uj.ac.za](mailto:idubery@uj.ac.za); Tel.: +27-011-559-2401

Received: 7 May 2018; Accepted: 4 June 2018; Published: 13 June 2018



**Abstract:** A new era of plant biochemistry at the systems level is emerging, providing detailed descriptions of biochemical phenomena at the cellular and organismal level. This new era is marked by the advent of metabolomics—the qualitative and quantitative investigation of the entire metabolome (in a dynamic equilibrium) of a biological system. This field has developed as an indispensable methodological approach to study cellular biochemistry at a global level. For protection and survival in a constantly-changing environment, plants rely on a complex and multi-layered innate immune system. This involves surveillance of 'self' and 'non-self,' molecule-based systemic signalling and metabolic adaptations involving primary and secondary metabolites as well as epigenetic modulation mechanisms. Establishment of a pre-conditioned or primed state can sensitise or enhance aspects of innate immunity for faster and stronger responses. Comprehensive elucidation of the molecular and biochemical processes associated with the phenotypic defence state is vital for a better understanding of the molecular mechanisms that define the metabolism of plant-pathogen interactions. Such insights are essential for translational research and applications. Thus, this review highlights the prospects of metabolomics and addresses current challenges that hinder the realisation of the full potential of the field. Such limitations include partial coverage of the metabolome and maximising the value of metabolomics data (extraction of information and interpretation). Furthermore, the review points out key features that characterise both the plant innate immune system and enhancement of the latter, thus underlining insights from metabolomic studies in plant priming. Future perspectives in this inspiring area are included, with the aim of stimulating further studies leading to a better understanding of plant immunity at the metabolome level.

**Keywords:** metabolomics; plant defence; plant-microbe interactions; priming; pre-conditioning

**1. Introduction: Multi-Layered Molecular and Cellular Networks Ensure Effective Adaptation to Changing Environments**

Evolution dictates that living systems constantly adapt to ever-changing environments in a context-dependent manner. Such adaptation and/or response to environmental or genetic alterations implies complex and dynamic cellular reprogramming [1–3]. These biological responses—which can be phenomenologically described by understanding the cellular or organismal physiological state—are kinetic and highly dynamic events that span the whole cellular biological information network [4–7]. Reflecting on the plant kingdom, one of the epitomes of such adaptation is the constant fine-tuning of physiologies and cellular-scale morphologies, and the dynamic (and complex) biosynthesis of an array of structurally and functionally diverse chemistries [8–10].

*Int. J. Mol. Sci.* **2018**, *19*, 1759; doi:10.3390/ijms19061759

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