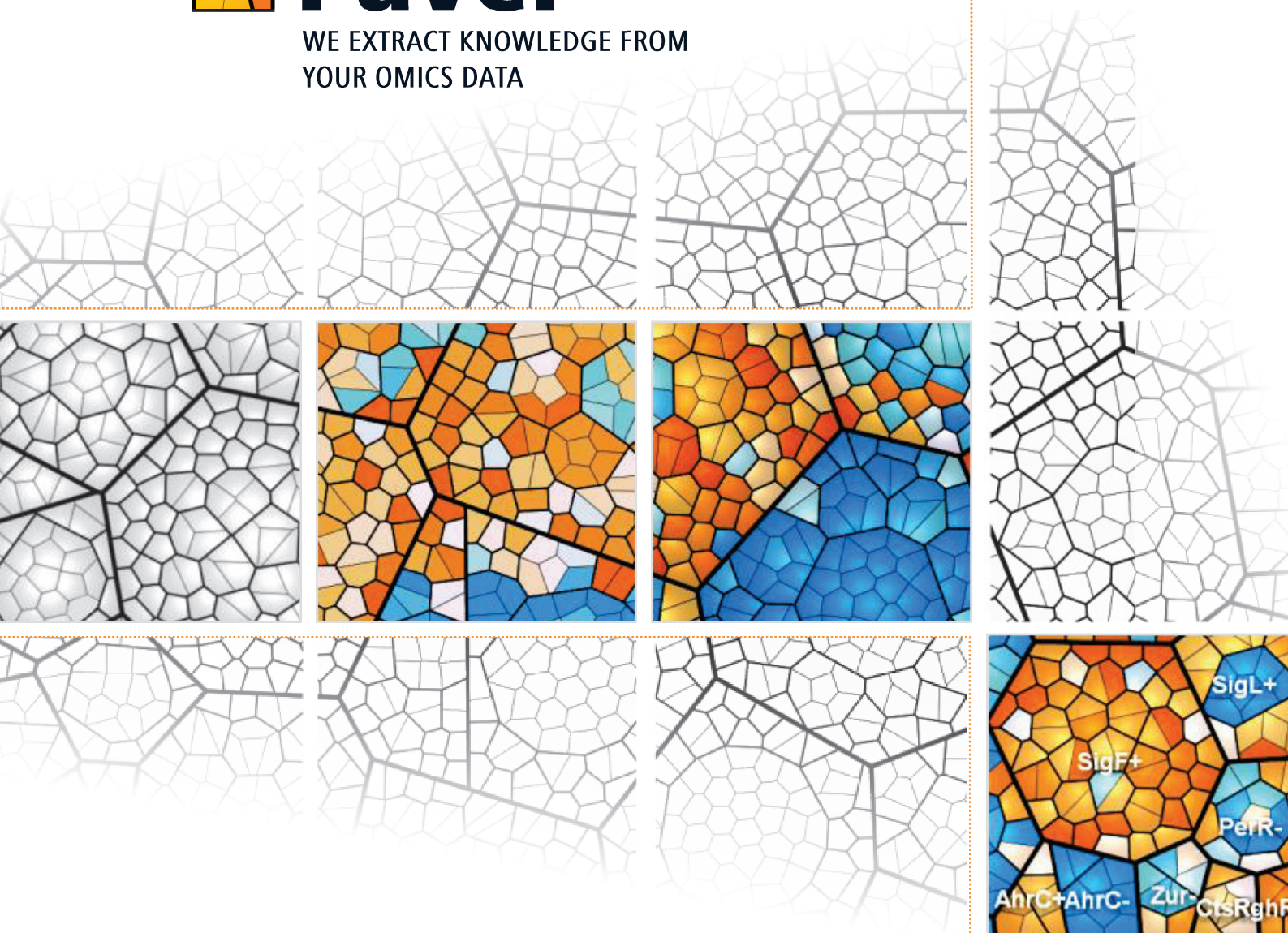




Paver

WE EXTRACT KNOWLEDGE FROM
YOUR OMICS DATA



Visualize high-level expression patterns

Paver is a DECODON service for the analysis and visualization of large OMICs data sets, including data from transcriptome, proteome and / or metabolome analyses. A newly developed integrated visualization technique aggregates complete sets of expression data with available biological knowledge from a variety of gene functional classification systems on a minimum of screen space. This makes it possible to visualize expression sets as a whole without any kind of pre-filtering.

Paver combines expression data and functional classification to build a visual display of all detected mRNAs or proteins of the biological system under investigation. In contrast to other approaches Paver can integrate the whole set of experimental data with a maximum of biological knowledge already available.

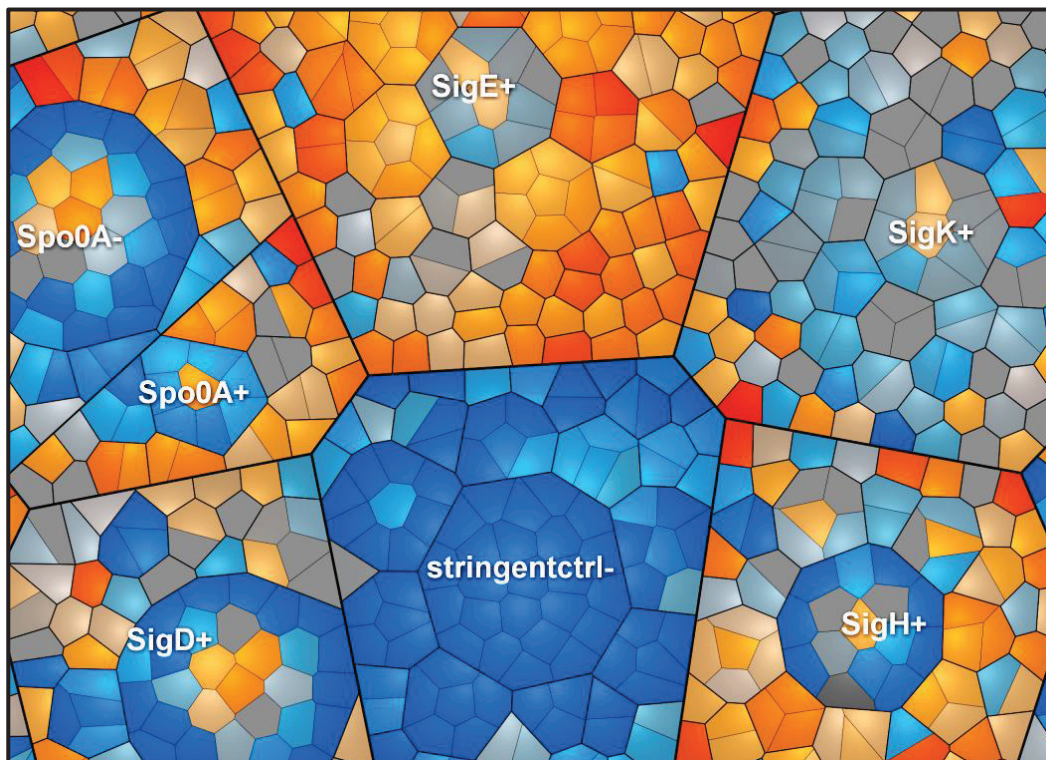
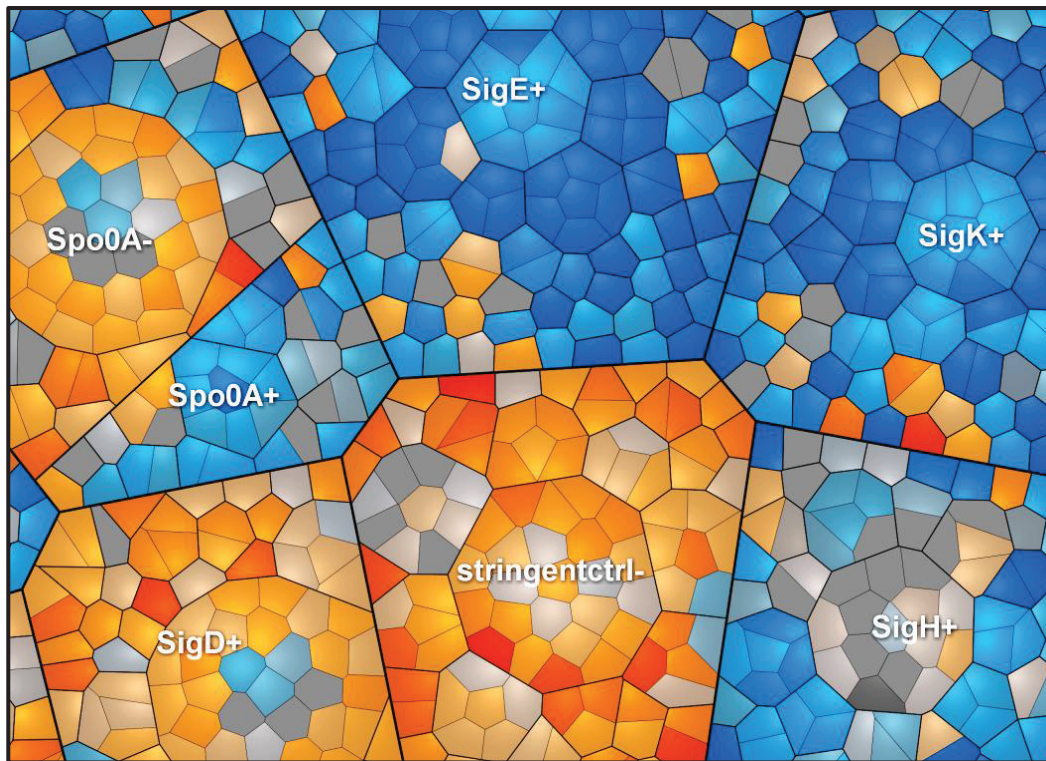
Gene functional classification systems organize genes / proteins according to their function in (quasi-)hierarchical systems. Paver supports:

- Gene Ontology
- KEGG Brite
- Riley scheme derivatives (e.g. TIGR classifications, Genolist classifications)
- Clusters of Orthologous Groups (COG)
- Open Biology Ontology (OBO)
- gene regulatory data
- custom classification schemes

Paver finds and clearly highlights genes and proteins that behave similarly; grouping by function makes them available for further interpretation and analysis. This allows bio-scientists to find interesting functional coherencies within biological systems and to discover new patterns never seen before in their expression data.

Paver's data visualization ►

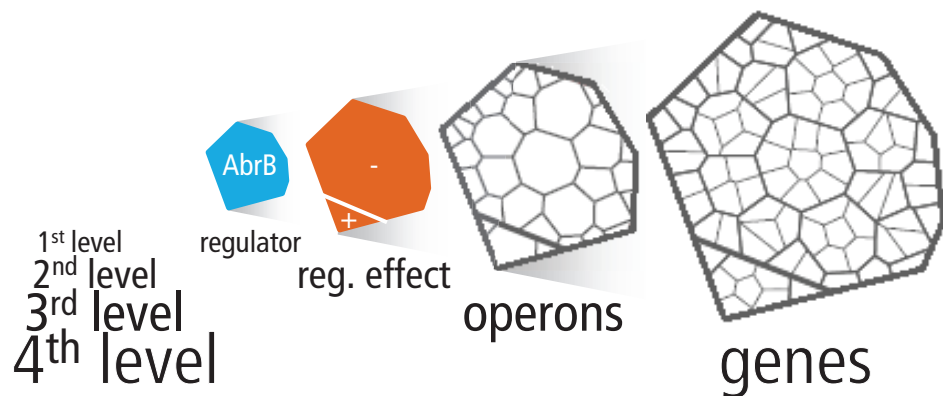
Bacterial gene expression data were mapped into a gene regulatory classification scheme. Expression levels are color-coded (expression levels: blue-low; white-average; orange-high combined with confidence: bright color-high; gray shaded color-low confidence). Expression data of genes (smallest tiles) is grouped by operon (next higher level clusters). The Voronoi treemap shows clearly how the activity of regulators (labels of highest level clusters) is tuned by the bacterial cell under two analyzed conditions (top – exponential growth, bottom – stationary phase).



Voronoi Treemaps – Paver’s technology for data visualization

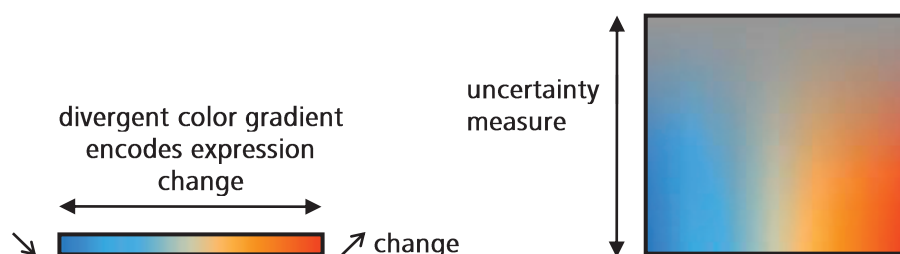
Treemaps were established by Ben Shneiderman from Maryland in the mid 90’s to display hierarchical data using nested (rectangular) areas. Each branch of a classification hierarchy is represented by a rectangular area. Subbranches tile them into rectangular subshapes and so on. This efficiently uses available screen space but the use of rectangular shapes makes perception of hierarchical structure difficult.

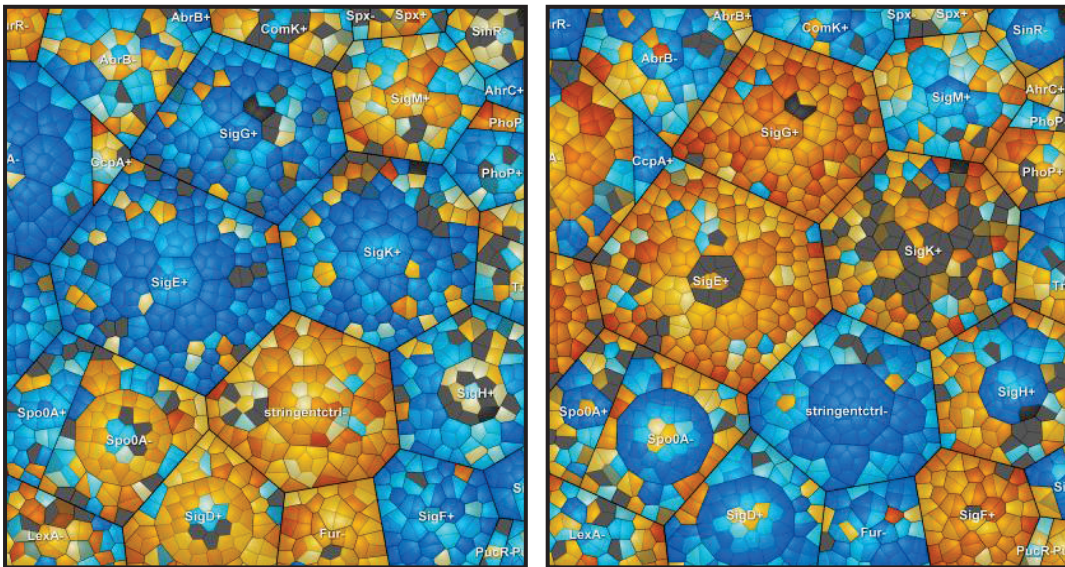
Voronoi treemaps replace the rectangular areas by convex Voronoi shapes (Balzer & Deussen). These shapes provide improved visual perception of hierarchy levels and related entities. When applied to a regulatory classification scheme from bacteria, the layout of a section of a treemap looks as follows:



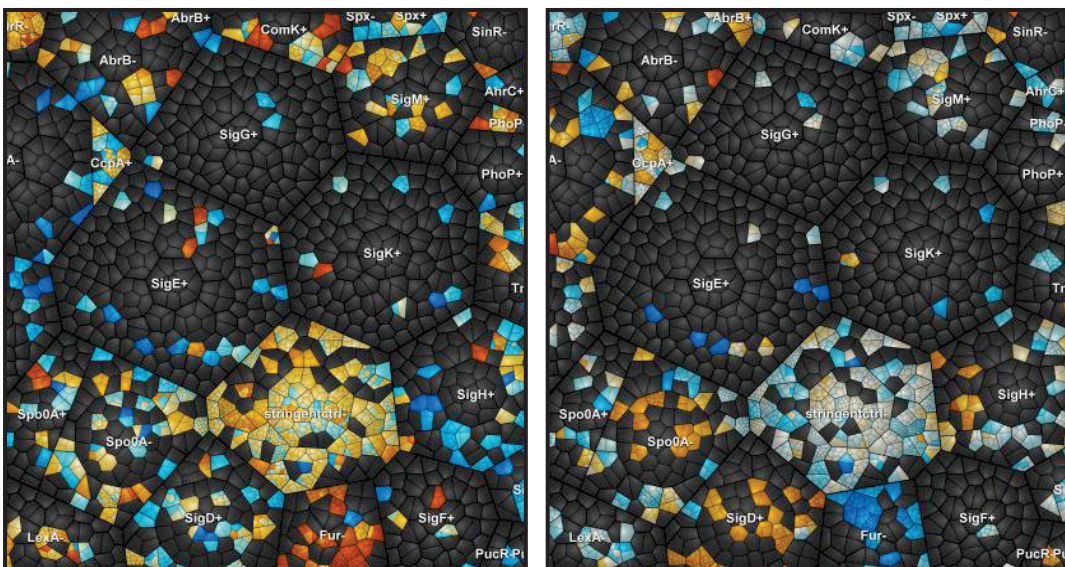
In a similar manner layouts based on Voronoi treemaps can be applied to any imaginable functional classification system.

Changes in expression levels for genes or proteins are visualized using a color gradient. Multivariate data (expression change combined with uncertainty and amount of biomolecules) may be represented using gray shading (i.e. saturation – see figure) or variation of brightness.





Global mRNA of a *Bacillus subtilis* 168 glucose starvation experiment was analyzed (Otto et al). Samples were obtained during exponential growth phase (left) and 30 min after entry into stationary phase (right). Z-transformed expression data were visualized within a regulon annotation map. During the exponential growth phase, particularly stringent controlled genes (growth involved) are active. In addition, Fur-dependent genes (ion recruitment) are depressed, CodY-activated genes, Pur-repressed genes, SigD-dependent genes and others are active. In the stationary phase, most of the genes are contrarily expressed.



The same data as shown above analyzed on protein level (left: exponential growth; right: stationary phase). Protein tiles are further subdivided to represent quantities on the peptide level. Area of subtiles corresponds to peptide length. In addition to protein expression levels, this Voronoi treemap also visualizes homogeneity of expression changes as measured across various parts of the whole protein molecule.

The Paver service

Expression data from any field of OMICS technologies are mapped to gene functional classification systems and analyzed. DECODON's service team guides you through the whole analysis process. New (customized) classification schemes of interest can be implemented if necessary. You'll be provided with sets of visualizations, statistical data on significantly influenced functional groups.

Development

Paver's underlying engine has been developed in a collaborative effort of DECODON GmbH and the group of Dr. Jörg Bernhardt at the Ernst-Moritz-Arndt-University of Greifswald bringing together the experience in software development, bioinformatics and OMICS centric biology. Until now Paver and its underlying technology have been applied in molecular medicine (human cell lines, treatment of blood products), pathogenomics (host pathogen interaction, response of human cell lines to infection) as well as microbial physiology (*B.subtilis*, *S.aureus* strains, *Pseudomonas* strains) and MetaOMICS related studies.

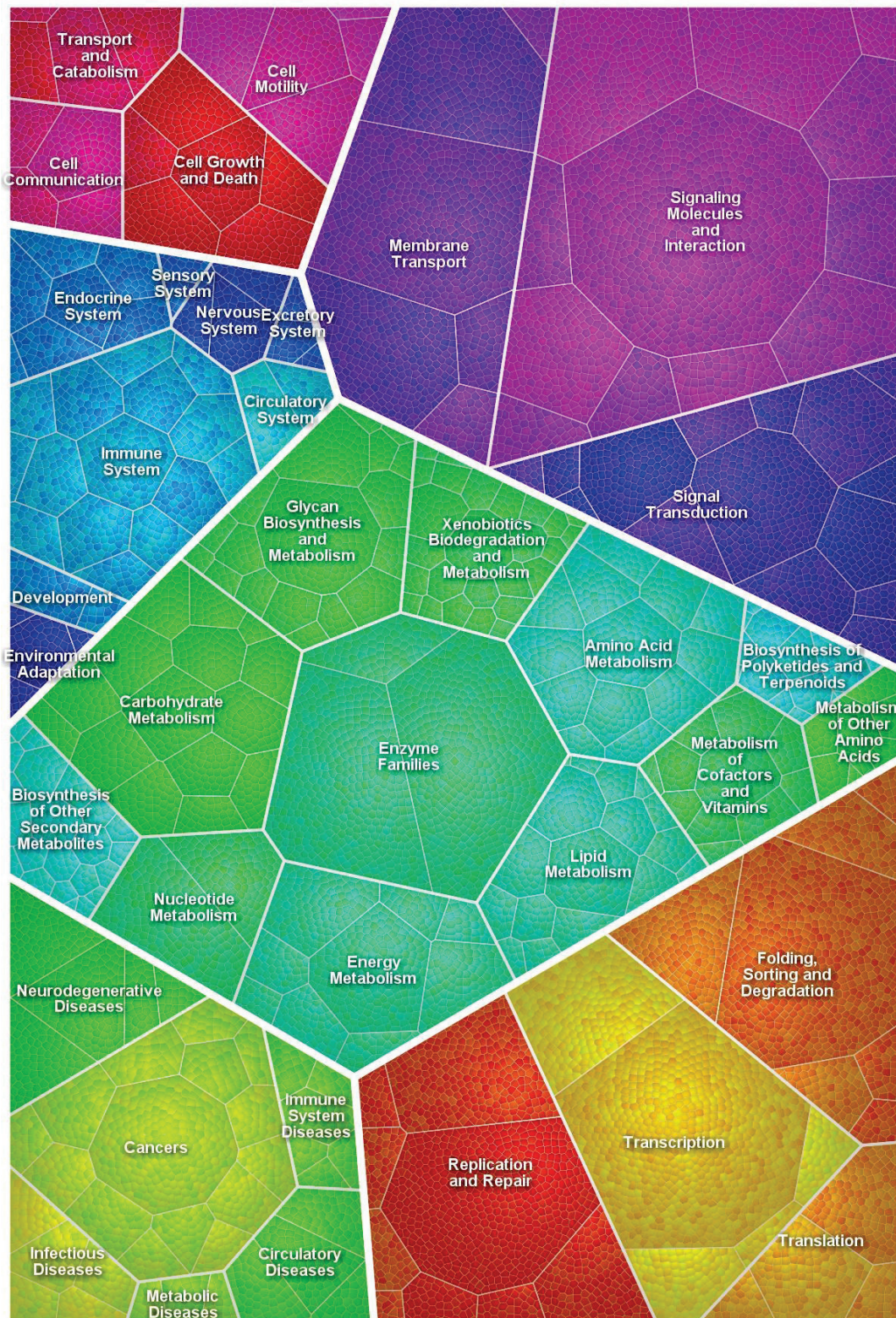
Learn more

Just send an email to info@decodon.com with the subject "Paver information request".

We are looking forward to hearing from you!

References

- Bernhardt, J, H Mehlan, J Schüler, M Hecker.** 2011. OntologyMaps. <http://vizbi.org/2011/Posters/Collection/?poster=D10>, Awarded as Best Poster at VizBi 2011 (Visualization in Biology) Conference at BROAD Institute in Boston
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Voronoi treemap for the KEGG Brite classification system



DECODON GmbH
Walther-Rathenau-Str. 49a
17489 Greifswald, Germany

www.decodon.com
info@decodon.com
phone: +49(0)3834 515230
fax: +49(0)3834 515239

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