

# Meeting Protocol

## Meeting Members

Prof. Dr. Kurt Zatloukal  
[kurt.zatloukal@meduni-graz.at](mailto:kurt.zatloukal@meduni-graz.at)

Dr. Peter Abuja  
[peter.abuja@meduni-graz.at](mailto:peter.abuja@meduni-graz.at)

DI Michael Kalkusch  
[kalkusch@icg.tu-graz.ac.at](mailto:kalkusch@icg.tu-graz.ac.at)

Marc Streit  
[mstreit@icg.tugraz.at](mailto:mstreit@icg.tugraz.at)

## Place

Pathologie - LKH Graz

## Date

December 12<sup>th</sup>, 2006

# 1 Heatmap

## 1.1 Dataset from Karl Kashofer can be used in GenView Project

Dataset consists of tumor probes from human tumor in mice and human tumor in humans.

(-> provides good scenarios for publications)

# 2 Heatmap <-> Pathway Interaction

## 2.1 Selection of genes in heatmap

2.1.1 Highlight selections in pathway (see concept described in 4.2)

## 2.2 Propagate neighborhoods also between pathways and heatmap

## 2.3 Reduction of gene data using pathways -> reduced data can then be applied to all KEGG pathways (e.g. scrolling the KEGG pathways)

## 2.4 Panther is a nice tool but information is simplified and abstracted (sometimes too much).

(The PANTHER, Protein ANalysis THrough Evolutionary Relationships [7] )

Classification System is a unique resource that classifies genes by their functions)

## 2.5 „Scrolling“ through pathways

2.5.1 Highlight components of pathway in heatmap (see concept described in 4.2)

2.5.2 Like in 2.5.1 but with own color for each pathway

2.5.3 Render only components of pathways in the heatmap – the rest transparent with frame

## 2.6 "Scrolling" through pathways in 3D via "Acordion view" (Concept proposed by Dieter)

# 3 Pathways

## 3.1 Radial Graph Layout in 2 ½ D

## 3.2 Depth search with arbitrary depth (i.e. neighborhood visualization)

## 3.3 Depth search from nodes in pathway via directed edges

3.3.1 forward in direction of edges

3.3.2 backwards against direction of edges

## 3.4 Kirchhoff's circuit laws [1][2] (Elektrotechnik)

3.4.1 Consider node throughput

3.4.2 Consider Kirchhoff's loop rule (Maschenregel)

## 3.5 Continuity equation [3][4] (Strömungslehre)

Is energy balance possible?

## 3.6 Bernoulli's Energy Equation [5][6]

## 3.7 sklenfreie Netzwerke (Barabasi) [8]

## 3.8 Construction of simplified pathways without metabolites (i.e. „semantic zoom“)

## 3.9 Layered pathway view: Show same pathway several times, but for different patient data.

e.g. 1 Pathway + 3 Patient data => 3 Planes with pathways in 3D (incl. activation visualization from heatmap (2½D view))

### 3.10 User Interface: List of pathways

3.10.1 currently selected pathways based on neighborhood visualization of enzymes and metabolites

3.10.2 currently selected pathway based on heatmap selection

3.10.3 arbitrary arranged list of pathways

3.11 Editable graphs with meta knowledge

3.12 Special (simple) handbuild pathways (2D)

3.13 Showing protein regulation in pathways (extracted from gene expression data)

3.14 Pathway connections to external pathways are very interesting

(Note: in XML already contained)

3.15 Cofactors are important but later on in the project relevant

3.16 Contacting KEGG: Presenting our tool keeps potential.

To be present in the KEGG community and to submit a useful application could increase the visibility of the Graz BioInformatics group.

3.17 Petri-Nets could be useful

## 4 Concepts

4.1 Consistent color coding in heatmap and pathways

4.2 Linking:

4.2.1 Heatmap ==> Pathway

4.2.1.1 Heatmap => Selection linked with Pathway

4.2.2 Pathway ==> Heatmap

4.2.2.1 Pathway => Selection highlighted in Heatmap

4.2.2.2 Whole pathway => Highlight only these genes

4.3 Slider

4.3.1 Slider for lower bound and upper bound

4.3.2 Lower and upper bound sliders should be represented by one single slider widget

4.3.3 Possibly connected to MIDI device

## 5 Contacts

- Berlin, Max-Planck Institute of Molecular Genetics  
*Hans Lehrach, Ralf Herwig* ([http://www.molgen.mpg.de/~lh\\_bioinf/team/](http://www.molgen.mpg.de/~lh_bioinf/team/))
- Proteomics: Protein - Protein Interaction  
*Erich Wanker*, Berlin, Max-Delbrück-Center (<http://www.mdc-berlin.de/>)
- LKH Graz:  
*Karl Kashofer*, Investigates Heatmap Pathway connection

## 6 Next Meetings

Thursday 14 <sup>th</sup> of Dec. 2006	09:00 Meeting with Karl Kashofer, Pathology 1 <sup>st</sup> Floor
Thursday 14 <sup>th</sup> of Dec. 2006	10:00 Meeting with Karl Kashofer & Kurt Zatloukal
Tuesday 19 <sup>th</sup> of Dec. 2006	9:00- 9:30 Prof. Bartsch meets Prof. Trajanoski
Tuesday 19 <sup>th</sup> of Dec. 2006	9:30-11:00 Prof. Bartsch, Meeting with Makus Grabner (ICG)
Wednesday 31 <sup>st</sup> of January 2007	Prof Zatloukal travels to Innsbruck, Meeting with Prof. Bartsch?

## 7 References

- [1] [http://de.wikipedia.org/wiki/Kirchhoffsche\\_Regeln](http://de.wikipedia.org/wiki/Kirchhoffsche_Regeln)
- [2] [http://en.wikipedia.org/wiki/Kirchhoff's\\_circuit\\_laws](http://en.wikipedia.org/wiki/Kirchhoff's_circuit_laws)
- [3] <http://de.wikipedia.org/wiki/Kontinuit%C3%A4tsgleichung>
- [4] [http://en.wikipedia.org/wiki/Continuity\\_equation](http://en.wikipedia.org/wiki/Continuity_equation)
- [5] [http://de.wikipedia.org/wiki/Bernoullische\\_Energiegleichung](http://de.wikipedia.org/wiki/Bernoullische_Energiegleichung)
- [6] [http://en.wikipedia.org/wiki/Bernoulli%27s\\_equation](http://en.wikipedia.org/wiki/Bernoulli%27s_equation)
- [7] <http://www.pantherdb.org/tools/>
- [8] Albert-László Barabási, „Skalenfreien Netzwerke“, [http://de.wikipedia.org/wiki/Albert-L%C3%A1szl%C3%B3\\_Barab%C3%A1si](http://de.wikipedia.org/wiki/Albert-L%C3%A1szl%C3%B3_Barab%C3%A1si)