

**Seminar „Systembiologie/Formelseminar“
Sommersemester 2010**

Jeweils Dienstags, 13.30 Uhr Härtelstr. SR 109

Date	Title	Referent	Abstract
08.06.	What happens on earth? A short introduction to geophysics.	Jens Przybilla	
15.06.	Some Examples of Statistics in Life Science	Carsten Wiuf	<p>Since I'm here for 6 months, I see the talk as an opportunity to introduce some examples of the work I've been involved in. I hope these examples might provide basis for further discussion and potential collaboration. The two first topics relate to analysis of microarray data.</p> <p>(i) Determination of DNA copy numbers from SNP microarray data in tumor cells has turned out to be a big statistical challenge. I will mainly discuss some work based on Hidden Markov Models, but also briefly mention a more pragmatic approach, we currently are working on.</p> <p>(ii) Methylation array data have among other things been used for classification of different tissue samples. Here, I discuss a simple statistical model that are able to depict global differences in methylation patterns between tissue types. The model uses information about CpG content and is applied to colon cancer samples (MSI, MSS and adenomas).</p> <p>(iii) The last topic relates to analysis of protein interaction data (PIN).</p> <p>Despite PIN data are very noisy, we might be able to learn about the evolution and size of an organism' interactome (the collection of all proteins and their interactions in an organism) from analysis of a PIN data set. I will discuss different statistical methods we have developed for that purpose.</p>

22.06.	3-Dimensional Reconstruction of Basal Cell Carcinoma	Patrick Scheibe	<p>This work presents a complete processing-chain for a 3D-reconstruction of Basal Cell Carcinoma (BCC). BCC is the most common malignant skin cancer with a high risk of local recurrence after insufficient treatment. Therefore, we have focused on the development of an automated image-processing chain for 3D-reconstruction of BCC using large histological serial sections. We introduce a novel kind of image-processing chain (core component: non-linear image registration) which is optimised for the diffuse nature of BCC.</p> <p>For full-automatic delineation of the tumour within the tissue we apply a fuzzy c-means segmentation method, which does not calculate a hard segmentation decision but class membership probabilities. This feature moves the binary decision tumorous vs. non-tumorous to the end of the processing chain, and it ensures smooth gradients which are needed for a consistent registration. We used a multi-grid form of the onlinear registration effectively suppressing registration runs into local minima (possibly caused by diffuse nature of the tumour). To register the stack of images this method is applied in a new way to reduce a global drift of the image stack while registration.</p> <p>Our method was successfully applied in a proof-of-principle study for automated tissue volume reconstruction followed by a quantitative tumour growth analysis.</p>
25.06.	Evolutionary and functional characterization of primate transcription factors	Katja Nowick (MPI MolGen Berlin)	t.b.a
29.06.	t.b.a.	Verena Zuber	<p>We study feature selection in classification by recently proposed Higher Criticism Tresholding (HCT) and derive an alternative formulation of the method using local false non discovery rates. We investigate missclassification error under the influence of feature selection and show that HCT tries to minimize a certain approximation to this error. Based on this approximation of the missclassification error we suggest an extension of the HCT method to the multi-class case.</p>
06.07.	Higher Criticism "und" False Discovery Rates	Bernd Klaus	<p>We study feature selection in classification by recently proposed Higher Criticism Tresholding (HCT) and derive an alternative formulation of the method using local false non discovery rates. We investigate missclassification error under the influence of feature selection and show that HCT tries to minimize a certain approximation to this error. Based on this approximation of the missclassification error we suggest an extension of the HCT method to the multi-class case.</p>

13.07. Diff-GI Modelle für "Signaling Cascades" Elisenda Feliu

One of the principal mechanisms by which signals are transmitted in living cells is by post-translational modification of proteins catalyzed by enzymes. In particular, classic signaling pathways are shaped by a cascade consisting of a series of post-translational modification cycles whose activated protein acts as the modifier enzyme in the next cycle.

Cascades may differ in length as well as in the number of modification sites required for activation. These features, together with the abundance of the involved chemical species and rate constants, confer how the signal is transmitted. For instance, one of the most common signaling cascades, the MAPK cascade, consists of a one site phosphorylation layer followed by two layers of two site phosphorylations. Although this cascade has been extensively studied, both experimentally and theoretically, it is still poorly understood why nature is keeping such a sophisticated mechanism to transform a given stimulus to a certain response.

Due to the huge amount of variables involved, theoretical conclusions are usually based either on the addition of extra assumptions (which might not always hold) or on evidences depicted from randomly generated parameters.

During my visit to Carsten Wiuf at the Bioinformatics Research Center in Aarhus, Denmark, we have developed a mathematical approach to analyze signaling cascades that exploits the modularity of the system and with no further assumptions than mass-action kinetics on the set of chemical reactions. In this talk I will discuss our results on the number of steady states, stimulus-response curves and switch-like behavior of signaling cascades.

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