

StemCellMathLab 2016

8th International Workshop on Models and Concepts of Stem Cell Organization

Systems Medicine of Leukemia

June 16th - 18th, 2016 - Hamburg, Germany



Scientific Programme

Thursday, 16th June 2016

14:00-14:15 *Welcome and Opening*
Ingo Roeder, Ingmar Glauche

Model-based data interpretation

Central questions to be discussed:

- What are current open questions in understanding basic biological principles that underlie hematological malignancies and how can these be addressed by mathematical models?
- Which are the major limitations, caveats, and restrictions of datasets and of experimental models that make the application of mathematical approaches necessary?
- Is the benefit for the understanding of biological principles higher than the cost of (over-)simplification? Or: How simple can/should models be?

Session Chair: Markus Loeffler

14:15-14:35 *Introductory Talk*
Connie Eaves
"Single-cell analyses flatten the Waddington concept of early stages of hematopoiesis"

14:35-14:45 Discussion

14:45-14:55 **Adam MacLean**
"Identifiability of leukemia models and testing of *relative* hypotheses"

14:55-15:05 Discussion

15:05-15:15 **Ingmar Glauche**
"Necessary ingredients for predicting CML relapse"

15:15-15:25 Discussion

15:25-15:35 **Dominique Bonnet**
"Dynamics and frequency of Leukemia-initiating cells during short-term ex vivo culture informs outcomes in AML patients"

15:35-15:45 Discussion

15:45-16:30 **Coffee Break**

16:30-16:40 **Kerstin Cornils**
"BcrAbl Barcoding - what we can learn from mathematical models"

16:40-16:50 Discussion

16:50-17:00 **Tim Brümendorf**
"Using telomere data to model stem cell kinetics"

17:00-17:10 Discussion

17:10-17:20 **David Kent**
"Using next generation sequencing to track clonal hematopoiesis in normal individuals"

17:20-17:30 Discussion

17:30-17:40 **Bertie Göttgens**
"Computer models may still come short even if we incorporate as much experimental data as we can"

17:40-17:50 Discussion

19:00 **Dinner/BBQ at Elsa-Brändström-Haus**

Friday, 17th June 2016

Theoretical perspectives/Model philosophy

Central question to be discussed:

- Is the primary aim of mathematical models the prediction of clinical outcomes (i.e. “decision-making”) or are models more useful when treatments don’t work (i.e., in “understanding”)?
- Because uncertainty in model predictions is inevitable, is it possible to define acceptable bounds on the uncertainty such that model predictions are: (i) useful; (ii) clinically viable?
- Which degree of simplification (that is inherent to models) is acceptable for clinical applications?
- Are “machine learning” approaches, based on “omics” data sufficient to predict biological/clinical outcomes or is a mechanistic understanding (still) necessary?
- What are good/useful strategies to combine “omics”-based bioinformatic analyses with mechanistic modelling? What does “data-integration” actually mean?

Session Chair: Connie Eaves

08:30-08:50	<i>Introductory Talk</i> Markus Loeffler “Mathematical models in biology and medicine: potentials, impact and limitations”
08:50-09:00	Discussion
09:00-09:10	Christoph Baldow “Plaque or cholera? Quantification of hematopoietic tissue remodeling and predictions of cancer break-out”
09:10-09:20	Discussion
09:20-09:30	Walter de Back “The impact of uncertainty propagation for model predictions”
09:30-09:40	Discussion
09:40-09:50	Ingo Roeder “The impact of different variance components on prediction accuracy”
09:50-10:00	Discussion
10:00-10:10	Fabian Theis "Constraining predictions by a mechanistic signaling model improves accuracy for cancer drug treatment"
10:10-10:20	Discussion
10:20-11:00	Coffee Break
11:00-11:10	Jens Przybilla “Targeting DNA methylation in myeloid malignancies”
11:10-11:20	Discussion
11:20-11:30	Benjamin Werner “Integrating mathematical modelling and cancer genomic data”
11:30-11:40	Discussion
11:40-11:50	Florian Büttner “Probabilistic machine learning facilitates interpretable models with high predictive power - examples from single-cell omics data”
11:50-12:00	Discussion

12:00-12:10	Andreas Schuppert “Computational Biomarkers”
12:10-12:20	Discussion
12:20-14:30	Lunch Break
<u>Clinical perspectives/Practical relevance of mathematical models</u>	
<i>Central questions to be discussed:</i>	
<ul style="list-style-type: none"> • Which is/should be the role of mathematical models in study design/clinical decision-making? • How can the knowledge on basic biological principles be exploited in clinical practice? • Under which conditions and for what reasons do biologists and clinicians rely/not rely on mathematical predictions? • Can/should classical prognostic parameters (e.g. cell counts, pathological scores) be replaced by “omics”-signatures, in the era of “big data”? 	
<i>Session Chair: Ingmar Glauche</i>	
14:30-14:50	<i>Introductory Talk</i> Andreas Schuppert “Practical relevance of mathematical models”
14:50-15:00	Discussion
15:00-15:10	Martin Bornhäuser “How can functional data and 'omics' be integrated into 'ad hoc' models for individual (cancer/Leukemia) patients?”
15:10-15:20	Discussion
15:20-15:30	Dominik Beck “Profiling expression levels as prognostic parameters across multiple patient cohorts”
15:30-15:40	Discussion
15:40-15:50	Nina Cabezas “The use of ‘omics’-signatures as prognostic factors”
15:50-16:00	Discussion
16:00-16:10	Lisa Hopcroft “How can single cell omics translate to the clinic?”
16:10-16:20	Discussion
16:20-16:30	David Kent “Using mathematical modelling to understand the impact of single mutations on the growth and differentiation of single blood stem cells.”
16:30-16:40	Discussion
16:40-17:30	Coffee Break
18:15	Departure of the bus from Elsa-Brändström-Haus
18:45	Cruise at the river Elbe
20:00	Dinner in the Portuguese Quarter of Hamburg

Saturday, 18th June 2016

Clinical perspectives/Practical relevance of mathematical models (continued)

Central questions to be discussed:

- Which is/should be the role of mathematical models in study design/clinical decision-making?
- How can the knowledge on basic biological principles be exploited in clinical practice?
- Under which conditions and for what reasons do biologists and clinicians rely/not rely on mathematical predictions?
- Can/should classical prognostic parameters (e.g. cell counts, pathological scores) be replaced by “omics”-signatures, in the era of “big data”?

Session Chair: Ingo Roeder

09:00-09:10	Joëlle Guilhot “Understanding long term molecular remission in Chronic Myeloid Leukemia (CML): how can it be addressed by mathematical models?”
09:10-09:20	Discussion
09:20-09:40	Lucie Laplane & Eric Solary “How to understand the progression from normal to clonal hematopoiesis to CMML to AML?”
09:40-09:50	Discussion
09:50-10:00	John Pimanda “Using functional properties of dysplastic hematopoietic stem cells to improve drug sensitivity”
10:00-10:10	Discussion
10:10-10:20	Connie Eaves “Utility of in vitro functional assays to predict neutrophil recovery in vivo post-transplant”
10:20-10:30	Discussion
10:30-11:00	Coffee Break
11:00-12:30	Summary discussion and closing remarks
12:30	End of meeting – departure Transfer to Wilsede (for participants of the Wilsede meeting)