TrainERS

Symposium and Workshop in

Applied Systems Biology and Personalized Medicine

Stuttgart Research Center Systems Biology

University of Stuttgart

Tuesday 9th - Thursday 11th October 2018

funded by the EU's Horizon 2020 research and innovation programme under the Marie Sklodowska-Curie grant 675448

jointly organised by:

SRCSB University of Stuttgart | University of Stuttgart Germany | ZPM | Eberhard Karls Universität Tübingen

Stuttgart Research Center Systems Biology Center for Personalized Medicine Tübingen

presented by:

EASYM EUROPE

European Association for Systems Medicine

Tuesday 9th October – Open Symposium

Plenary meeting: University of Stuttgart, Lecture Theatre 0.267, Pfaffenwaldring 9, D-70569 Stuttgart		
Time	**Speakers**	**Topic**
9.00-9.10	***Markus Morrison***	***Welcome***
9.10-9.55	Prof Julio Vera (Univ. Erlangen)	Cancer Network Biology. From data processing to network-based hypotheses.
9.55-10.35	Prof Nicole Radde (Univ. Stuttgart)	Systems theory and parameter estimation for biological networks
10.35-11.05	***Coffee***	
11.05-11.50	Prof Kathrin Thedieck (Univ. Groningen)	Systems proteomics and metabolomics
11.50-12.35	Prof Carlos Lopez (Vanderbilt Univ.)	Nature's design for a MIMO signal integrator
12.35-14.00	***Lunch***	
14.00-14.45	Prof Nico Pfeifer (Univ. Tübingen)	Medical Informatics and Precision Medicine
14.45-15.30	Prof Markus Morrison (Univ. Stuttgart)	Modelling and data processing for biomarker development and clinical deployment
15.30- 16.00	***Coffee, Open Discussion with Speakers***	
19.30	**TRAIN-ERS and Speakers dinner (incl. career perspectives)**	**Restaurant Leonhardts, Fernsehturm Stuttgart, Jahnstrasse 120, D-70597 Stuttgart**

Wednesday 10th October, 2018

Allmandring 31, 70569 Stuttgart

Modelling and -Omics Workshop (ESRs only)	
Course topics: Symposium speakers conduct hands on courses	
9.00 – 13.00	Prof Carlos Lopez (Vanderbilt Univ.) Biological models as programs in Python
13.00-14.00	***Lunch***
14.00-17.00	Prof Julio Vera (Univ. Erlangen) Visualize and analyse high throughput data
18.00	**ESR social event (tent. Kraftpaule beer tasting)**

Thursday 11th October, 2018

Allmandring 31, 70569 Stuttgart

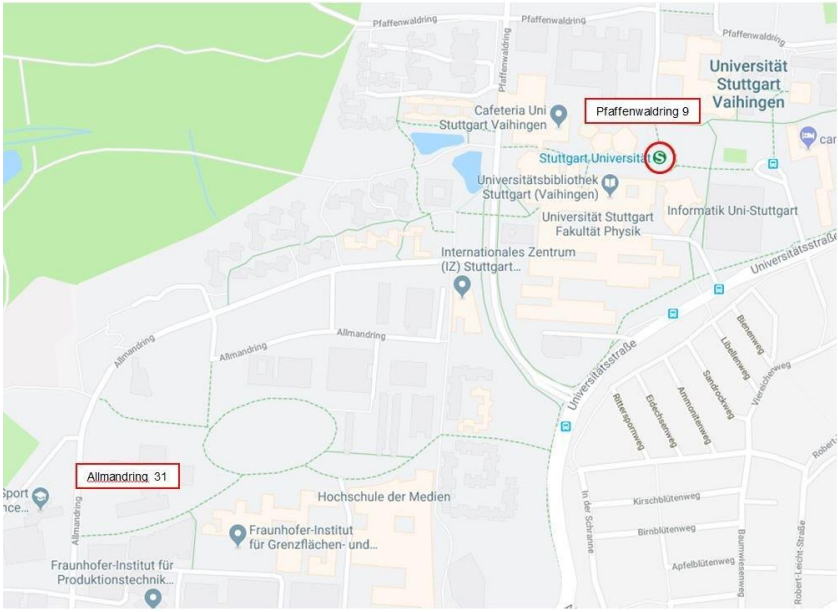
Modelling and -Omics Workshop (ESRs only)	
Course topics:	
9:00 – 13:00	Cristiano Guttà (Univ. Stuttgart): From Omics to patient survival analysis (TCGA - ER stress use case)
13.00-14.00	***Lunch***
14.00-17.00	Gavin Fullstone (Univ. Stuttgart): Building, testing and applying a prototype differential equations model (cell death use case)

Accommodation

Novum Hotel Rieker Stuttgart City
Friedrichstr. 3
D-70174 Stuttgart

Venue

Pfaffenwaldring 9
Lecture Theatre 0.267
University of Stuttgart, D-70569 Stuttgart



Learning outcomes and Advance preparation for hands-on workshop:

Prof Carlos Lopez:
Learning outcomes: Make the users aware of different tools and methods available in Python for the scientific community. Present PySB and MAGINE tools to attendees.
Advance preparation: Recommends carrying out a Python or SciPy tutorial rather than reading a paper in advance.

Prof Julio Vera:
Learning outcomes: In the session we will introduce the use of biochemical networks as a strategy to visualize and analyze high throughput data in the context of cancer. We will learn about methods and tools used to reconstruct networks, visualize data and derive core regulatory networks. We will use public available web tools, as well as our network platform www.vcells.net/melanoma. One could also use Cytoscape, but only if it is installed in the computers that students will use.
Advance preparation:

Cristiano Gutta:
Learning outcomes: Hands-on experience in how to conduct a survival analysis based on TCGA data, including considerations regarding TCGA data curation.
Advance preparation: ESR representative to collect favourite (ER stress) gene from all participants. Optimally avoiding overlap.

Dr Gavin Fullstone:
Learning outcomes: Experience in building a simplistic ODE model. Hands-on experience in using a semi-automated systems model of apoptosis execution. Understand features such as molecular switches and response robustness.
Advance preparation: Familiarise with canonical apoptosis execution network.