systems medicine disease maps

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The 3rd Disease Maps Community Meeting (DMCM2018) is hosted by the Computational Systems Biology of Cancer group, Institut Curie.

The programme and the abstract booklet are available here

Objectives

The objective of the 3rd DMCM is to consolidate efforts around the disease map projects and extend the Disease Maps Community. The 3rd DMCM will expose progress of the projects from the Disease Maps Community and beyond. The representative examples of network maps generation, their applications for disease data analysis, disease comorbidity, drug response prediction, advances in tools development and modelling approaches will be presented.

Topics

Among others, the following topics will be discussed: biocuration of prior knowledge related to different human diseases; creation and maintenance of disease network maps following common standards; sharing sub-maps with mechanisms implemented into different human diseases; providing technical solutions for network maps complexity management, mathematical modelling of maps and web-tools for explorations in maps. **Topic-specific roundtable discussions** will be organised to identify bottleneck problems and ways to overcome them.

Hands-on tutorials

Part of the meeting will be dedicated to **demos and hands-on tutorials** on major tools supporting the disease maps. The downloadable materials are available at the tutorial description in the meeting programme.

Programme

21 June

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Amphithéâtre BDD

08:30 - 09:00 Arrival and registration

09:00 - 09:05 Opening session and welcome

Emmanuel Barillot, Institute Curie, Paris, France

Reinhard Schneider, Luxembourg Centre for Systems Biomedicine, Belval, Luxembourg

09:05 - 09:15 Aims and perspectives of the DMCM2018 meeting

Alexander Mazein, European Institute for Systems Biology and Medicine, Lyon, France

Inna Kuperstein, Institute Curie, Paris, France

Session 1: Disease maps resources

09:15 - 09:30 Integrating disease maps using a graph database approach

Irina Balaur, European Institute for Systems Biology and Medicine, Lyon, France

Abstract

09:30 - 09:45 A disease map for the blood pressure and glomerular filtration regulatory network on which antihypertensive and analgesic drugs act

Francisco J. Lopez Hernandez, University of Salamanca, Salamanca, Spain

<u>Abstract</u>

09:45 - 10:00 Towards a molecular map of cystic fibrosis mechanisms

Catarina Pereira and Andre Falcao, University of Lisbon, Lisbon, Portugal

Abstract

10:00 - 10:30 Coffee break at BDD Hall

Session 2: Disease maps resources II

10:30 - 10:45 The AsthmaMap: computational representation of disease mechanisms using domain expert knowledge

Alexander Mazein, European Institute for Systems Biology and Medicine, Lyon, France

<u>Abstract</u>

10:45 - 11:00 A multiscale signalling network map of immune response in cancer reveals signatures of cell heterogeneity and functional polarization

Maria Kondratova, Institute Curie, Paris, France

Abstract

11:00 - 11:15 Parkinson's disease map facilitated gene expression analysis reveals new insights in PD pathogenesis

Stephan Gebel, Luxembourg Centre for Systems Biomedicine, Belval, Luxembourg

Abstract

11:15 - 11:30 Computational systems biology approach for the study of rheumatoid arthritis: from a molecular map to a dynamical model

Anna Niarakis, Universite d' Evry Val d' Essonne, Evry Val d' Essonne, France

<u>Abstract</u>

11:30 - 12:30 Invited talk: WikiPathways: curation, visualization and analysis of biological pathways

Martina-Summer Kutmon Maastricht University, Maastricht, the Netherlands

<u>Abstract</u>

12:30 - 13:30 Lunch and collaborations discussion at BDD Hall

13:30 - 15:00 Hands-on tutorials: parallel sessions

Time/Place	Amphi BDD	Annexes 1-3 BDD
13:30 - 14:10	Tutorial 1	Tutorial 3
14:10 - 14:15	Break	Break
14:15 - 14:55	Tutorial 2	Tutorial 4

Tutorial 1: Constructing and visualizing pathways with web-based SBGN editor Newt

Ugur Dogrusoz, Bilkent University, Ankara, Turkey

Abstract

Tutorial 2: MINERVA for visualization of disease maps

Piotr Gawron, Marek Ostaszewski, Luxembourg Centre for Systems Biomedicine, Belval, Luxembourg

Abstract

Requirements and downloads: To follow this tutorial, is recommended to install CellDesigner. All tutorial files are available here. Additionally, all files will be available on LCSB's ownCloud (Password: DMCM2018)

Tutorial 3: rROMA, a tool for module activity calculation from omics data and networks

Luca Albergante, Urszula Czerwinska, Andrei Zinovyev, Loredana Martignetti, Institute Curie, Paris, France

Abstract

Requirements and downloads: To follow this tutorial, is recommended to install R or R Studio and to download these files

Tutorial 4: COBRA toolbox for visualisation and map manipulation through CellDesigner and MatLab environment

Jennifer Modamio, Ronan Fleming, Luxembourg Centre for Systems Biomedicine, Belval, Luxembourg Nicolas Sompairac, Andrei Zinovyev, Inna Kuperstein, Institute Curie, Paris, France

Abstract

Requirements and downloads: To follow this tutorial, is recommended to install MATLAB (Paying license needed), CellDesigner and the COBRAToolBox . The files for the tutorial can be downloaded here

Session 3:Maps of biological processes and disease

15:00 - 15:10 The adult neurogenesis map

Rupert Overall, German Center for Neurodegenerative Diseases, Dresden, Germany

Abstract

15:10 - 15:20 The Ras/Raf/Mek/Erk Signaling Pathway - Attention to Details

Maria Dost, Humboldt-Universität zu Berlin, Berlin, Germany

Abstract

15:20 - 15:30 Is cellular senescence a prerequisite for tumor invasion?

Mathieu Boissan, Centre de recherche St-Antoine, Paris, France

Abstract

15:30 - 16:00 Coffee break at BDD Hall

Session 4: Maps for drug assessment and disease comorbidity

16:00 - 16:10 Comprehensive signaling network of regulated cell death: comparison of cell death modes in Alzheimer's neurodegenerative disease and cancer

Cristobal Monraz, Institute Curie, Paris, France

Abstract

16:10 - 16:20 Predicting personal activation potential of CD4 T cells

Feng He, Luxembourg Institute of Health, Luxembourg, Luxembourg

Abstract

16:20 - 16:30 Reconstruction of integrated maps for drug efficacy assessment

Tatiana Serebriyskaya, Moscow Institute of Physics and Technology, Moscow, Russia

<u>Abstract</u>

16:30- 16:40 Metabolic and signalling network map integration: application to cross-talk studies and omics data analysis in cancer

Nicolas Sompairac, Institute Curie, Paris, France

Abstract

16:45- 17:00 Group photo

17:00 - 18:15 Marie Curie museum and garden visit

http://musee.curie.fr

22 June

Amphithéâtre BDD

Session 5:Methods resources and models

09:00 - 09:15 Access and Discover Biological Pathway Information from Pathway Commons

Augustin Luna, Dana-Farber Cancer Institute/Harvard University, Boston, United States

Abstract

09:15 - 09:30 Community resources connecting chemistry and toxicity knowledge to environmental observations

Emma Schymanski, Luxembourg Centre for Systems Biomedicine, Belval, Luxembourg

Antony Williams, National Center for Computational Toxicology, Office of Research and Development, U.S. Environmental Protection Agency, Durham, USA

Abstract

09:30 - 09:45 Differential metabolic activity and discovery of therapeutic targets using summarized metabolic pathway models

Joaquin Dopazo, Fundación Progreso y Salud, Sevilla, Spain

Abstract

09:45 - 10:00 A computational model of the circadian clock and its application to understanding renal disease

Tom Freeman, The University of Edinburgh, Edinburgh, United Kingdom

Abstract

10:00 - 10:30 Coffee break at BDD Hall

Session 6: Large Reconstructions and integrations

10:30 - 10:45 Status report: parameter estimation of a large-scale mechanistic model for mast cells in asthma

Thomas S. Ligon, Ludwig-Maximilians-Universitat, Munich, Germany

Jan Hasenauer, Helmholtz Zentrum Munchen, Munich, Germany

Abstract

10:45 - 11:00 Application of disease maps to rare diseases: as muscular dystrophies

Cecilia Jimenez Mallebrera, Hospital Sant Joan de Deu, Barcelona, Spain

Abstract

11:00 - 11:15 Maps of influence and interactions of infectious and cancer diseases from Wikipedia networks

Dima Shepelyansky, Laboratoire de Physique Theorique CNRS, Universite Paul Sabatier, Toulouse, France

Abstract

11:15 - 11:30 Integrating ontological representation and reasoning into a disease map: application to Alzheimer's disease

Vincent Henry, ICM Brain and Spine Institute, Paris, France

Abstract

11:30 - 12:30 Invited talk: Reactome multi-scale pathway visualization

Henning Hermjakob, Molecular Systems services EMBL-EBI, Cambridge, United Kingdom

Abstract

12:30 - 13:30 Lunch and collaborations discussion at BDD Hall

13:30 - 15:00 Hands-on tutorials: parallel sessions

Time/Place	Amphi BDD	Annexes 1-3 BDD
13:30 - 14:10	Tutorial 5	Tutorial 7
14:10 - 14:15	Break	Break
14:15 - 14:55	Tutorial 6	

Tutorial 5: From interaction maps to dynamical models with Cell Collective: a hands-on tutorial

Tomas Helikar, University of Nebraska-Lincoln, Lincoln, United States

Abstract

Requirements and downloads: To follow this tutorial, is recommended to create a free acount on the Cell Colective website

Tutorial 6: mEPN and yEd: a graphical and computational modelling platform for biological pathways

Tom C. Freeman, University of Edinburgh, Edinburgh, UK

Abstract

Requirements and downloads: To follow this tutorial, is recommended to download and install yEd and Graphia Professional

Tutorial 7: A tutorial of hipathia, a mechanistic model of pathway activity

Martha R Hidalgo, Centro de Investigación Principe Felipe, Valencia, Spain Joaquin Dopazo, Fundación Progreso y Salud, Sevilla, Spain

Abstract

15:00 - 15:30 Invited talk: Share FAIR - Data management and standards for Systems Medicine

Martin Golebiewski, Heidelberg Institute for Theoretical Studies, Heidelberg, Germany

Abstract

15:30 - 16:00 Coffee break at BDD Hall

Session 7: Visualization and modeling frameworks

16:00 - 16:10 Instantiation of patient-specific network-based logical models with multi-omics data allows clinical stratification of patients

Jonas Beal, Institute Curie, Paris, France

Abstract

16:10 - 16:20 Visual analytics of biological networks using VANTED and its SBGN-ED add-on

Hanna Borlinghaus, University of Konstanz, Konstanz, Germany

Abstract

16:20 - 16:30 MINERVA API and plugin architecture: new data visualization interfaces for disease maps

Piotr Gawron, Luxembourg Centre for Systems Biomedicine, Belval, Luxembourg

Abstract

16:40 - 17:15 Thematic discussion groups (suggested topics):

Integration of maps in a shared repository

Tools for maps generation

Applications of disease maps in research and clinics: what is missing to close the gap?

Maps to models: curation standards to allow easy transformation of networks into executable models

Maps' complexity management approaches

Disease pathways vs. healthy pathways: how different are they?

17:15 - 17:30 Conclusions and closing session

Emmanuel Barillot, Institute Curie, Paris, France

Reinhard Schneider, Luxembourg Centre for Systems Biomedicine, Belval, Luxembourg

Abstract submission

Submit abstracts (up to 400 words) via **the submission link** for oral presentations and/or posters. Indicate 4 keywords to allocate it into the suitable session.

Registration

The registration is free but mandatory. Fill in the **registration form here**.

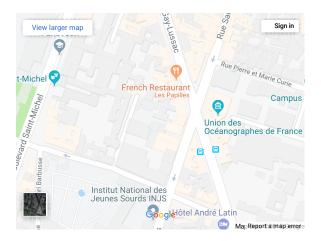
Location

Batiment de biologie du developpement et cancer (BDD building)

11 rue Pierre et Marie Curie 75005, Paris

France

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Accommodation

Recommended hotels:

Les Jardins Du Luxembourg

5 Impasse Royer-Collard, 75005 Paris, France

Hotel Elysa-Luxembourg

6 Rue Gay Lussac, 75005 Paris, France

Hotel du Brésil

10 rue Le Goff, 75005 Paris, France

Hotel Michelet Odeon

6 Place De L Odeon, 75006 Paris, France

Hotel de l'Avenir

65 rue Madame, 75006 Paris, France

Hôtel Des Mines

125 Bd Saint Michel, 75005 Paris, France

Contact

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