Maastricht University Helis Academy Training Developments

Maastricht University (UM) has developed different training programs and variations thereof within the context of the Helis Academy project. Large datasets of biological information such as genomics and transcriptomics data are becoming more widely available, and both researchers and professionals in the life sciences field will require an understanding of how to utilize this data. Hence, UM has developed trainings under the context of the Helis Academy to provide and understanding of omics data pre-processing, biological pathways, pathway analysis, biological networks, and network analysis. The trainings have been developed for both generic use and for use within specific contexts such as the understanding of rare diseases as well as pancreatic cancer.

Need for training

We now live in a world of big data, especially when it comes to the healthcare field. Technology is continuously developing that allows us to understand more and more about science. We can even sequence a person's entire genome. That is a ton of data that can prove really useful for understanding not only healthy functions of the body, but also pathological situations. However, we need to understand how to analyze this amount of data and what we can use it for. Particularly, biologists do not understand how to analyze the big data that they are generating. They instead send it to a bioinformatician to perform some magic. We want to offer a course using tools that are accessible and easy to use for those who are not comfortable with intensive computational techniques or coding themselves.

General Setup of Courses

The courses all contain both theoretical and practical aspects. We typically begin each course with a lecture to provide the necessary theoretical framework for the course participants. Lectures serve to make sure all of the participants have the same basic knowledge required to perform and understand the practical applications for the course because the backgrounds of the participants can sometimes be very diverse. In addition to the theoretical lectures, the courses all contain hands on practical exercises for the participants to apply the theoretical knowledge they have just learned. All of the practical materials are made available on Github pages so that they are freely accessed. Additionally, we develop a quiz for the end of the day for most of the courses to give the participants an indication of how much they've learned.

Target Audience

The courses developed by Maastricht University within the context of the Helis Academy project aim to reach professionals, students, and academics in the life sciences field. The majority of our courses aim to help those researchers and industry workers in the life sciences domain who want to learn how to analyze the omics data that they are producing. With more advanced courses we aim to reach bioinformaticians as well as other scientists who have some experience with programming.

Courses

Omics data analysis through data integration - using biological pathways, networks, and linear models

Description

The first Helis Academy Omics Data Analysis course is a collaborative effort between Maastricht University and VIB in which you will learn about transcriptomics data analysis and multi-omics data integration. We will begin the course addressing how you obtain published data from data repositories and then cover basic pre-processing steps. We will continue by introducing you to molecular pathways, from what they are, to how to make your own, to how to use them in advanced omics data analysis (transcriptomics, proteomics, metabolomics) and how this compares Gene Ontology analysis. The course will continue by zooming out to utilize your pathway analysis in a broader network analysis so you can see the bigger picture. Finally, we will finish with a day to show you how to integrate Omics data sets in an unsupervised statistical way using linear models.

UM Contribution

Materials: https://laurendupuis.github.io/Helis-Academy-Omics-June-2019/

Learning Outcomes

1. Understand the biology of biological pathways and networks
2. Normalize your data using ArrayAnalysis
3. Learn to utilize the biological pathway editor PathVisio to create your own pathway model or to edit an existing model.
4. Understand the concepts behind an enrichment analysis.
5. Perform an enrichment analysis using PathVisio
6. Perform a Gene Ontology Analysis using Gorilla
7. Perform a network analysis using Cytoscape

Schedule

11 June 2019:

11:30 - 12:30 Lecture: Introduction to pathways

12:30 - 13:30 Lunch

13:30 - 13:45 Lecture: Introduction to PathVisio and WikiPathways

13:45 - 15:00 Practical: WikiPathways academy

15:00 - 15:30 Break

15:30 - 17:00 Practical: Draw your own pathway in PathVisio

17:00 - 17:30 Wrap up (Quiz and Q&A)

12 June 2019:

09:30 - 10:30 Lecture: Data repositories and data-preprocessing

10:30 - 12:30 Practical: Pre-processing hands-on with ArrayAnalysis

12:30 - 13:30 Lunch

13:30 - 14:00 Lecture: Pathway analysis

14:00 - 15:00 Practical: Pathway analysis

15:00 - 15:30 Break

15:30 - 16:00 Lecture: Gene Ontology Analysis

16:00 - 17:00 Practical: Gene Ontology Analysis

17:00 - 17:30 Wrap up (Quiz and Q&A)

13 June:

09:30 - 10:30 Lecture: Network Biology

10:30 - 11:45 Practical: Pathways as a source for network biology

11:45 - 12:30 Gene Ontology-analysis in Cytoscape

12:30 - 13:30 Lunch

13:30 - 15:00 Lecture and practical: Protein-Protein Interactions

15:00 - 15:30 Break

15:30 - 16:30 Practical: Automation demo or work on your own dataset

16:30 - 17:00 Wrap up (Quiz and Q&A)

Trainers

Lauren Dupuis (Maastricht University)

Martina Summer-Kutmon (Maastricht University)

Susan Steinbusch (Maastricht University)

Friederike Ehrhart (Maastricht University)

Alexander Botzki (VIB & Elixir Belgium)

https://training.vib.be/all-trainings/helis-academy-course-omics-data-analysis-through-data-integration-using-biological

Handling of High-Throughput Transcriptomics (HTT) Data for Modeling

7 – 9 October, 2019 – The materials were developed and disseminated in Maastricht, the Netherlands, but the first version of the course was carried out in Barcelona, Spain

Description

The Helis Academy and the EUToxRisk project have collaborated to develop course materials for the Handling of High Throughput Transcriptomics (HTT) Data for Modeling. The proposed training activity will focus on the handling of HTT data for modelling and exploitation by the use of advanced computational tools. The audience will be introduced to the application of advanced computational tools for the acquisition and pre-treatment of HTT data by the use of practical examples. Hands-on sessions will allow the attendants to get familiar with these tools.

Learning Outcomes

1. Understand the basics of data acquisition, normalization, and scaling
2. Understand how to create an Adverse outcome pathway
3. Understand the basics of data visualization on pathway models
4. Perform a GO analysis
5. Perform a network analysis

Schedule

Day 1 – Mon. 7 Oct

Time	Topic	Speakers
	Introductory part (facultative for advanced and expert participants)	
13:00 - 14:00	**Theory (1)** Introduction	Florian Caiment (UM)
14:00 - 16:00	**Theory (2)** Basic data handling. Data acquisition, normalization and scaling. 1) Finding data (using repositories of toxicogenomics data) 2) Basic data treatment 3) Basic statistical modelling (find changed genes)	Florian Caiment (UM)
16:00 - 16:30	Coffee break	
16:30 - 18:30	**Hands-on (I)**	All

Day 2 – Tue. 8 Oct

Time	Topic	Speakers
	Pathway analysis and GO analysis	
8:30 - 10:30	**Case study (I)** 1) Understanding and creating pathway (using WikiPathways, feature the AOP portal) 2) Basic pathway analysis with data visualisations 3) GO-analysis	Lauren Dupuis (UM), Marvin Martens (UM), Chris Evelo (UM)
10:30 - 11:00	Coffee-break	
11:00 - 13:00	**Hands-on (II)** 1) Pathway analysis in PathVisio (1.5h) 2) Recap of pathway analysis, discuss findings and future directions (0.5h)	Lauren Dupuis (UM), Marvin Martens (UM), Chris Evelo (UM)
13:00 - 14:30	Lunch	
	Advanced data handling and machine learning	
14:30 - 16:00	**Theory (III)** Advanced data handling. Differential gene expression from a set of compounds for a specific endpoint.	Olivier Taboureau (UCPH), Alejandro Orozco (UCPH)
16:00 - 16:30	Coffee-break	
16:30 - 17:30	**Case study (II)** Use of HTT data in machine learning	Olivier Taboureau (UCPH), Alejandro Orozco (UCPH)
17:30 - 18:30	**Hands-on (III)**	Olivier Taboureau (UCPH), Alejandro Orozco (UCPH)

Day 3 – Wed. 9 Oct

Time	Topic	Speakers
	Network analysis and network extension (Facultative for not-advanced participants)	
8:30 - 10:00	**Case study (III)** 1) Converting pathways found into networks 2) Extending networks with transcription factors and/or miRNAs (using CyTargetLinker) 3) Looking for active nodes and showing them.	Lauren Dupuis (UM), Marvin Martens (UM), Chris Evelo (UM)
10:00 - 10:30	Coffee break	
10:30 - 12:30	**Hands-on (IV)** 1) Creating a network in Cytoscape 2) Extending the network with CyTargetLinker 3) Recap network analysis and discuss findings.	Lauren Dupuis (UM), Marvin Martens (UM), Chris Evelo (UM)
12:30 - 13:00	**Conclusions and wrap-up**	Manuel Pastor (UPF)

Trainers

Manuel Pastor (UPF)

Florian Caiment (UM)

Lauren Dupuis (UM)

Denise Slenter (UM)

Olivier Taboureau (UCPH)

Alejandro Aquayo Orozco (UCPH)

Workshop and Hackathon: Molecular pathways for rare disease (FAIR) data analysis

26. - 29.11.2019 in Maastricht – The Netherlands

Description

The Helis Academy and European Joint Program on Rare Diseases are collaborating to develop the course and workshop titled Molecular pathways for rare disease (FAIR) data analysis. You will learn about biological pathway creation and curation as well as FAIR data. The course will focus on rare disease applications.

Materials: https://laurendupuis.github.io/Helis-Academy-Omics-June-2019/

Learning Outcomes

6. Understand the basics of biological pathways
7. Learn to utilize the biological pathway editor PathVisio to create your own pathway model or to edit an existing model.
8. Understand how to utilize the pathway database WikiPathways
9. Understand the basics of FAIR data

Schedule

Day 1 Tuesday 26.11.19

Focus of the day: Introduction and exploring WP/PV - making of pathways

12:00 – 13:00 (including lunch)	Participants registration (UNS60, Co Greepzaal (5th floor))	
13:00 – 14:00	Introduction and welcome (Chris Evelo)	Introduction to WikiPathways-PathVisio, network and RDF applications, aims and goals of the workshop Introduction of participants, background and expectations

14:00 – 15:00	How to make and curate pathways	Introduction lecture and hands on (by Lauren Dupuis)
15:00 - 15:30	Coffee break	
15:30 – 17:30	Create your own pathway!	Start working on new pathways (in small groups)
17:30	End of day 1	

Day 2 Wednesday 27.11.19

Focus of the day: Combining data and pathways and making the results FAIR

09:00 – 12:00 (coffee break included)	Continue work on pathways or explore curation task list to help improve pathways.	
	Continue working on pathways in small teams (with help from Marvin Martens)	For curation group - introduction to WikiPathways curation by Lauren Dupuis
12:00 – 13:00	Synthesis discussion - presentation of the results	
13:00 – 13:45	Lunch break	
13:45 – 15:00	Introduction and exploring neXtProt model	Presentation by Lydie Lane (SIB)
15:00 – 15:30	Coffee break	
15:30 – 17:00	Pathway and network analysis	Lecture and hands on (by Lauren Dupuis)
17:00 – 17.30	Discussion – Pathway analysis input data	
17:30	End of day 2	

Day 3 Thursday 28.11.19

Focus of the day: Next steps - identification of tasks and preparation of hackathon, hackathon

09:00 – 13:00	2 parallel groups	
(coffee break included)	Discussion of impressions from previous days and preparation of hackathon: 1. How to make data FAIR in such a way that it allows group-based pathway analysis 2. How to make pathway analysis results FAIR 3. How to improve the rare disease portal Evaluate, present, check different common methods in separate groups (Metadata description methods, Bioschemas, and for the pathways: Pathway RDF, Pathway ontology, Nanopubs for references, BridgeDb for ID mapping build in, with explicit resource-based IDs, and Applets for integration into other approaches)	BYOD session (Bring Your Own Data) Possibility for supervised data analysis - especially for ERN members and other data owners (supervision by Susan Coort) PS: if you can't bring your own data you can work in groups or download data from repositories (e.g. GEO or ArrayExpress).
13:00 – 13:45	Lunch break	
13:30 – 17:30 (coffee break included)	Discussion and start of hackathon, identification of next steps, goals for hackathon	
17:30	End of day 3	

Trainers

Chris Evelo (Maastricht University)

Lauren Dupuis (Maastricht University)

Friederike Ehrhart (Maastricht University)

Lydie Lane (SIB)

Comprehensive Introduction to Omics Data Analysis

April 2020, eLearning

Description

The Comprehensive Introduction to Omics Data Analysis course, offered by the Helis Academy, takes you from the procurement of biological data through to the analysis using biological pathway and network analysis techniques. We will begin the course with a description of multiple relevant biological databases where useful data can be procured. We will address the steps to get published data from data repositories and then cover basic pre-processing steps. We will continue by introducing you to molecular pathways, from what they are, to how to make your own, to how to use them in advanced omics data analysis (transcriptomics, proteomics, metabolomics) and how this compares Gene Ontology analysis. The course will continue by zooming out to utilize your pathway analysis in a broader network analysis so you can see the bigger picture. Finally, we will finish with a day to show you how to integrate Omics data sets in an unsupervised statistical way using linear models.

Materials: https://laurendupuis.github.io/Helis_Academy_April_2020/

Learning Outcomes

1. Understand the biological databases available and how to procure data from them
2. Normalize your data
3. Understand the basics of biological pathways and networks
4. Learn to utilize the biological pathway editor PathVisio to create your own pathway model and curate an existing model.
5. Perform an enrichment analysis using PathVisio
6. Perform a Gene Ontology Analysis using GOrilla
7. Perform a network analysis using Cytoscape

Schedule

eLearning Course, follow at your own pace

Program

Introduction to Biological Databases

Lectures: Introduction to Biological Databases

Tutorials: <u>Use of Online Data Resources for Molecular Biology</u>

Introduction to Biological Pathways

Lectures

- **Introduction to Pathway Modeling** by Dr. Lauren Dupuis (slides prepared by Dr. Kristina Hanspers and Dr. Lauren Dupuis)

Tutorials

- You will need to learn how to draw pathways using PathVisio. **Make sure to follow the <u>WikiPathways Academy</u> to get an interactive introduction to pathway drawing.**
- Once you have followed all of the steps of the WikiPathways Academy, you will be ready to get started drawing your own pathways in PathVisio. Before you start drawing or editing pathways, **follow the <u>Getting Started Guide</u>.** This guide will help you create a <u>WikiPathways</u> account, install the <u>WikiPathways plugin</u> in PathVisio, and select the proper <u>BridgeDb</u> mapping files.
- Now you are ready to draw some simple pathways of your own. **<u>Try drawing these pathways</u>**.

Introduction to Pathway Analysis

Lectures

- **Introduction to Pathway Analysis** by Dr. Lauren Dupuis (slides prepared by Dr. Martina Kutmon and Dr. Lauren Dupuis)

Tutorials

- **<u>This beginner's tutorial</u> will give you a hands-on introduction** to pathway analysis in PathVisio.

Introduction to Gene Ontology

Lectures

- **Introduction to Gene Ontology** by Dr. Lars Eijssen

Tutorials

- Complete this tutorial on GO Analysis using GOrilla

Introduction to Biological Networks

Lectures

- **Introduction to Biological Networks** by Dr. Martina Summer-Kutmon

Tutorials

- Complete this Network Analysis tutorial using Cytoscape.

Trainers

Lauren Dupuis (Maastricht University)

Martina Summer-Kutmon (Maastricht University)

Susan Steinbusch (Maastricht University)

Friederike Ehrhart (Maastricht University)

Lars Eijssen (Maastricht University)

CAKUT Pathway Curation Workshop

4-5 February, 2021 online

Description

The Helis Academy, in collaboration with the European Joint Program on Rare Diseases, has developed a new type of workshop that allows all participants and instructors to learn from one another. While the instructors teach participants about biological pathways and the tools to create and curate them, the participants teach the instructors about pathways relating to Congenital Anomalies of the Kidney and Urinary Tract (CAKUT). WikiPathways [http://wikipathways.org] is an open community created, community and expert curated pathway database. CAKUT is one of the use cases for which we create workflows and data pipelines in the European Joint Programme on Rare Diseases (EJP-RD) [https://www.ejprarediseases.org/]. Within the rare disease portal of WikiPathways [http://raredisease.wikipathways.org] we created a group of CAKUT pathways to allow disease network creation and omics data analysis but in the department of Bioinformatics (BiGCaT) in Maastricht are no experts on this particular disease. To create an expert curated pathway we held on February 4th the first online pathway curation workshop. For this workshop we invited CAKUT experts through the network of EJP-RD member Franz Schäfer. 12 Experts from Canada, France, Germany, Israel, UK, USA and the Netherlands joined the workshop. After a short welcome and introduction in "how to read and make pathway models in WikiPathways" by BiGCaT member Lauren Dupuis, the experts took over, supported by pathway modelling experts from BiGCaT. After the session we have removed two pathways, created two new pathways and modified another one. The follow up is still ongoing, we still get papers with comprehensive drawings or interaction provenance to be added to the pathways. It was a successful meeting, showing that modeling specialists collaborate best with domain experts to create pathways for data analysis.

Learning Outcomes

1. Understand the basics of biological pathway modeling
2. Learn to utilize the biological pathway editor PathVisio to create your own pathway model or to edit an existing model.
3. Understand how to develop a pathway model from a publication on CAKUT.

Schedule

15:00-15:10 CET	Welcome and introduction to the workshop goals (Franz Schäfer, Chris Evelo, Friederike Ehrhart)
15:10 – 15:40	How to draw and read pathways – a short introduction (Lauren Dupuis)
15:40 – 16:45 CET	Break up in focus groups around specific pathways or pathway groups. Each group will be accompanied by a member of the Bioinformatics department to help with pathway curation.

Group 1	Group 2	Group 3	Group 4

16:45 – 17:00 CET	Wrap up and conclusions
5 February	Follow up and continue development of the pathways

Trainers

Chris Evelo (Maastricht University)

Lauren Dupuis (Maastricht University)

Friederike Ehrhart (Maastricht University)

Franz Schäfer (EJP-RD)

Yanis Mimouni (EJP-RD)

PanCanNet Pathway Curation Workshop

13 April, 2021 online

Description

The Helis Academy, in collaboration with the European Joint Program on Rare Diseases and now the PancCanNet, has developed a new type of workshop that allows all participants and instructors to learn from one another. While the instructors teach participants about biological pathways and the tools to create and curate them, the participants teach the instructors about pathways relating to pancreatic cancer. WikiPathways [http://wikipathways.org] is an open community created, community and expert curated pathway database. Pancreatic cancer is one of the use cases for which we create workflows and data pipelines for the PancCanNet community. Within the pancreatic cancer portal of WikiPathways we created a group of pathways to allow disease network creation and omics data analysis but in the department of Bioinformatics (BiGCaT) in Maastricht are no experts on this particular disease. To create an expert curated pathway we held an online pathway curation workshop.

Learning Outcomes

1. Understand the basics of biological pathway modeling
2. Learn to utilize the biological pathway editor PathVisio to create your own pathway model or to edit an existing model.
3. Understand how to develop a pathway model from a publication on pancreatic cancer.

Schedule

morning	Introduction (Martina Summer Kutmon and Lauren J. Dupuis)
	How to draw and read pathways – a short introduction (Lauren Dupuis)
afternoon	Break up in focus groups around specific pathways or pathway groups. Each group will be accompanied by a member of the Bioinformatics department to help with pathway curation.
	Wrap up and conclusions

Trainers

Lauren Dupuis (Maastricht University)

Martina Summer Kutmon (Maastricht University)

Meet the Expert Pathway and Network Analysis Workshop

25 May, 2021 online

Description

The Helis Academy hosts a new type of workshop that allows all participants and instructors to learn from one another. While the instructors teach participants about biological pathways and networks and the tools to create, curate, and analyze them, the participants teach the instructors about data and pathways relating to their fields of interest.

Learning Outcomes

1. Understand the basics of biological pathway modeling
2. Learn to utilize the biological pathway editor PathVisio to create your own pathway model or to edit an existing model.
3. Perform a pathway analysis with PathVisio.

Schedule

morning	Introduction (Friederike Ehrhart and Lauren J. Dupuis)
	How to draw and read pathways – a short introduction (Lauren Dupuis)
afternoon	Work independently on pathway analysis using the tools learned in the workshop

Trainers

Lauren Dupuis (Maastricht University)

Friederike Ehrhart (Maastricht University)