

BioSB Research School

Education Programme



Version March 2017

Introduction

The BioSB education programme covers essential topics of the wide-ranging fields of bioinformatics and systems biology. It offers a wide variety of training courses that enable life scientists to apply modelling and computational approaches in addressing scientific challenges.

The programme consists of three types of courses:

1. **Introductory courses**

Courses intended for novices. These courses can either be face-to-face or e-learning courses. The format differs per course. The course length ranges from 1 to 5 days. The frequency varies, but the aim is to have these courses at least once a year.

2. **Core courses**

Courses for PhD students and other researchers in bioinformatics and systems biology. The topics and themes in the core programme form a coherent curriculum. The courses have a format of 5 days, with additional extra work (before and after) with a total study load of 3 EC. These courses will be offered once per two years.

3. **Specific courses**

Other courses and workshops that do not fit in the above-mentioned categories. These courses may have a different format and be offered occasionally only (e.g. summerschools). Some of them have successive editions while others may be one-time only events.

The BioSB education programme builds on the training programmes developed over the past years by the Netherlands Bioinformatics Centre, the Netherlands Consortium for Systems Biology, and their partners. The large group of tutors and staff that is already involved and the best practices that have been developed constitute a solid basis for the BioSB research school.

This document gives an overview of the BioSB Education Programme. For each course, brief information is given about the course, and the upcoming and earlier editions. Also the reference is given to the full course information (webpage). In addition, on the BioSB website, the BioSB Course Portfolio Page gives access to up to date information about the dates of upcoming courses and also provides links to the specific course pages for each course. For courses that are not open for registration it is possible to pre-register to indicate your interest for this course, after which you will get notified when the course is open for registration.

Many of the courses shown are being organised by BioSB in collaboration with other organisations. Existing collaborations and/or partnerships with other research schools and graduate schools, such as ASCI (www.asci.tudelft.nl), EPS (www.graduateschool-eps.info), PE&RC (www.pe-rc.nl), Molmed (www.molmed.nl), MCISB (www.mcisb.org), and the Groningen Graduate School of Medical Sciences (<http://www.rug.nl/research/gradschool-medical-sciences/>) will be extended and new partnerships will be established.

BioSB Course Portfolio

Introductory courses <i>1- 5-days; once per year</i>
<u>Programming in Python</u> <u>Kick-start R</u> <u>Programming in Matlab</u>
<u>E-course Biology</u> <u>E-course Modelling</u> <u>E-course Calculus</u>
<u>Discovering Systems Biology Principles</u>

Core Courses <i>5-days; once per 2 years; 3 ECTS</i>
<u>Pattern Recognition</u>
<u>Managing and Integrating Information in the Life Sciences</u>
<u>Optimisation Techniques in Bioinformatics and Systems Biology</u>
<u>Multi-scale modelling</u>
<u>Comparative Genomics: from Evolution to Function</u>
<u>Protein Structures: Production, Prowess, Power, Promises, and Problems</u>
<u>Algorithms for Biological Networks</u>
<u>Quantitative and Predictive Modelling</u>

Specific courses <i>1-5-days; frequency more irregular</i>
Regular Courses with successive editions
<u>Constraint-Based Modelling</u>
<u>Metagenomics applications and Data Analysis</u>
<u>RNA-seq Data Analysis</u>
<u>NGS in DNA Diagnostics</u>
<u>Next-generation sequence data analysis</u>
<u>Life Sciences with Industry</u>
<u>Python for Life Scientists</u>
<u>Systems Medicine: Modelling epigenetics</u>
One time only and/or few editions
<u>Exploring System Properties Using Various Modelling Approaches</u>
<u>Advanced de novo assembly and resolving complex genomic regions</u>
<u>EPS Postgraduate course 'Genome Assembly'</u>
<u>Data Integration in the Life Sciences</u>
<u>Biological Network Analysis</u>

Note: the **purple highlights** indicate courses in which bioinformatics and systems biology approaches are fully integrated.

BioSB Introductory courses

Programming in Python

Note: See below for Python course in the BioSB Specific Courses Track

Coordinators <names>

Dates <yyyyMMdd> (previous editions: none)

Venue <venue>

Website <www>

Study load 1 EC

Description/Keywords

Programming principles, software tools, Python.

Kick-start R

Coordinator Douwe Molenaar (VU)

Date 19 May 2017 (previous editions: 2012, 2013, 2014, 2015)

Venue VU University, Amsterdam

Website <http://biosb.nl/education/course-portfolio/course-kick-start-r/>

Study load 1 EC

Description/Keywords

This is a one-day introduction to the possibilities of the statistical calculation environment R for those who would like to use it, or have already started using R for statistical data analysis but would like to obtain a bit more background. We will start with a lecture in which the philosophy behind the R-language will be explained. An understanding of the data structures in R allows you to work more efficiently with R. We will show some of the advanced possibilities of R as well as where to find tutorials if you want to know more about those techniques. Most of the day will be devoted to a hands-on tutorial. The tutorial contains material from an introductory master course that is taught at the VU University. The manual contains material and references to material for self-study.

Topics that we will discuss: R language basics, installing R and R-packages, finding help, using R-studio, making dynamic reports, model fitting, reading/writing data from/to files, making publication-ready graphs, books and tutorials on the use of R.

Programming in Matlab

Coordinator Hans Stigter (WUR)

Date March 13, 2017 (previous edition: 2015)

Venue Wageningen

Website <http://biosb.nl/education/course-portfolio-2/course-matlab/>

Study load 1 EC

Description/Keywords

This is a one-day introduction to the possibilities of Matlab as a programming environment for simulation and analysis of biological models. We will start with a simple introduction of the basics of Matlab (matrices, vectors, manipulation of matrices and presentation of data). Having obtained some basic programming knowledge (writing of simple scripts and functions in Matlab), we will move on to more advanced topics. These include programming and solving ordinary differential equation models (ODEs) and the concept of “vectorized thinking” while writing Matlab-code. Finally, calibration of parameters in ODE type of models using measured data will be discussed and examples will be given. The course also includes the basics of presenting your results (graphing) in various types of plots that can easily be drawn in Matlab. Participants will, of course, get hands-on experience with Matlab and write code themselves in a practical.

Keywords: Programming principles, software tools, Matlab.

E-course Biology: Biomolecular Principles of the Cell (‘basic biology for non-biologists’)

Coordinator Bert Groen

Dates continuous, can be started any time (previous: 2009-2013) [*temporarily on hold*]
Venue Internet
Website <http://biosb.nl/education/course-portfolio-2/biosb-ecourses/>
Study load 3 EC

Description/Keywords

This e-course gives scientists that have no training in biology an introduction in basic biomolecular and cell biological concepts. The e-courses are fully web-based and are carried out individually. They consist of (a) readings, (b) recorded lectures, (c) assignments to monitor progress and (d) online-interaction with a tutor.

E-course Modelling: Modelling of Biological Processes ('basic modelling for biologists')

Coordinator Hans Stigter (WUR)
Dates continuous, can be started any time (previous: 2009-2013) [*temporarily on hold; will be available in 2017*]
Venue Internet
Website <http://biosb.nl/education/course-portfolio-2/ecourse-modelling/>
Study load 3 EC

Description/Keywords

This module introduces biologists to basic quantitative modelling. The e-courses are fully web-based and are carried out individually. They consist of (a) readings, (b) recorded lectures, (c) assignments to monitor progress, and, (d) online-interaction with a tutor.

E-course Calculus: Elementary Calculus in Systems Biology

Coordinator Hans Stigter (WUR)
Dates continuous, can be started any time (previous: 2012- 2013) [*temporarily on hold; will be available in 2017*]
Venue Internet
Website <http://biosb.nl/education/course-portfolio-2/ecourse-calculus/>
Study load 3 EC

Description/Keywords

This e-course provides a basic introduction to some mathematical concepts such as the derivative of a function, power series and Taylor series, the chain rule of differentiation, and more.

The aim of this e-course is to prepare students for the type of mathematics that, ultimately, can be used to create a mathematical model of a biological system. This e-course can therefore also be considered as an introduction to the e-course 2 on 'Modelling of Biological Processes'.

The e-courses are fully web-based and are carried out individually. They consist of (a) readings, (b) recorded lectures, (c) assignments to monitor progress, and, (d) online-interaction with a tutor.

Discovering Systems Biology Principles

Coordinators Frank Bruggeman (VU))
Dates 2017 (previous editions: 2015)
Venue Science Building, VU University, De Boelelaan 1085, 1081HV Amsterdam
Website <http://biosb.nl/education/course-portfolio-2/course-discovering-systems-biology-principles/>
Study load 3 EC

Description/Keywords

This course enables the student to discover biological principles that underlie biological networks. The course will first acquaint the student with the concepts of concentrations, rates, fluxes, steady state, production and transport. Several phenomena will be explained based on these biological principles: (i) production and transport are correlated, (ii) fluxes in a network may be correlated at steady state, (iii) control of function tends to be distributed (no rate-limiting step), (iv) networks may engage in energy waste through futile cycling, (v) cell function may be regulated at the level of transcription, translation, signalling and metabolism at the same time to different extents, (vii) networks may have multiple steady states and lead to pattern formation, (viii) drug targets may not be where they are traditionally expected, (ix) networks enhance robustness and engage in (near) perfect adaptation. The course will use existing models

of relevant networks which the student will interrogate using the web-based live model repository JWS. No mathematical experience is required.

Emergence of function, in silico discovery, network principles, cooperativity, control and regulation of cell function, self-organization, principles of biology.

BioSB Core courses

Pattern Recognition

Coordinators Perry Moerland (UvA), Dick de Ridder (WUR), Lodewyk Wessels (NKI, TUD)

Dates 25-29 September 2017 (previous editions: 2009, 2011, 2013, 2015)

Venue Amsterdam

Website <http://biosb.nl/education/course-portfolio/pattern-recognition>

Study load 3 EC

Description/Keywords

The course introduces basic techniques from the fields of pattern recognition and machine learning to solve bioinformatics problems. After having followed this course, a student should have an overview of basic pattern recognition techniques and be able to recognize what method is most applicable to classification problems (s)he encounters in bioinformatics applications.

Full description: Many problems in bioinformatics require classification: prediction of the class to which a certain object (i.e. a gene, protein, cell, patient, ?) belongs. This calls for algorithms that can assign the most likely label (discrete output) to an object, given one or more measurements on that object. For most interesting problems, the underlying physics are too complex to explicitly formulate such an algorithm. In such cases, a machine learning approach is taken: an algorithm is constructed, with parameters that are tuned based on an available dataset of training examples. The algorithm should predict the labels for these examples as well as possible, yet still generalize, i.e. perform well on objects not seen before. Some examples of classification problems in bioinformatics are gene finding (sequence in, gene presence out), diagnostics (microarray data in, diagnosis out), data integration (measurements in, probability of interaction out), etc. In this course, we will introduce basic techniques from the fields of pattern recognition and machine learning to solve such problems. We will introduce the pattern recognition pipeline: measuring, feature extraction and selection, classification and evaluation. The first two days will introduce the basic classification problem and a number of classic approaches to solve it. Next, methods for selecting or extracting informative features from a large set of measurements will be introduced. This will be followed by an introduction to a number of unsupervised techniques, that allow to find natural groupings or probabilistic descriptions of (unlabeled) data. The course will end with a cursory introduction to a number of intricate classifiers, artificial neural networks and support vector machines, and an overview of approaches to solve the generalization problem. For a large number of the methods discussed, we will turn to recent bioinformatics literature for examples.

Managing and Integrating Information in the Life Sciences

Coordinators Marco Roos (LUMC), Katy Wolstencroft (UL)

Dates 2017 (previous editions: 2009, 2011, 2013, 2015)

Venue Utrecht

Website <http://biosb.nl/education/course-portfolio/course-managing-and-integrating-information-in-the-life-sciences/>

Study load 3 EC

Description/Keywords

This course introduces modern techniques for the management of life science data and knowledge for bioinformatics applications. After following this course students should be able to start creating their first applications based on these technologies or make more informed design decisions for their current application. In this course participants will learn about:

1. Linked Data and the Semantic Web technologies that underpin it
2. How you can use Linked Data for data and knowledge integration in the Life Sciences
3. Available Linked Data resources in the public domain and large-scale projects that use these resources
4. How you can integrate your own data with Linked Data resources

5. How you can combine data integration and analysis over distributed resources, using Web Services and workflows

Optimisation techniques in Bioinformatics and Systems Biology

Coordinators Jaap Kaandorp (UvA), Jaap Molenaar(WU), Hans Stigter (WU), Cajo ter Braak (WU)

Dates TBA (previous edition: 2010)

Venue TBA

Website www.nbic.nl/education/nbic-phd-school/course-schedule/optimisation-techniques

Study load 3 EC

Description/Keywords

In many different problems from bioinformatics and systems biology (e.g. multi parameter estimation, reverse engineering of gene networks, multi-alignment problem, 3D structure prediction etc.) various optimisation methods are applied. In this course you will get acquainted with the underlying mathematics of optimization and with a selection of local and global optimization methods. In addition, throughout this course a great variety of examples of optimization problems in life sciences will be presented and discussed.

Day 1: math refresher and univariate optimisation

Dag 2: local multivariate optimisation

Dag 3: global stochastic optimization (simulated annealing, evolutionary algorithms)

Dag 4: parameter estimation, systems control and optimisation

Dag 5: MCMC techniques

Multi-Scale Modelling

Coordinators Roeland Merks (UL, CWI), Matthias Reuss (University of Stuttgart, DE)

Dates TBD (previous editions: 2012, 2013, 2014)

Venue TBA

Website TBA

Study load 3 EC

Description/Keywords

Connecting different aggregation levels, spatial models, patterning, tissue modelling, physiology-based PK/PD modelling.

Comparative Genomics: from Evolution to Function

Coordinators Berend Snel (UU), Martijn Huynen (Radboudumc), Jaap Heringa (VU)

Dates 2018 (previous editions: 2011, 2014, 2016)

Venue TBA

Website <http://biosb.nl/education/course-portfolio/course-comparative-genomics/>

Study load 3 EC

Description/Keywords

Comparative genomics between species and between types of data facilitates the understanding of what these data really reflect about the underlying biological processes. Comparative genomics therewith relies on a solid understanding of basic elements of Bioinformatics like homology and orthology. Moreover it is important to know the assumptions and heuristics of bioinformatic methods for comparative genomics and hence we aim to let participants develop an understanding of why these methods sometimes fail (or misdetect) as a consequence of a variety of biological /evolutionary causes, and in which situations which method is most appropriate. The first two days of the course provide a basis for the course with the aim to move “beyond blast” in terms of the most sensitive homology searches, domain level analysis of protein evolution as well as more fine grained definitions of relatedness as can be obtained from the proper interpretation of gene trees (i.e. various levels of orthology). This foundation is used to discuss in the three following days in more detail three topics: (1) the study of functional and evolutionary consequence of (genome) duplications, (2) the evolution of interactions and complexes and (3) the prediction and evolution of genomic regulatory elements and of RNA structures.

Protein Structures: Production, Prowess, Power, Promises, and Problems

Coordinators Gert Vriend (Radboudumc), Daniel Hoffmann (University Duisburg/Essen, DE)

Dates Oct 30 – Nov 3 2017 (previous editions: 2011, 2013, 2015)

Venue Nijmegen

Website <http://biosb.nl/education/course-portfolio/protein-structures-production-prowess-power-promises-and-problems/>

Study load 3 EC

Description/Keywords

In the right hands, protein structures are a 'power'ful tool to answer bio-molecular questions. Knowledge of the structure is a pre-requisite for rational drug design, for biotechnology, for chemical biology, and for answering a whole series of biomedical questions. In this course we will discuss the 'production' of protein structures by NMR, X-ray, and homology modelling. These methods all have their pro's and cons so a certain 'prowess' is needed to follow all 'promises' and start attacking bio-medical 'problems' using protein structures. The course is split in three parts:

Part 1) Looking and seeing things in protein structures, learning to operate the software, understanding some of the algorithms.

Part 2) Protein structure determination (prediction) with NMR, X-ray, and homology modelling, and the possibilities and problems that come with each of these three techniques.

Part 3) Applying all that was learned in real-life example studies.

Keywords: Protein structure visualisation, analysis and scientific application.

Algorithms for Biological Networks

Coordinators Jeroen de Ridder (UMCU), Dick de Ridder (WUR), Marcel Reinders (TUD)

Dates 2018 (previous editions: 2010, 2012, 2014, 2016)

Venue Delft

Website <http://biosb.nl/education/course-portfolio/course-algorithms-for-biological-networks>

Study load 3 EC

Description/Keywords

In this course, we will first give a brief overview of molecular biology, the advent of high-throughput measurement techniques and large databases containing biological knowledge, and the importance of networks to model all this. We will highlight a number of peculiar features of biological networks. Next, a number of basic network models (linear, Boolean, Bayesian) will be discussed, as well as methods of inferring these from observed measurement data. A number of alternative network models more suited for high-level simulation of cellular behaviour will also be introduced. Building on the network inference methods, a number of ways of integrating various data sources and databases to refine biological networks will be discussed, with specific attention to the use of sequence information to refine transcription regulation networks. Finally, we will give some examples of algorithms exploiting the networks found to learn about biology, specifically for inspecting protein interaction networks and for finding active sub networks.

Keywords: Properties of biological networks, Network inference, Alternative network models, Integrative bioinformatics, Network algorithms.

Quantitative and Predictive Modelling

Coordinators Jaap Molenaar (WUR), Natal van Riel (TUE)

Dates June 26-30 2017 (previous editions: 2015)

Venue Wageningen

Website <http://biosb.nl/education/course-portfolio-2/course-quantitative-and-predictive-modelling/>

Study load 3 EC

Description/Keywords

In this Quantitative and Predictive Modelling course the participants learn how to describe the dynamic behaviour of biological systems and to integrate experimental data. Concepts of modelling are introduced

via a great variety of examples taken from diverse practices. The emphasis is on providing an introduction into modelling approaches rather than an in-depth treatment of a few techniques. So, the course provides a broad overview of Modelling in the Life Sciences and is as such useful for a broad audience. The course is a mixture of theory sessions and computer practicals. During the practicals Matlab is used. Participants not acquainted with Matlab will get an introduction. The course has to be completed with assignments in the form of practical exercises as homework afterwards.

BioSB Specific courses

In the Specific courses track we identify two types of courses:

- Courses that occur regularly and have or have had several successive editions
- Courses that will occur or have occurred one time only or a few times in the past.

BioSB Specific Courses - regular courses with successive editions

In silico life: constraint-based modelling at genome scale

Coordinators Bas Teusink (VU), Brett Olivier (VU)

Dates 2018 (previous edition: 2016)

Venue Amsterdam

Website <http://biosb.nl/education/course-portfolio-2/course-constraint-based-modelling-course/>

Description/Keywords

Metabolic modelling, Genome-Scale Metabolic Models, flux balance analysis. Constraint-based modelling is a powerful modelling methodology that is being used to model a diverse range of biological phenomena. These include both fundamental and applied questions relevant to biotechnology, microbiology and medicine. Central to constraint-based modelling is the use of a genome-scale reconstructions (GSR's) that maps out the metabolism of a cell as a biochemical reaction network. In this course you will be introduced to: techniques for the construction of a working GSR: tools, tricks and pitfalls; the underlying mathematical definition and description of a constraint-based model; methods for interrogating models and interpreting results, such as Flux Balance Analysis and Flux Variability Analysis; software and standards

Metagenomics Applications and Data Analysis

Coordinators Sacha van Hijum (Radboudumc/NIZO), Bas Dutilh (UU). *For the 2017 edition, new coordinators will be identified.*

Dates 2017 (previous editions: 2013, 2014)

Venue TBA

Website <http://biosb.nl/education/course-portfolio/course-metagenomics-approaches-and-data-analysis>

Description/Keywords

This metagenomics course covers metagenomics and metatranscriptomics of prokaryotes, eukaryotes and viruses. Topics are metagenomics-specific issues like calling taxa, functional annotation, metagenome assembly, and comparative Metagenomics.

Metagenomes, environmental sequencing, functional profiling, next-generation sequencing, NGS, comparative metagenomics, bacterial genomics, microbial ecology, taxonomy.

RNA-seq data analysis

Coordinators Peter-Bram 't Hoen (LUMC), Jan Oosting (LUMC)

Dates 2017 (previous editions: 2011, 2012, 2013, 2014, 2015, 2016)

Venue Leiden

Website <http://biosb.nl/education/course-portfolio/rna-seq>

Description/Keywords

This is an advanced course for people with experience in NGS. The course will consist of seminars and hands-on command line, Galaxy and R practicals and will cover the analysis pipelines for differential transcript expression and variant calling. Examples will be taken from human and mouse studies. The course does not cover prokaryotic RNA profiling nor plant- and metagenomics aspects.

Course topics: RNA-seq experimental approaches, Alignment and de novo assembly, Statistics for differential gene expression, eQTL analysis and allele specific expression, Variant calling and RNA editing, Fusion transcript detection, Small RNA profiling, Software for RNA-seq data analysis.

NGS in DNA Diagnostics

Coordinators Jasper Saris (ErasmusMC), Christian Gilissen (Radboudumc), Rob van der Luijt (UMCU), Johan den Dunnen (LUMC)

Dates Sept 19-21 2017 (previous editions: 2014, 2015, 2016)

Venue Rotterdam

Website <http://biosb.nl/events/ngs-in-dna-diagnostics/>

Description/Keywords

VKGL/VKGN 'NGS in DNA diagnostics' is a course aimed at Genomic Resequencing in a Medical Diagnostic Context, i.e. to apply Next Generation Sequencing data as diagnostic tool in the hospital. Lectures will be accompanied with hands-on exploration. Day 1 consists of an introduction to NGS techniques followed by specialized lectures on sample preparation, enrichment technologies and read mapping.

Day 2 will continue with lectures on variant calling, annotation and interpretation with a diagnostic emphasis applied to Gene Capturing Panels, Exome Screening and CNV analysis. The afternoon of Day 1 & Day 2 is reserved for workshops and software demonstrations. Real data will be used where possible in hands-on tutorials using both commercial and open source software. Day 3 focuses on impact of results in the lab and ethical and legal issues of NGS in the clinical application. Real-life applications of NGS in the clinic will be presented. A forum discussion between researchers and clinicians about mutual expectations, ethics, implications of NGS on diagnostics and data sharing concludes the day.

Next Generation Sequencing Data Analysis

Coordinators Jeroen Laros (LUMC), Wilfred van IJcken (ErasmusMC), Judith Boer (ErasmusMC), Johan den Dunnen (LUMC)

Dates 2017 (previous editions: 10 times during 2009-2016)

Venue Leiden

Website <http://biosb.nl/events/course-next-generation-sequencing-ngs-data-analysis/>

Description/Keywords

This course aims at PhD students, postdocs, and senior researchers who are interested in, planning, or already working with next-generation sequencing. We welcome researchers from both the genomics and bioinformatics fields. Currently available technologies as well as hardware and software solutions will be presented and discussed. The focus of the course will be on the data and ways to analyse these.

Life Sciences with Industry

Coordinators Roel van Driel (UvA), Gökhan Ertaylan (Maastricht University), Ellen Feddes (STW), Bas Teusink (UVA),

Dates April 3-7 2017 (previous editions: 2013, 2014, 2015)

Venue Oord Building, Lorentz Centre, Niels Bohrweg 2, 2333CA Leiden

Website <http://biosb.nl/events/life-sciences-with-industry-2017/>

Description/Keywords

Challenging R&D problems, formulated by (Dutch) life sciences companies, will be tackled by young researchers. They are expected to find creative solutions to real-life problems. Each R&D problem will be tackled by a group of eight young scientists, supported by a senior researcher from academia or industry. On the last day, each group will present their solution of the problem that was tackled. Participants are expected to make new contacts and develop future job perspectives. Participants are PhD students and postdocs.

Systems Medicine: Modelling epigenetics

Coordinators Hans Westerhoff (UvA/VU), Barbara Bakker (UMCG/RUG) *[in collaboration with ISBE-NL]*
Dates TBA (previous editions: 2012, 2013, 2014, 2015, 2016)
Venue Amsterdam
Website <http://biosb.nl/education/course-portfolio-2/course-systems-medicine/>
Study load tbd

Description/Keywords

Metabolic syndrome, Multiscale modelling, Cancer modelling, Next generation sequencing, PK/PD modelling, personalised medicine based on genome wide maps and systems biology.

Python for Life Scientists

Coordinators Nicola Bonzanni (ENPICOM)
Dates TBA (previous editions: two times in 2016)
Venue Amsterdam
Website <http://biosb.nl/events/python-for-life-scientists-2/>

Description/Keywords

Tailored for life scientists with little or no prior programming experience, this course, organized by ENPICOM, is driven by real-life use cases. Participants will learn by doing, completing snippets of code that they will be able to reuse in their everyday tasks. Extensive use of IPython Notebook (Jupyter) will encourage to annotate and document the code, building the basis for sound and reproducible data analysis.

BioSB Specific Courses - One time only and/or limited number of editions

Exploring System Properties Using Various Modelling Approaches

Coordinators Jaap Molenaar (WUR), Christian Fleck (WUR)
Dates TBA (previous editions: none)
Venue Wageningen

Description/Keywords

In this course the most common modelling approaches are dealt with in more detail via realistic examples. At the same time the strong relation between the experimental limitations and the choice of modelling approach is dealt with. Metabolic, regulatory, signalling, population models are put in ODE form and analysed via steady states, stability, phase plane analysis, tipping points, etc.. It is discussed when stochasticity is important and how it can be included in a model. Experimental design and data integration are introduced. The concepts of multi-scale modelling are introduced.

ODE models for metabolic, regulatory, signalling, population, and ecological processes, experimental design, data-integration, stochastic modelling, stochastic effects.

Data Integration in the Life Sciences

Coordinators Roel van Driel (UvA), Jaap Molenaar (WUR), Lodewyk Wessels (NKI, TUD), Hans Westerhoff (UvA/VU)
Dates 2015 February 02-06 (previous editions: none)
Venue Snellius Building, Lorentz Centre, Niels Bohrweg 1, 2333CA Leiden
Website <http://biosb.nl/events/training-course-data-integration-in-the-life-sciences/>

Description/Keywords

Biological systems function through the dynamic interplay of large numbers of components. At the molecular level these include genes, transcripts, proteins and metabolites. At higher organisational levels the main players are cells, tissues, organs and organisms. Understanding biological systems, for instance in the context of biomedical and industrial applications, requires combining multiple diverse data sets on all components and their interactions. This integration process is hampered by the fact that in modern data acquisition technologies each concentrates on one specific component of the system, e.g. a specific type of

molecule. Proteomics, metabolomics and transcriptomics are examples. To overcome this hurdle novel approaches are being developed, enabling the integration of disparate data sets in ways that are biologically sound and that provide insight into the architecture and dynamics of biological systems. The basic concept in this course is that diverse data sets can be integrated in predictive and quantitative computational models. Depending on the types of data and the research aim, optimal integration and modelling approaches must be selected. This training course is meant for PhD students and postdocs. It is organised in collaboration with ERASysAPP (www.erasysapp.eu).

Biological Network Analysis

Coordinators Christian Rausch (VUmc), Gunnar Klau (VU & CWI), Martina Kutmon (Maastricht University)

Dates 2015 September 17-18 (previous editions none)

Venue Amsterdam

Website <http://biosb.nl/events/biosb-course-biological-network-analysis/>

Description/Keywords

The course will discuss the concepts of networks, and their application to biological examples like gene interaction networks, metabolic pathways, gene regulation- and signal transduction pathways. We will introduce the graphical programs PathVisio and Cytoscape and use it in the practical training for data visualization and analysis. We will use pathways from public resources like WikiPathways to create pathway visualizations and analyze experimental data. Furthermore, we will analyze differential gene expression data and will identify the affected metabolic (sub)pathways (KEGG/ gene ontology).

Advanced de novo assembly and resolving complex genomic regions

Coordinators Johan den Dunnen (LUMC), Yahya Anvar (LUMC)

Dates 2015 June 22-26 (previous edition: 2013)

Venue Leiden

Website <http://biosb.nl/education/course-portfolio-2/course-advanced-de-novo-assembly-2nd-edition/>

Description/Keywords

This course is targeted at PhD students and Postdocs in Life Sciences or Bioinformatics with basic knowledge of next-generation sequencing (NGS) technology and data analysis. This course covers topics on what every biologist should know about de novo assembly and study design, overview of available technologies and sampling strategies, methodologies and framework for de novo assembly (haploid and polyploid genomes), gap closure, quality assessment and functional annotation. In addition, we will showcase recent achievements, novel discoveries and current limitations in resolving complex genomes. The practical sessions are designed in such a way to promote lively discussions on how to design your study, the best practices, dos and don'ts, and provide you with an outlook on how to move from sequencing data to high-quality assembly and meaningful biological interpretation. After following this course, participants will gain insights on how to design a genome assembly study and will have an overview of challenges and various techniques to choose the most fitting strategy in order to produce a high-quality genome assembly.

EPS Postgraduate course 'Genome Assembly'

Coordinators Gabino Sanchez-Perez (WUR), Sandra Smit (WUR), Hendrik-Jan Megens (WUR), Jan van Haarst (WUR)

Dates TBA (previous edition: 2013, 2015)

Venue Wageningen

Website <http://biosb.nl/events/eps-postgraduate-course-genome-assembly-2nd-edition/>

Description/Keywords

The aim of this course is to teach PhD students in the green life sciences about the process of genome assembly and annotation. We will cover topics such as sequencing technologies, assembly algorithms, genome annotation, assembly improvements, and assembly validation. The focus is on the assembly of (complex) eukaryotic genomes. After attending this course, students should understand the main

sequencing technologies; understand which steps are involved in producing an annotated genome sequence; have an overview of relevant tools, or know where to find them; be able to understand genome papers (assembly terminology and common analyses); be able to do a small genome assembly using Galaxy.