

Project No. **222886-2**

MICROME

The MICROME Project:
A Knowledge-Based Bioinformatics Framework for Microbial Pathway Genomics

Instrument: **Collaborative project**

Thematic Priority: **KBBE-2007-3-2-08: BIO-INFORMATICS - Microbial genomics and bio-informatics**

D7.6 Third MICROME Training Course

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Organisation name of lead contractor for this deliverable: SIB

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Dissemination Level		
PU	Public	PU

Contributors

Lead: SIB

Organization: EBI & SIB

Staff initially involved in the DOW: SIB, CEA, EMBL-EBI

Additional staff involved in the jamboree annotation: CERTH, Isthmus, ULB

INTRODUCTION

Deliverable reference number:

D7.6 Third MICROME Training Course

Training in metabolism-related bioinformatics with specific sessions for curators and bioinformaticians

Methods

The goal of the training course was to educate life scientists and bioinformaticians in the use of methods for the development and refinement of genome scale metabolic models, with a particular focus on the tools and resources developed in the context of the Microme project. Specific sessions were provided for curators and bioinformaticians (databases, curation tools, analysis tools), over a 2-day period. The training course involved 24 participants from X countries.

The training course was organized by Paul Kersey (EMBL-EBI) and Anne Morgat (SIB Swiss Institute of Bioinformatics), and was held at the Hinxton Genome campus (UK) from October 8th to October 10th, 2013. The course was supported by the EMBL-EBI training facilities. Teaching materials and tutorial sessions (slides, tutorials, sample files) were contributed by six Microme partners (CEA, CERTH, EBI, Isthmus, SIB, ULB) as well as two external tutors:

- Marco Pagni & Mathias Ganter (SIB Swiss Institute of Bioinformatics, MetaNetX, a project of the Swiss SystemX.ch initiative)
- Hubert Denise (EBI Metagenomics)

All teaching materials (slides, tutorials) were made available through a Web site (<http://www.ebi.ac.uk/training/course/bacterial-genomics>), which remains available after the training.

Results (if applicable, interactions with other workpackages)

Overview

Next generation sequencing techniques have led to the deciphering of thousands of bacterial genomes, and the accumulation of a wealth of information about the diversity of natural enzymatic functions. Yet accessing and mining this data remains a difficult problem. In this course, partners from the Microme project, a collaborative European effort to improve resources for bacterial metabolism, taught in a number of practical workshop sessions aimed at guiding the participants through the complexities of networks of metabolites and biochemical pathways within the current knowledge.

Attendance

This course was aimed at biologists already working on bacterial genomes, annotation and metabolism who were embarking upon projects that aim to mine large datasets. This course did not require prior knowledge of methods for metabolic reconstruction.

Country	Participants
Belgium	4
France	1
Finland	1
Italy	2
Ireland	1
Egypt	1
Poland	2
Spain	2
The Netherlands	1
United Kingdom	10
Total	24

Gender	Participants
Female	12
Male	12
Total	24

Affiliation	Participants
Academic	22
Private company	2
Total	24

Most of the attendees came from academia, with two participants from biotech companies (UK, France).

Learning Objectives

After this course the attendees were expected to be able to...

- Access public bacterial genome data through interactive and programmatic interfaces with the Ensembl platform
- Explore metabolic data in different contexts using UniProt and UniPathway web sites
- Review genome annotation in a comparative framework using MicroScope
- Use the power of comparative analysis to complete our knowledge of metabolic pathways and their evolutionary history
- Perform automated metabolic reconstruction and pathway design

Programme

Time	Topic	Trainer
Day 1 - 8 October 2013		
12:30	Registration and Lunch	
13:30	<u>Introduction</u> General introduction biochemistry reminder and metabolic data reconciliation issue. Exploring bacterial metabolism with UniProt/UniPathway resources	Anne Morgat
15:30	Coffee break	
16:00	<u>Exploring bacterial genomes with Ensembl</u> <u>Reaction Matrix</u> <u>Programmatic Access to Ensembl Bacteria</u> <u>Practical - Browsing Genomes with Ensembl Bacteria</u>	Paul Kersey/Lee Falin/Dan Staines
18:00	Close of day	
19:00	Workshop Dinner - Wellcome Trust Conference Centre	
Day 2 - 9 October 2013		
09:00	MicroScope, a collaborative platform for genome annotation, comparative genomics and microbial diversity exploration <u>Part 1 - Part 1 Exercise</u> <u>Part 2 - Part 2 Exercise</u> <u>Part 3</u>	Eugeni Belda & Claudine Medigue François Lefevre & Damien Mornico
10:30	Coffee break	
10:45	Reconstruction and expert curation of genome-scale metabolic networks with MicroScope	Eugeni Belda & Claudine Medigue François Lefevre & Damien Mornico
12:15	Lunch	
13:15	<u>Genome Scale Metabolic Networks: reconstruction, properties and applications</u> <u>Stoichiometric and Constraint-based Modeling</u> <u>Tutorial</u>	Marco Pagni & Mathias Ganter
15:00	<u>Metabolic CAD / Bioretrosynthesis</u>	Pierre-Yves Bourguignon
16:00	Coffee break	
16:30	Predicting operons, regulons and metabolic pathways from bacterial genomes	Jacques van Helden
18:00	Close of day	
19:00	Workshop Dinner - Red Lion, Hinxton	

Day 3 - 10 October 2013

09:00	Metagenomics Tutorial	Peter Sterk/Alex Mitchell/Hubert Denise
10:30	Coffee break	
11:00	Comparative genomics of metabolic pathways and the computational inference of their ancestral states	Fotis Psomopoulos & Christos Ouzounis
12:45	Concluding remarks and feedback	Paul Kersey & Anne Morgat
13:00	Close of workshop and Lunch	

Perspectives

This third MICROME Training course served primarily to promote the resources and tools developed in Microme to potential users.