

start: **09:15**    end: **10:15**

Len: 00:60:00    id: 839

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A History of Bioinformatics (in the Year 2039)

C. Titus Brown

A History of Bioinformatics (in the Year 2039)

# C. Titus Brown

start: **10:45**    end: **11:03**

Len: 00:18:00    id: 839

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ADAM: Fast, Scalable Genomic Analysis

Frank Austin Nothhaft

ADAM: Fast, Scalable Genomic Analysis

# Frank Austin Nothhaft

start: **11:03**    end: **11:21**

Len: 00:18:00    id: 839

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Automated RNA-seq Differential Expression Validation

Rory Kirchner

Automated RNA-seq Differential Expression Validation

# Rory Kirchner

start: **11:21**    end: **11:39**

Len: 00:18:00    id: 839

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New Frontiers of Genome Assembly with SPAdes 3.1

Andrey Prjibelski

New Frontiers of Genome Assembly with SPAdes 3.1

# Andrey Prjibelski

start: **11:39**    end: **11:57**

Len: 00:18:00    id: 840

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SigSeeker: An Ensemble for Analysis of Epigenetic Data

Jens Lichtenberg

SigSeeker: An Ensemble for Analysis of Epigenetic Data

# Jens Lichtenberg

start: **11:57** end: **12:15**

Len: 00:18:00 id: 840

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Galaxy as an Extensible Job Execution Platform

John Chilton

Galaxy as an Extensible Job Execution Platform

# John Chilton

start: **12:15** end: **12:30**

Len: 00:15:00 id: 840

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Open Bioinformatics Foundation (OBF) update

Hilmar Lapp

Open Bioinformatics Foundation (OBF) update

# Hilmar Lapp

start: **13:00**    end: **13:05**

Len: 00:5:00

id: 843

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Connecting computational steps for NGS, and beyond.

Laurent Gautier

Connecting computational steps for NGS, and beyond.

# Laurent Gautier

start: **13:05**    end: **13:10**

Len: 00:5:00

id: 843

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Updates to MISO, the open-source NGS LIMS project

Xingdong Bian

Updates to MISO, the open-source NGS LIMS project

# Xingdong Bian

start: **13:10**    end: **13:15**

Len: 00:5:00

id: 843

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Running Taverna Workflows within IPython Notebook

Alan Williams / Aleksandra Pawlik (TBC)

# Running Taverna Workflows within IPython Notebook

Alan Williams / Aleksandra Pawlik (TBC)

start: **13:15**    end: **13:20**

Len: 00:5:00

id: 843

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Reconstruction of ancestral genomes in presence of gene gain and loss

Shuai Jiang

Reconstruction of ancestral genomes in presence of gene gain and loss

# Shuai Jiang

start: **13:20**

end: **13:25**

Len: 00:5:00

id: 843

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Firehose in The Cancer Genome Atlas: Rigorous Open Science, At Scale

Michael Noble

Firehose in The Cancer Genome Atlas: Rigorous Open Science, At Scale

# Michael Noble

start: **13:25**

end: **13:30**

Len: 00:5:00

id: 843

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GEPETTO Update: An Open Source Framework for Gene Prioritization

Hoan Nguyen

GEPETTO Update: An Open Source Framework for Gene Prioritization

# Hoan Nguyen

start: **13:30**end: **13:35**

Len: 00:5:00

id: 843

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NeoPipe: An Open Source Framework for Protein sequence analysis

Hoan Nguyen

NeoPipe: An Open Source Framework for Protein sequence analysis

# Hoan Nguyen

start: **13:35**

end: **13:40**

Len: 00:5:00

id: 843

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MyGene.info updates: scalable gene-centric web services with user contributions

Chunlei Wu

MyGene.info updates: scalable gene-centric web services with user contributio

# Chunlei Wu

start: **13:40**

end: **13:45**

Len: 00:5:00

id: 843

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Aiding the journey from data to publication in the plant sciences

Robert Davey

Aiding the journey from data to publication in the plant sciences

# Robert Davey

start: **13:55**    end: **14:00**

Len: 00:5:00

id: 843

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Bio2RDF mobile: an app for biological semantic web databases

Maxime Deraspe

Bio2RDF mobile: an app for biological semantic web databases

# Maxime Deraspe

Veyepar: TalkSigns.rfxml

start: **14:00**    end: **14:18**

Len: 00:18:00    id: 840

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WormGUIDES: an Interactive Informatic Developmental Atlas at Subcellular Resolution

Anthony Santella

WormGUIDES: an Interactive Informatic Developmental Atlas at Subcellular Resolution

# Anthony Santella

Veyepar: TalkSigns.rfxml

start: **14:18**    end: **14:36**

Len: 00:18:00    id: 840

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BioJS: an Open Source Standard for Biological Visualisation

Manuel Corpas

BioJS: an Open Source Standard for Biological Visualisation

# Manuel Corpas

start: **14:36**    end: **14:54**

Len: 00:18:00    id: 840

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Biodalliance: a Fast, Extensible Genome Browser

Thomas Down

Biodalliance: a Fast, Extensible Genome Browser

# Thomas Down

start: **14:54** end: **15:12**

Len: 00:18:00 id: 840

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TGAC Browser: Visualisation Solutions for Big Data in the Genomic Era

Anil S. Thanki

TGAC Browser: Visualisation Solutions for Big Data in the Genomic Era

# Anil S. Thanki

start: **15:12**    end: **15:30**

Len: 00:18:00    id: 840

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Explore, Analyze, and Share Genomic Data Using Integrated Genome Browser

Ann Loraine

Explore, Analyze, and Share Genomic Data Using Integrated Genome Browse

# Ann Loraine

start: **16:00**    end: **16:12**

Len: 00:12:00    id: 840

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BioMart 0.9 - Introducing Tools for Data Analysis and Visualisation

Luca Pandini

BioMart 0.9 - Introducing Tools for Data Analysis and Visualisation

# Luca Pandini

start: **16:12**    end: **16:24**

Len: 00:12:00    id: 840

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Biocaml: The OCaml Bioinformatics Library

Ashish Agarwal

Biocaml: The OCaml Bioinformatics Library

# Ashish Agarwal

start: **16:24**    end: **16:36**

Len: 00:12:00    id: 841

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BioRuby and Distributed Development

Pjotr Prins

BioRuby and Distributed Development

# Pjotr Prins

start: **16:36** end: **16:48**

Len: 00:12:00 id: 841

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Biopython Project Update

Wibowo Arindrarto

# Biopython Project Update

# Wibowo Arindrarto

start: **16:48** end: **17:00**

Len: 00:12:00 id: 841

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Shared Bioinformatics Database Within Unipro UGENE

Ivan Protsyuk

Shared Bioinformatics Database Within Unipro UGENE

# Ivan Protsyuk

start: **17:00**    end: **17:05**

Len: 00:5:00

id: 841

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Fostering the Next Generation of Data-driven Open Science with R

Karthik Ram

Fostering the Next Generation of Data-driven Open Science with R

# Karthik Ram

start: **17:07**    end: **17:12**    Len: 00:5:00    id: 844

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Tripal: an Open Source Toolkit for Building Genomic and Genetic Data Websites and Databases

Margaret Staton

Tripal: an Open Source Toolkit for Building Genomic and Genetic Data Websites

# Margaret Staton

start: **17:14** end: **17:19**

Len: 00:5:00

id: 841:

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PLUTo: Phyloinformatic Literature Unlocking Tools

Ross Mounce

PLUTo: Phyloinformatic Literature Unlocking Tools

# Ross Mounce

start: **17:21**

end: **17:26**

Len: 00:5:00

id: 841

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A Publication Model that Aligns with the Key Open Source Software Principles

Michael L. Markie

A Publication Model that Aligns with the Key Open Source Software Principles

# Michael L. Markie

start: 09:00

end: 09:15

Len: 00:15:00

id: 841

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Codefest 2014 Report

Brad Chapman

# Codefest 2014 Report

# Brad Chapman

start: **09:15**    end: **10:15**

Len: 00:60:00    id: 841

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Biomedical Research as an Open Digital Enterprise

Philip Bourne

Biomedical Research as an Open Digital Enterprise

# Philip Bourne

start: **10:45**    end: **11:03**    Len: 00:18:00    id: 841

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Pathview: an R/Bioconductor Package for Pathway-based Data Integration and Visualization

Weijun Luo

Pathview: an R/Bioconductor Package for Pathway-based Data Integration and

# Weijun Luo

start: **11:03**

end: **11:21**

Len: 00:18:00

id: 842

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Use of Semantically Annotated Resources in the Moby2 Web Framework

Hervé Ménager

Use of Semantically Annotated Resources in the Moby2 Web Framework

# Hervé Ménager

start: 11:21

end: 11:39

Len: 00:18:00 id: 842

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Towards Ubiquitous OWL Computing: Simplifying Programmatic Authoring of and Querying with OWL Axioms

Hilmar Lapp

Towards Ubiquitous OWL Computing: Simplifying Programmatic Authoring of a

# Hilmar Lapp

start: **11:39** end: **11:57**

Len: 00:18:00 id: 842

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Integrating Taverna Player into Scratchpads

Robert Haines

Integrating Taverna Player into Scratchpads

# Robert Haines

start: **11:57** end: **12:15**

Len: 00:18:00 id: 842

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Small Tools for Bioinformatics

Pjotr Prins

## Small Tools for Bioinformatics

# Pjotr Prins

start: **13:00**    end: **13:05**    Len: 00:5:00    id: 844

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Tripal: an open source toolkit for building genomic and genetic data websites and databases

Margaret Staton

Tripal: an open source toolkit for building genomic and genetic data websites a

# Margaret Staton

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Tripal: an open source toolkit for building genomic and genetic data websites and databases

Margaret Staton

Tripal: an open source toolkit for building genomic and genetic data websites a

# Margaret Staton

start: **13:05**

end: **13:10**

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id: 844

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BioBuilds: A Model for Long Term Sustainability of Open Source Bioinformatics

Chris Mueller

BioBuilds: A Model for Long Term Sustainability of Open Source Bioinformatics

# Chris Mueller

start: **14:00**    end: **14:18**

Len: 00:18:00    id: 842

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SEEK for Science: A Data Management Platform which Supports Open and Reproducible Science

Carole Goble

SEEK for Science: A Data Management Platform which Supports Open and Re

# Carole Goble

start: **14:18**    end: **14:36**

Len: 00:18:00    id: 842

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Arvados: Achieving Computational Reproducibility and Data Provenance in Large-Scale Genomic Analyses

Brett Smith

Arvados: Achieving Computational Reproducibility and Data Provenance in Lai

# Brett Smith

start: **14:36**

end: **14:54**

Len: 00:18:00

id: 842

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Enhancing the Galaxy Experience through Community Involvement

Daniel Blankenberg

Enhancing the Galaxy Experience through Community Involvement

# Daniel Blankenberg

start: **14:54** end: **15:12**

Len: 00:18:00 id: 842

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Supporting Dynamic Community Developed Biological Pipelines

Brad Chapman

Supporting Dynamic Community Developed Biological Pipelines

# Brad Chapman

start: **15:12**    end: **15:30**

Len: 00:18:00    id: 842

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'Open' as a Strategy for Durability, Reproducibility and Scalability

Jonathan Rees

'Open' as a Strategy for Durability, Reproducibility and Scalability

# Jonathan Rees

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Panel : Reproducibility: Rewards and Challenges

Phil Bourne, Titus Brown, Varsha Khodiyar, Kaitlin Thaney

Panel : Reproducibility: Rewards and Challenges

Phil Bourne, Titus Brown, Varsha Khodiyar, Kaitlin Thaney■