

GALAXY IN SKIN SCIENCES RESEARCH/ TRAINING / ELIXIR-CNV COMMUNITY

Krzysztof Poterlowicz

Centre for Skin Sciences, Bradford UK

@bioinfbrad

Summary

- Galaxy in Skin Sciences Research
- Usegalaxy.eu TlaaS /BCB Master programme
- Elxir CNV community update

Centre for Skin Sciences (CSS)

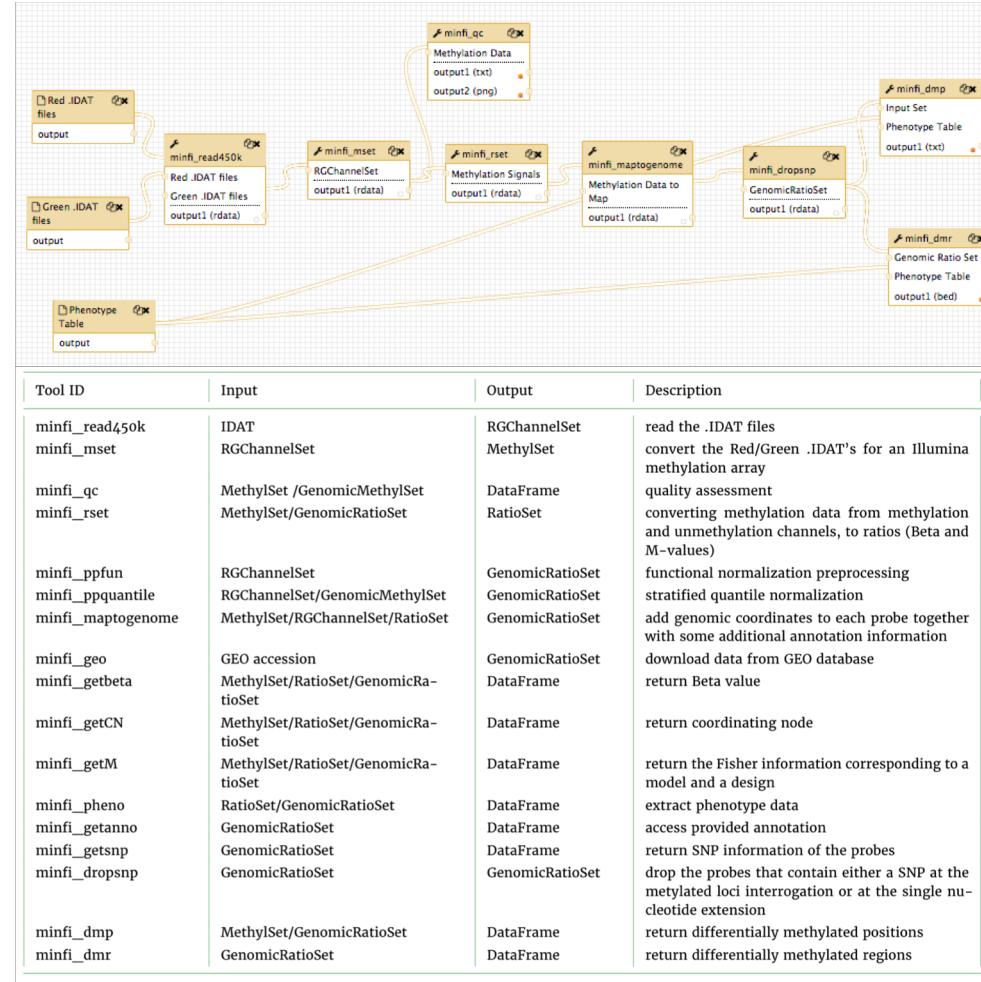


Galaxy in CSS research

- small local server available for CSS lab's members <https://goo.gl/ffv23p>
- also on-demand AWS based instances available
- used for research of:
 - epigenetics and transcriptomics of skin development, regeneration and disorders (mainly)
 - Genetics of skin disorders (i.e Lupus)
 - would like to use for burn image clustering but collaborators use Matlab
- Over the years CSS generated large number of skin i.e (Rna-Seq, ChIP-seq, 4C, 5C, imaging: immunocytochemistry and immunohistochemistry, burns, DNA and RNA fish), just acquired internal funds for systemization of these data (skin research public galaxy instance)

Epigenetic-Wide Association Studies Analysis in Galaxy (EWAS_Galaxy Suite)

- EWAS analyse genome-wide activity of epigenetic marks in different individuals
- aim to find associations between epigenetic variation and phenotype.
- With its high accuracy and low input DNA requirements, the Illumina 450k Methylation one of the most comprehensive EWAS study solutions.
- Existing software not user friendly



github.com/kpbioteam

EWAS data analysis of 450k data

Overview

- What is a epigenome-wide association studies?
- Why is a EWAS analysis useful?
- Why 450k data?

Objectives

- Learn how to perform reproducible EWAS analysis

Requirements

- Galaxy introduction
- Quality control
- Mapping

Introduction

The field of cancer genomics has demonstrated the power of massively parallel sequencing techniques to inform on the genes and specific alterations that drive tumor onset and progression. Although large comprehensive sequence data sets continue to be made increasingly available, data analysis remains an ongoing challenge, particularly for laboratories lacking dedicated resources and bioinformatics expertise. To address this, we have provide training based on Galaxy tools ewas suite that represent many popular algorithms for detecting somatic genetic alterations from cancer genome and exome data.

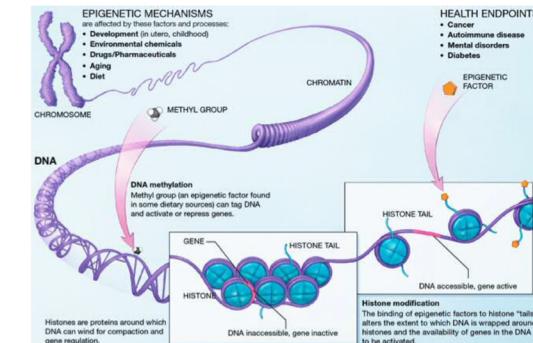


Figure 1: How epigenetics mechanism can effect health (adapted from <https://commonfund.nih.gov/epigenomics/figure>)

galaxyproject.github.io/training-material/topics/epigenetics/tutorials/ewas-suite/tutorial.html

Usegalaxy.eu TlaaS / BCB Master Programme

Find A Masters > Masters Courses > Search Masters Degrees

Bioinformatics and Computational Biosciences - MSc •

 University of Bradford > Faculty of Life Sciences
 Bradford > United Kingdom

[Email Now](#) > [Visit Website](#) >

Course content

Bioinformatics is a branch of the life sciences that focus on analysing and integrating big data acquired in biomedical experimentation.

Over the last couple of years 'omics' technologies have transformed healthcare practice, biomedical research and industry, and there is a shortage of biomedical graduates with bioinformatics training in the advanced healthcare sector.

Our programme will provide

[Read More...](#)



UNIVERSITY of
BRADFORD

Study Type
Full time available

Subject Areas
Biological Sciences

Start Date
September

Galaxy Freiburg
Team
Thank you !

Principles of Bioinformatics

Module code: BIS7017-B

Module Aims

To provide a comprehensive understanding of bioinformatics and its application to Biology. To develop student autonomy in the use of web-based platforms for analysing and annotating biomedical big data.

Outline Syllabus

Data standards and formats in bioinformatics Galaxy workbench and its application in biomedical sciences, Galaxy workflows, tools and histories, quality control analysis, analysis of RNA sequencing data, analysis of ChIP-Seq data, identification of the genetic variation using the exome sequencing, transcriptomics, background and application of specialist databases and genome browsers.

ELIXIR-CNV COMMUNITY (IN DEVELOPMENT)

- Kick off meeting in September 2018, Hinxton
- Define optimal CNV detection pipelines
- Create reference datasets
- Define a data exchange format to allow comparison of NGS data
- Develop and provide access to innovative bioinformatics tools to target potential disease-causing genes
- Galaxy for interoperability of tools and training

CSS,UoB

Dr J Boyne

Dr N Botchkareva

Prof V Botchkarev

Dr M Fessing

Dr I Malashchuk

Dr A Mardaryev

Dr G Westgate

Prof D Tobin

Thank you !

Future Galaxy community plans

- epigenetics.usegalaxy.eu ??

My small lab:

- K Murat
- Dr K Smith
- L Bytie
- K Agyeman