

Sharing code, figures and tables in the laboratory ...

... using GitHub



Sergio Martínez Cuesta

Overview

- The laboratories and context
- The past: Redmine
- The present: GitHub
 - ✓ Structure
 - ✓ Case study: The glioblastoma project

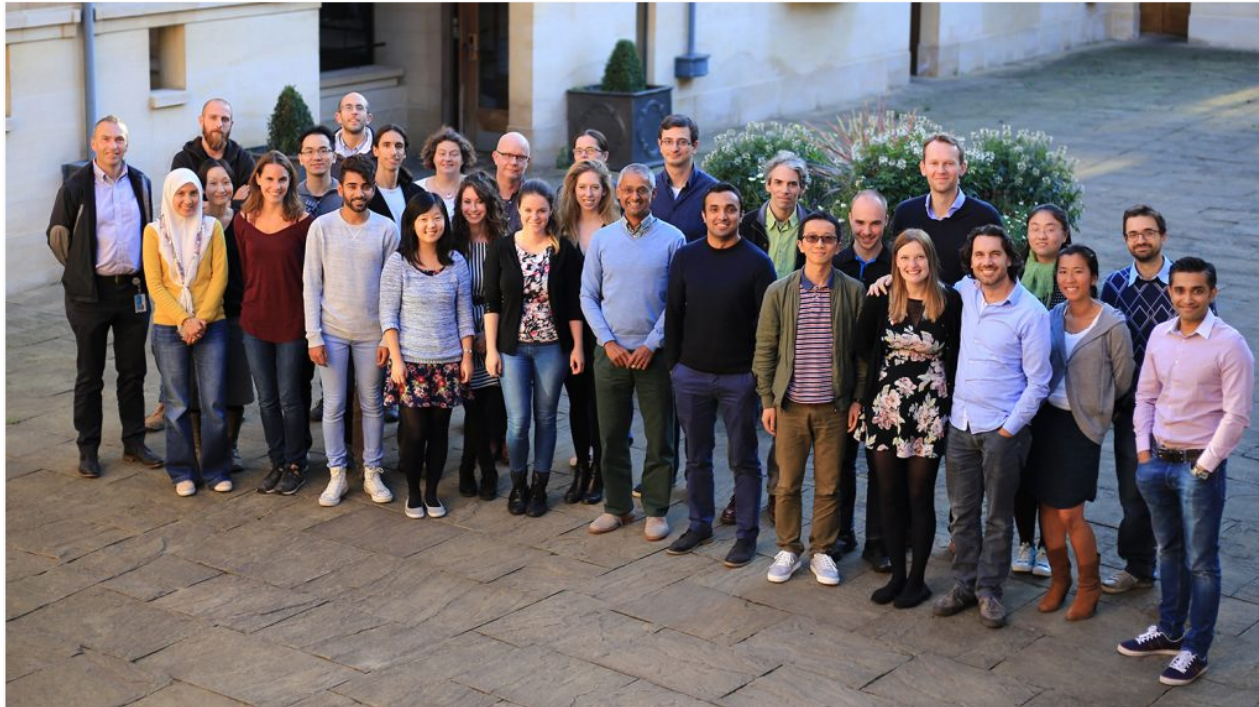
Materials available at ...



<https://github.com/semacu/talks>
folder:
20170703_GitHubintheLab_CRUK-CI/

The laboratories

The Balasubramanian group



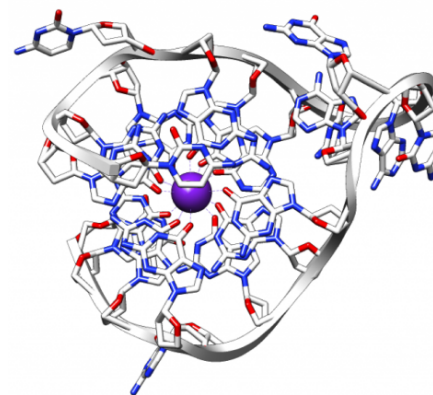
The laboratories

Nucleotide modifications

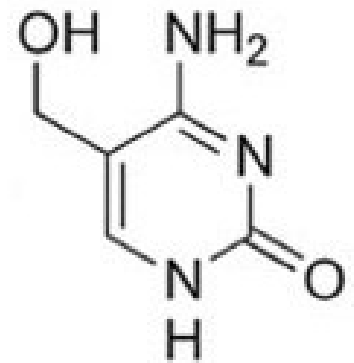
- Mapping modified bases (e.g. 5hmC and 5fC) in genomes and transcriptomes
- Quantifying abundances using mass spectrometry
- Chemical synthesis

G-quadruplexes

- Mapping in DNA and RNA
- Biophysical characterization
- Drug discovery



G4



5hmC

The context

- Most projects have both an experimental and a computational leader
- Classical ways of sharing:



The needs

We strive for an environment where:

Computational colleagues can ...

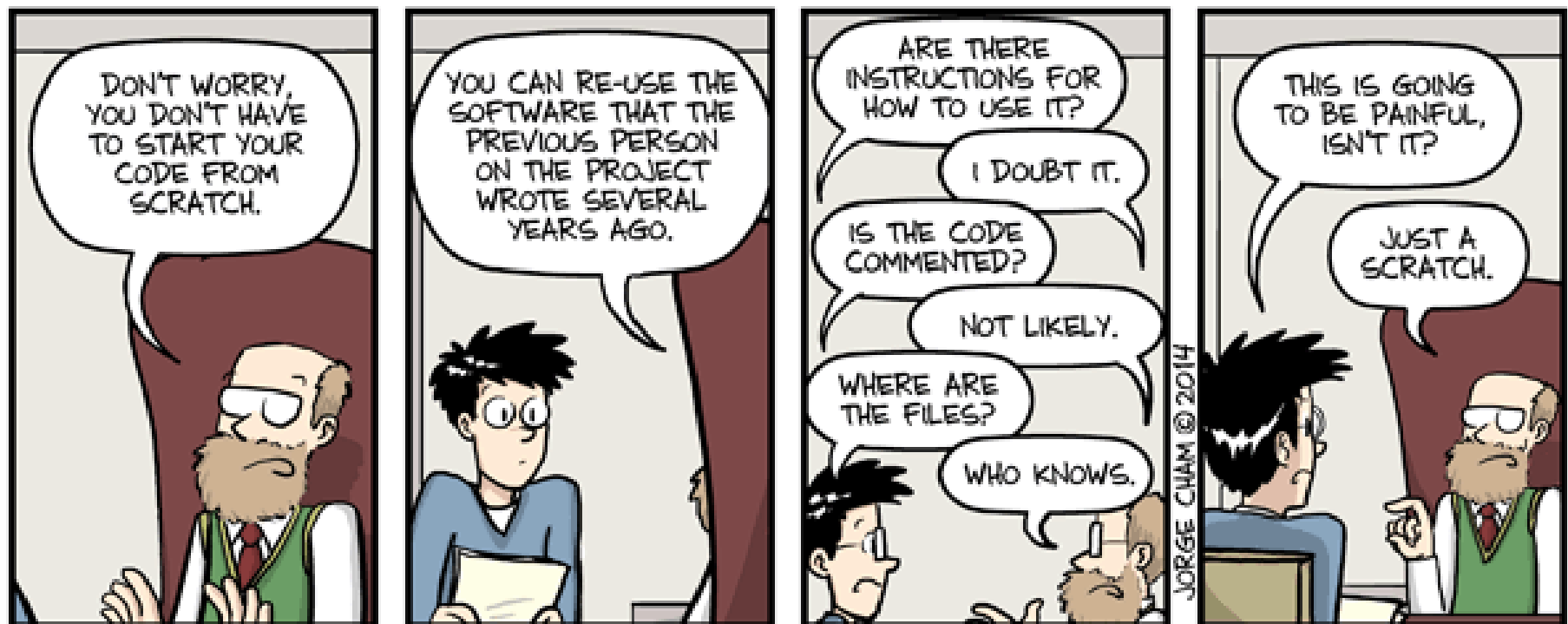
- ... share code and results
- ... review work
- ... get credit for the collaborative project work

Experimental colleagues can ...

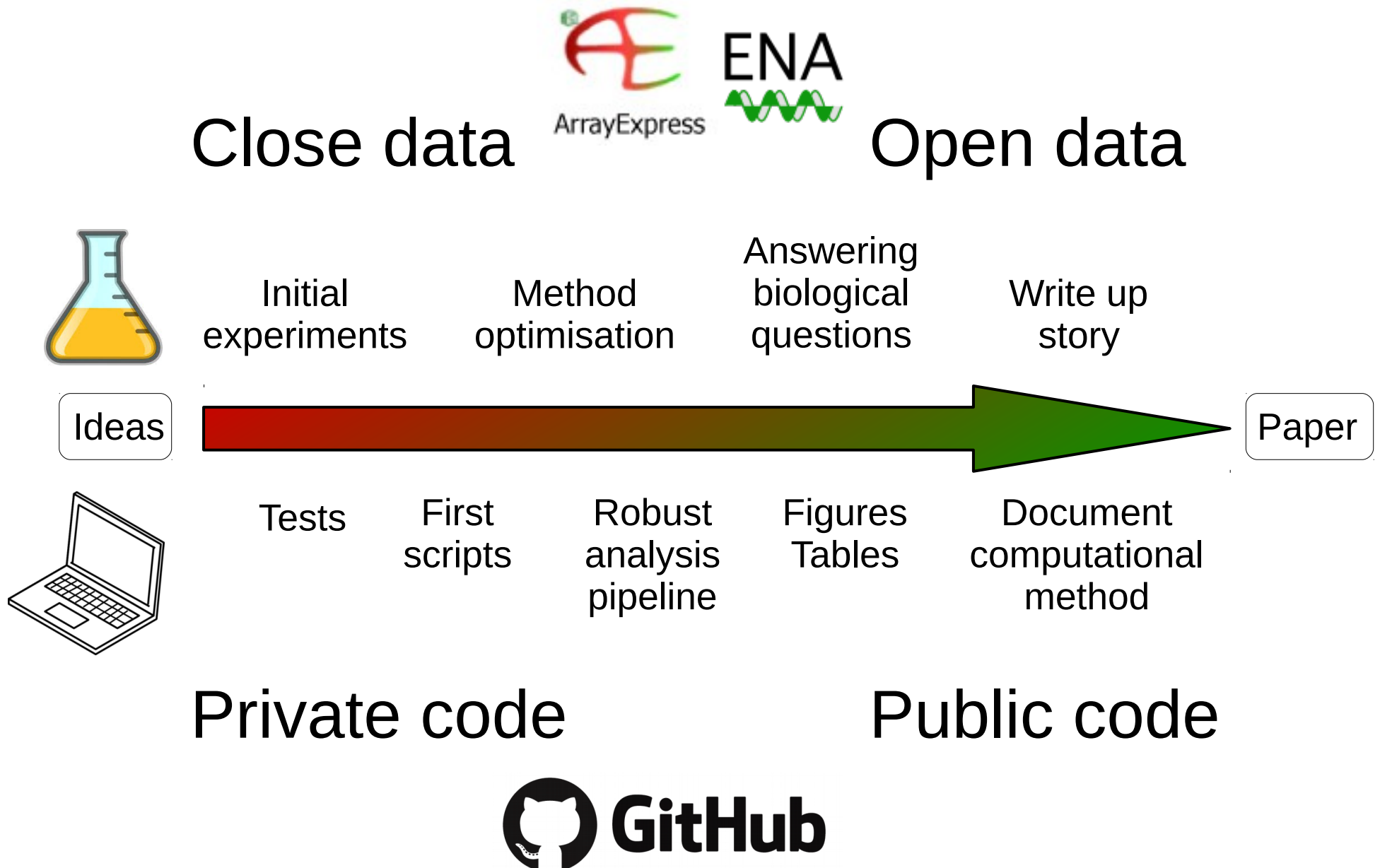
- ... follow development
- ... access results
- ... learn computational methods

The needs

Reproducibility



Project timeline



The past: Redmine

The screenshot shows the Redmine web application interface. At the top is a browser window with the address bar showing '10.20.192.25:3000/projects?utf8=✓&closed=1'. Below the browser window is the Redmine header with navigation links: Home, Projects, Help. On the right of the header are links for Sign in and Register. The main content area is titled 'Redmine @ sblab' and features a search bar. Below this, there is a 'Projects' section with a list of project entries. Each entry includes a date, a project title, and a brief description. The right sidebar contains a 'Projects' section with a checkbox for 'View closed projects' and an 'Apply' button.

10.20.192.25:3000/projects?utf8=✓&closed=1

110%

Search

Most Visited NBIS Sweden Biostars jobs Wolfson College ...

Home Projects Help Sign in Register

Redmine @ sblab Search:

Projects View all issues | Overall spent time | Overall activity

01-05-2015 Methylation in brain
Tumor brain project in collaboration with Illumina

09-03-2015 Gordon redBS mESC
Sequencing of 5fC candidate sites via redBS. Sites identified by pull down.

20-08-2015 Tobi cisplatin
Mapping of cisplatin binding in the genome via pull down enrichment and sequencing

2013_10_29_Vicki_stop-assay

20150820 - Shiqing - Duplex Sequencing
Kennedy2015 Nature Protocol by Shiqing
<http://www.nature.com/nprot/journal/v9/n11/full/nprot.2014.170.html>

Single Cell Methylome
Analysis the single cell methylome data, try to link up methylation profile on both strands

scRRBS
[[<http://genome.cshlp.org/content/23/12/2126.full>]]
[[<http://www.nature.com/nprot/journal/v10/n5/full/nprot.2015.039.html>]]

scBS (Wolf Reik)
[[<http://www.nature.com/nmeth/journal/v11/n8/full/nmeth.3035.html>]]...

20150929 - Barbara - Domains
Obtain uniprot and pfam domains for list of uniprot ids interacting with RNA G4

Projects

☒ View closed projects

Apply

The past: Redmine

 Open source

 Accessibility

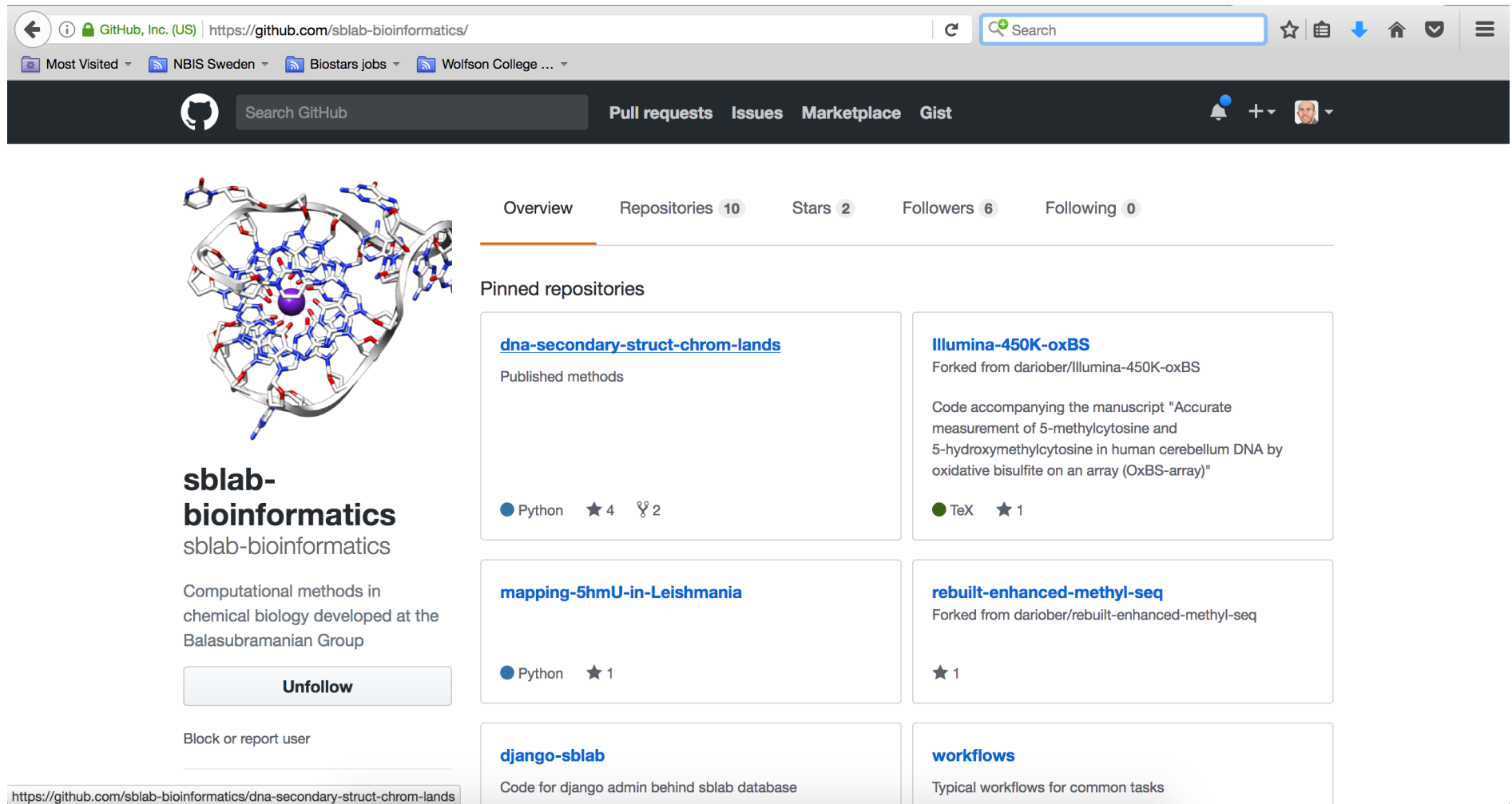
 Multiple projects

 Version control

 Documentation
and wikis

 Discontinued
Feb 2015

The present: GitHub



The screenshot shows the GitHub profile page for the user **sblab-bioinformatics**. The browser address bar shows the URL `https://github.com/sblab-bioinformatics/`. The GitHub navigation bar includes a search bar, links for Pull requests, Issues, Marketplace, and Gist, and a user profile icon.

sblab-bioinformatics
sblab-bioinformatics

Computational methods in chemical biology developed at the Balasubramanian Group

Unfollow

Block or report user

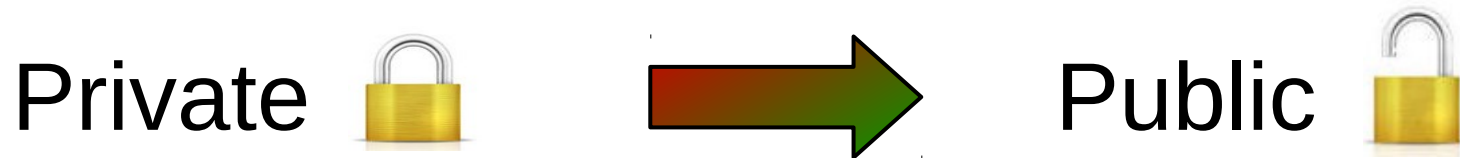
Overview Repositories **10** Stars **2** Followers **6** Following **0**

Pinned repositories

- [dna-secondary-struct-chrom-lands](#)**
Published methods
Python ★ 4 🍴 2
- [Illumina-450K-oxBS](#)**
Forked from dariober/Illumina-450K-oxBS
Code accompanying the manuscript "Accurate measurement of 5-methylcytosine and 5-hydroxymethylcytosine in human cerebellum DNA by oxidative bisulfite on an array (OxBS-array)"
TeX ★ 1
- [mapping-5hmU-in-Leishmania](#)**
Python ★ 1
- [rebuilt-enhanced-methyl-seq](#)**
Forked from dariober/rebuilt-enhanced-methyl-seq
★ 1
- [django-sblab](#)**
Code for django admin behind sblab database
- [workflows](#)**
Typical workflows for common tasks

`https://github.com/sblab-bioinformatics/dna-secondary-struct-chrom-lands`

Structure



/projects/20150501_methylation_brain

/epigenetics-of-glioblastoma

/projects/FAIRE-seq_Robert

/dna-secondary-struct-chrom-lands

Early stages

Pre/post-publication stage

Documentation ...



Structure

{ Contributors: computational colleagues
{ Collaborators: computational and experimental colleagues

Costs ...

sbilab-bioinformatics developer plan

- private (\$) and public (free) repositories
- USD \$7 / month

<https://github.com/pricing>

Case study: The glioblastoma project

Early 2014:

- Investigate relationship between nucleotide modifications (5mC and 5hmC) and genomic variation in human glioblastoma samples
- Collaboration with neurosurgeons (Addenbrooke's) and Illumina

2014 – 2016: development

- In *projects/* private repository

Feb – Oct 2016: pre-publication

- In *epigenetics-of-glioblastoma/* private repository

Case study: The glioblastoma project

Oct 2016: submission

- *epigenetics-of-glioblastoma/* goes public

March 2017: published

BRIEF COMMUNICATION **OPEN**

Base resolution maps reveal the importance of
5-hydroxymethylcytosine in a human glioblastoma

Eun-Ang Raiber¹, Dario Beraldi¹, Sergio Martínez Cuesta¹, Gordon R. McInroy², Zoya Kingsbury³, Jennifer Becq³, Terena James³, Margarida Lopes³, Kieren Allinson⁴, Sarah Field¹, Sean Humphray³, Thomas Santarius⁵, Colin Watts⁵, David Bentley³ and Shankar Balasubramanian^{1,2,6}

2017: post-publication

- continue development of public *epigenetics-of-glioblastoma/*

Future?

Thanks!

Acknowledgements

The Balasubramanian group

Dario Beraldi