

The Benefits of an Open-Science Approach in Student Research Projects

Emma MacKenzie, Sophie Winterbourne, Edward Wallace, Flic Anderson @ Edinburgh Open Research Conference

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Why we're here...

Co-authored an article in The Biochemist:

The benefits of an open-science approach in student research projects (2021) <u>https://doi.org/10.1042/bio_2021_198</u>





Movement to allow scientific information, data and outputs to be more widely accessible and reusable. This includes within research groups, where participants share their data, analysis code, ideas and feedback.

riboviz



riboviz is open source software which processes & analyses ribosome profiling (sequencing) data



Developed from 1.0 to 2.0 in collaborative project BBSRC-NSF funded project - working with experts in UK & USA



Aims: use **software engineering** techniques to create more **robust** & **reliable** code -> *more researcher time for biological questions*



Ribosome profiling data helps unlock details of translation: how the cell creates proteins from genetic code (DNA, RNA)



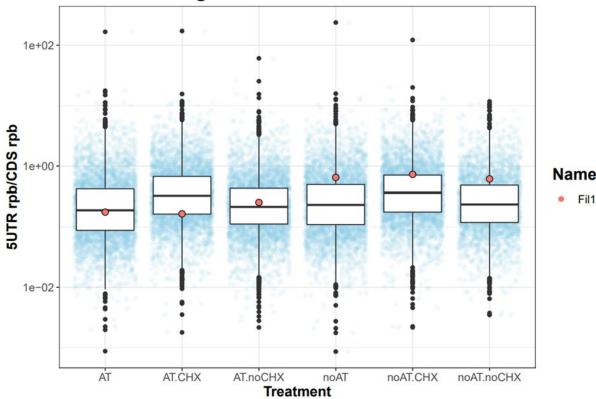
riboviz helps researchers check **quality control** & understand the **characteristics** of the experimental data - ie. do different experimental conditions change how the cell translates proteins from genes?



riboviz 2.0 publication: <u>https://doi.org/10.1093/bioinformatics/btac093</u> (2021) Bioinformatics riboviz on GitHub: <u>https://github.com/riboviz/riboviz</u>

Student Project Background

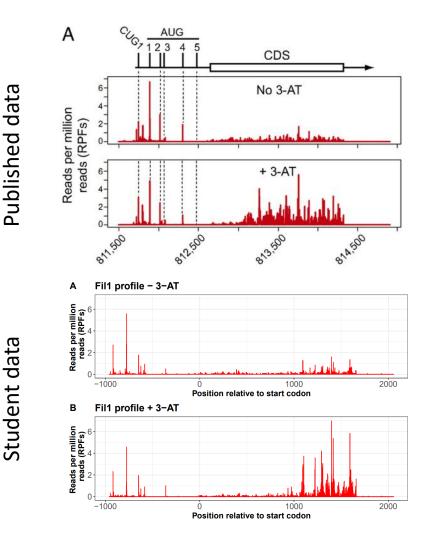
- Wallace lab uses riboviz to analyse translation dynamics in fungal datasets
- Several successful student projects so far using riboviz!
- 2(+) heads are better than one:
 similar projects = peer learning!
- Adjusting scopes as we gain more experience in successful open (software) projects.



5UTR:CDS usage in different conditions

Thesis image. Data reanalysed from Duncan et al. 2018. <u>https://www.pnas.org/doi/full/10.1073/pnas.1713991115</u>

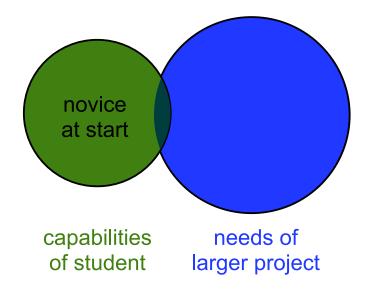
What Makes a Good Student Project?



- Recreating published results works well
- Adding new features to the codebase to address specific research questions
- Comparing datasets from different organisms
- Developing new visualizations to explore data
- Getting credit is important: all previous students co-authored riboviz 2 publication for contributing to the software

Published data from Duncan et al. 2018 – figure 5. https://www.pnas.org/doi/full/10.1073/pnas.1713991115

Student Skills & Project Requirements (At Kickoff)



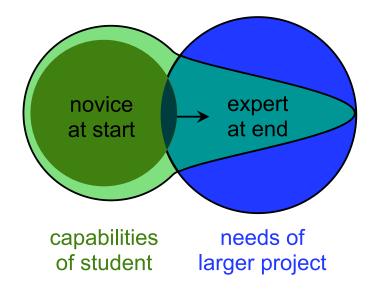
- Students are **expert novices** let them identify and combat your 'expert blind-spots'!
- They have time and motivation to contribute to code, documentation and publications (and get credit for these!)
- Overlapping goals: aim for a project where project tasks help progress lab goals
- Plan a structured pathway from novice to expert for students, using authentic research tasks...

Structured Skills Pathway: Bioinformatics Example

Skill Level	Example Student Task	Learning / Skills Gained
Novice	Installing riboviz software and running built-in 'vignette' small test dataset	Installation, setup, understanding output files, troubleshooting
Confident Beginner	Run existing full-size example dataset & improve documentation as needed	Data size problems, navigating directory structures, contributing to documentation
Competent Practitioner	Analyse a published dataset from an existing annotation (organism-specific files already exist)	Learning about adapter removal in sequencing data, other common bioinformatics tasks
Expert	Identify, adapt and run a new dataset with a new genome annotation (create new organism-specific files)	Tricky task with organism-specific quirks, potential data availability or format issues

Gradually builds skills, confidence and understanding needed to successfully undertake expert-level tasks

Student Skills & Project Requirements (By Wrap-Up)



• Student has expanded their capabilities generally...

- ... and is expert in their specific project skills!
- Student project has contributed significantly to overall project needs (Happy PI time!)

 'Open science' project has contributed to lab culture (e.g. skill-sharing, demonstrating new tools, encouraging asking for help when stuck)

Open Tools Help Develop Experts: Invest Early!

ΤοοΙ	What's It Good For?	
Hackathons	Build momentum, progress leaps	
Stand-ups (daily update)	Check-ins & day-to-day planning	
Slack (chat-like service)	Informal discussion, questions, sharing successes	
Videocall Supervision Meetings	Review progress, in-depth explanations, code demos, troubleshooting, pair-programming	
Open Documentation & Courses	Accessible any time, pro-active solution-finding and learning (e.g. Carpentries courses, lab guides, documentation)	
Git (version control)	Developing & managing code, pinging scripts back and forth for checking, testing, review, traceability	
Issue Tickets @ GitHub	Assigning/investigating issues, asking questions	
Kanban Boards @ GitHub	Prioritising/managing project tasks & tracking progress	

Professional Skills: Day-To-Day Supervisor

- Develop teaching/supervisory skills while progressing my work; students bring new insights & overlapping goals
- Open Tools are great supervision tools easily track what students are working on / stuck with, train and support progress
- Working in (temporarily) larger team, improve my collaboration and 'open science' skills
- Visible skills my commits / comments are visible to future employers or collaborators!
- **Communication**: publications, posters, lab meetings, presentations...

'Open' Mindset: Day-To-Day Supervisor

- Keeping an 'Open' Mind:
 - Visibly & frequently ask questions & seek help
 - Sharing ideas: less reluctant to put own ideas forward
 - Errors showing/explaining avoids reoffending
- Stand-ups for research: sharing priorities, achievements and problems helps project planning, brings support
- Open & inclusive lab culture –

cooperative, welcoming and positive environment encourages academic and personal growth

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# 'Open' Mindset: Student's View

- New and scary
- Uncomfortable admitting mistakes and seeking help
- Only markers saw our work in previous assignments
- Errors or unexpected results were not exciting due to expected outcomes in lab work
- Had to **develop** over the project
- Development is clear in how we communicated problems



### Before 'Open' Mindset

- Confusing screenshots
- Sent over Slack so not accessible to others
- Only providing useful information when prompted
- Difficult to identify problem and the solution
- Does not provide long term documentation of error and solution

```
ss samples
    sample logs dir, run config)
  File "/home/sophie/riboviz/riboviz/tools/prep riboviz.py", line 302, in proce
ss sample
    run confia)
  File "/home/sophie/riboviz/riboviz/workflow.py", line 155, in cut adapters
    run config.is dry run)
  File "/home/sophie/riboviz/riboviz/process_utils.py", line 130, in run_logged
 command
    run command(cmd, f, f)
  File "/home/sophie/riboviz/riboviz/process utils.py", line 22, in run command
    assert exit_code == 0, "%s failed with exit code %d" % (cmd, exit_code)
AssertionError: ['cutadapt', '--trim-n', '-0', '1', '-m', '5', '-a', 'TCGTATGCC
GTCTTCTGCTTG', '-o', 'W_Sc_2016/tmp/Cerevisae_RPF/trim.fq', 'W_Sc_2016/input/W_
Sc_2016_40000.fastq.gz', '-j', '0'] failed with exit code 1
Finished processing 1 samples, 1 failed
Processing error: ../example-datasets/fungi/saccharomyces/Weinberg 2016 RPF 3 s
amples CDS w 250utrs config.yaml
Exception
Traceback (most recent call last):
  File "/home/sophie/riboviz/riboviz/tools/prep_riboviz.py", line 832, in prep_
 riboviz
    run workflow(config file, is dry run)
  File "/home/sophie/riboviz/riboviz/tools/prep riboviz.py", line 711, in run w
orkflow
    raise Exception("No samples were processed successfully")
Exception: No samples were processed successfully
(riboviz) sophie@sophie-VirtualBox:~/riboviz$
```

### After 'Open' Mindset

- Improved readability
- On GitHub accessible
- Provide useful information making it easier to solve the problem
- Long term record of how problem was overcome
- New mindset, same mistakes, better solutions

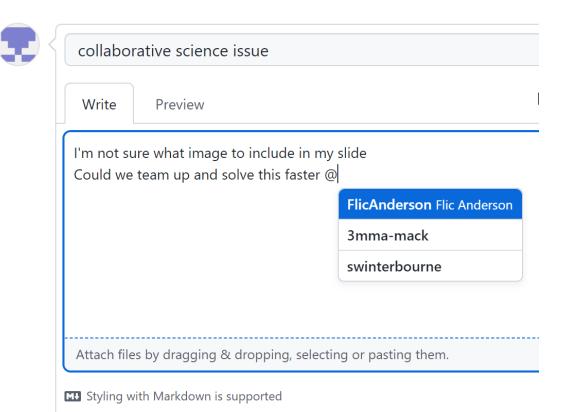


Having a look, the line library(getopt, quietly = T) appears on line 28 of Bam_to_H5.R, and the package is also present in the wallace_rna/Rlibrary folder on eddie, so I don't understand why it is failing here. I have started a run of the Duncan et al Schizosaccharomyces dataset to see if the error occurs for that dataset as well, as I successfully ran the Duncan et al dataset on the 23rd.

This is being run in the develop branch of riboviz, with the latest commit being 106a204bc64525db8de7d18e99d5421be1246394, on the 21st of June.

### Collaborative Learning

- Documenting mistakes helps future users if they run into the same error
- Using issue tickets can solve problems faster – more knowledgeable people can jump in and help
- Learn from and adapt existing code
- If there is a mistake to be made, a student will make it



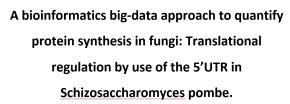
### Gain Life and Professional Skills

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Before student project	After student project	
Poor <b>communication</b> , struggling to work collaboratively	Experience working collaboratively, communicating issues effectively	
Inconsistent documentation of tasks and solutions, need encouragement to provide relevant information	Improved approach to documenting tasks in future projects. Write with knowledge that notes may be used by others in future	
Need guidance on how to approach tasks	Understanding of processes and able to provide guidance to new users	
Uncomfortable making mistakes, assume unexpected results are due to own error	Comfortable communicating mistakes and working towards collaborative solutions	

## Open Research Leads To Positive Outcomes

- Evidence of work
- Good projects
- Data re-analyzed
- Publications
- Conferences



The benefits of an open-science approach in student research

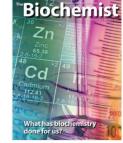
Emma MacKenzie 💿 ; Sophie Winterbourne 💿 ; Felicity Anderson 💿 ; Edward Wallace 🛥 💿

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projects FREE

Check for updates

Biochem (Lond) (2021) 43 (6): 66-73. https://doi.org/10.1042/bio_2021_198



#### riboviz 2: a flexible and robust ribosome profiling data analysis and visualization workflow $\widehat{\partial}$

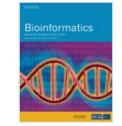
Alexander L Cope, Felicity Anderson, John Favate, Michael Jackson, Amanda Mok, Anna Kurowska, Junchen Liu, Emma MacKenzie, Vikram Shivakumar, Peter Tilton, Sophie M Winterbourne, Siyin Xue, Kostas Kavoussanakis, Liana F Lareau 🕿, Premal Shah 🕿, Edward W J Wallace 🕿

Bioinformatics, Volume 38, Issue 8, 15 April 2022, Pages 2358–2360, https://doi.org/10.1093/bioinformatics/btac093 Published: 14 February 2022 Article history ▼



Edinburgh Open Research Initiative

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Edinburgh ReproducibiliTea

An excellent read detailing the experience of applying #OpenResearch principles to student projects in The Wallace Lab https://t.co/JOe7UTr5E5! https://t.co/BAR8f4Qca6 With insights from students Emma MacKenzie, Sophie Winterbourne, supervisor @Flic_Ande

21 Dec 2021

A bioinformatics big-data approach to quantify protein synthesis in fungi: investigating translational control by inhibitory codon pairs



### Thanks for Listening!

### Any Questions?



### Student Vs Lab?

	Student Project	Lab Research Project
Question Scope:	Something achievable	Something novel
They Aim To:	Learn new skills, get good grades, build research experience	Discover new insights, progress lab research outcomes, adopt new methods
They Need This To:	Achieve their degree (=> career goals)	Contribute high-quality <pre>publishable results (=&gt; secure future funding)</pre>
Timescale:	SHORT! 1 x Semester	LONG Multi-year

Very different goals – how can Open Science approaches help resolve this? ... Think of students as instant collaborators!