

# CAB newsletter 1 November 2023

You are receiving this as a member of the Centre for Applied Bioinformatics (CAB)

**Not yet joined CAB?** Well if you are receiving this you already have joined, but if you know anyone who would like to join, then please forward this message and they can now sign up using a simple web form from the members page at <https://www.appliedbioinformatics.com.au/Members.php>

## News:

### **Nominations are open for the 2023 Australian Bioinformatics and Computational Biology Society (ABACBS) Executive Committee**

Nomination deadline: 11:59 pm AEST November 14, 2023  
Nominations for all elected roles are invited, including:

**Ordinary Member:** Group of 4 members that have voting rights within the National Executive Committee. Also helps with other major society initiatives and can represent other ABACBS sub-committees when required

**Postdoctoral Representative:** Representative of Postdoctoral members at the National Executive Committee

**Professional Bioinformatician Representative:** Representative of Professional Bioinformaticians at the National Executive Committee

**Student Representative:** Representative of student members at the National Executive Committee

**Treasurer:** Responsible for financial management and reporting for the society

**Secretary:** The major organisational role within the society, responsible for regular member communications and executive governance

**Vice President:** Delegate leader of the society under the President and responsible for leading major society projects, including the ABACBS Awards Committee

**President (special criteria apply):** Leads National Executive Committee meetings and overall governance of the society.

To nominate, please send by email to [committee@abacbs.org](mailto:committee@abacbs.org) prior to the deadline: November 14, 2023, 11:59 pm AEST. Please include a candidate statement of up to 400 words. Per the society's constitution, roles which receive multiple nominations will trigger an election by current members.

### **ARDC implement a National Machine Learning Service**

Details available here: <https://tinyurl.com/36acyhk8>

## Conferences and Presentations:

Cold Spring Harbor Laboratory: **Plant Genomes, Systems Biology & Engineering**  
November 29 - December 02, 2023  
See <https://meetings.cshl.edu/meetings.aspx?meet=plants&year=23> for details

**Australian Bioinformatics And Computational Biology Society (ABACBS) annual conference** will be held 4 – 8 December in Brisbane, for the first time in collaboration with the International Society of Computational Biology. Save the date!

**EMBO workshop: Computational structural biology**, 6 – 9 December 2023, EMBL Heidelberg and Virtual. Details available at <https://tinyurl.com/ynm7s5wd>

### **Plant webinars and tutorials available from EBI**

The plant webinar series and a few useful online tutorials are now in an open access curated collection - <https://www.ebi.ac.uk/training/online/courses/data-driven-plant-sciences/>

### **EMBL AI and biology symposium**

12– 15 March 2024, EMBL Heidelberg and Virtual  
Information available here: <https://tinyurl.com/mvdcdb4h>

## Infrastructure:

### **How to apply for Nimbus servers:**

Would you like some free Linux servers with up to 16 cores and 64 GB RAM through Pawsey? Dr Sarah Beecroft has helpfully provided a 'how to apply' video available at <https://www.youtube.com/watch?v=mpFQC5sXSHQ> Users have full access to these machines and we have prepared an image that supports many standard bioinformatics tasks that can run on this scale of machine.

**Pawsey have found a nicer way to handle the many tiny files that Conda makes, as well as some processes that make many files.**

The docs are here: <https://support.pawsey.org.au/documentation/display/US/How+optimise+filesystem+usage+with+SquashFS>

Basically, they have developed a way to write your conda env into a squashFS image, which you can then mount with singularity. No more breaking the quota, and you can move your environments and store them on Acacia!

## Training:

### **Integrative analysis of multi-omics data**

27 February – 1 March 2024, EMBL Heidelberg

Are you a PhD student or post-doc in computational biology aiming to improve your skills in multi-omics data integration methodologies? Then join #EMBOMultiOmics, our advanced practical course which aims to convey conceptual and mathematical foundations that underpin existing and emerging integrative multimodal data strategies and practical trade-offs between various methods.

Information available here: <https://tinyurl.com/3396bdfz>

### **EMBL Course: Analysis and integration of transcriptome and proteome data**

4 – 9 February 2024, EMBL Heidelberg

Information available here: <https://tinyurl.com/2p97yhtd>

### **CAB plans to support local training sessions for R and single cell analysis,**

please contact Asad Prodhan [asad.prodhan@uwa.edu.au](mailto:asad.prodhan@uwa.edu.au) (R) and Chuck Herring [herring.charles.a@gmail.com](mailto:herring.charles.a@gmail.com) (single cell analysis) for more information.

If you would like to **host a bioinformatics masters student** for approximately 6 months to undertake a research project or host a student intern, please contact [dave.edwards@uwa.edu.au](mailto:dave.edwards@uwa.edu.au) and I can distribute your information to the students.

## **Calling all bioinformatics students:**

COMBINE is the Australian Computational Biology and Bioinformatics Student Society and looking to coordinate events here in WA. If you are not a member of COMBINE, you can join here for free <https://forms.gle/Rg1g3Kj1GLpacb6EA>. If you could like to contribute to COMBINE social or training events in WA, please contact Carissa at [cche5029@uni.sydney.edu.au](mailto:cche5029@uni.sydney.edu.au).

## **Postdoc position available:**

### **Computational biology position available at the Peter MacCallum Cancer Centre in Melbourne.**

The Trigos lab focuses on understanding how different -omics layers in tumour cells and the microenvironment adapt and co-evolve as an ecosystem to drive cancer progression, resistance and metastasis with the goal of identifying novel biomarkers and targets for treatment. The position closes November 13.

The Postdoctoral Research will lead projects understanding spatial cell-cell interactions from spatial transcriptomics and proteomics data, including the integration with other data modalities, such as single-cell RNAseq and ATACseq, genome sequencing and methylation. The Postdoctoral Researcher will have the opportunity to develop projects together with the lab head, design and carry out analyses and method development (as required) with unique patient -omics datasets to address key translational questions.

Here is the link to view the full position description and to apply:

<https://careers.petermac.org/job/MELBOURNE-Postdoctoral-Fellow-Computational-Biology-VIC-3000/945024010/>

## PhD Scholarship available

Based at Griffith University Centre for Planetary Health and Food Security  
The details of the position can be found here:  
<https://www.griffith.edu.au/research-study/scholarships/developing-a-genomic-platform-and-resources-for-australian-papaya>

## Casual position wanted

Ali Afrasiabi is looking for a casual bioinformatics position:

Skills:

A) I possess expertise in analyzing a wide range of high-throughput sequencing data (both bulk and single cell resolution), including DNAseq, RNAseq, scRNA-seq, ATAC-seq, nanopore, CITE-seq and more. I'm proficient in utilizing conventional pipelines and can develop custom ones as required.

B) My proficiency in R and bash equips me to handle both downstream tasks (such as data analysis, interpretation, and visualization) and upstream tasks (including the preparation and processing of raw data).

Please contact Ali directly at Ali Afrasiabi <[ali.afraziabi@wimr.org.au](mailto:ali.afraziabi@wimr.org.au)>

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