CAB newsletter 5th September 2022

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:

Do you need access to HPC? The applications for access to Pawsey through the partner scheme and the NCMAS are open. Details are below. We have recently set up some new nimbus servers for applied bioinformatics provided by Pawsey. If you plan to set up a bioinformatics nimbus server and would like some help with the application/set up, please see below.

Want to work with the University of Arizona? CAB is organising a virtual symposium of short presentations with University of Arizona researchers to try to identify potential collaborations 8am on 21st October. If you would like to attend or present at the virtual meeting, please email Dave.Edwards@uwa.edu.au

Twitter addicts, get your fix of the latest bioinformatics tweets at @UWABioinfo

Promote your publications through CAB tweets! Please email any of your recent publications and we can promote through the CAB newsletter and twitter account @UWABioinfo

Missed a previous newsletter? Fear not, they are now all available online at: https://www.appliedbioinformatics.com.au/Newsletters.php

Interesting papers:

Please send information on interesting papers that I can promote in the newsletter/CAB twitter feed.

Title: Temporally restricted activation of IFNβ signaling underlies response to immune checkpoint therapy in mice
Summary: The authors used bulk and single-cell RNA sequencing to map what happens over time during immunotherapy, identifying key differences between cancers that respond to immunotherapy and those that do not.
Link: https://rdcu.be/cUnhZ
Tags: @RachaelZemek @NatureComms @telethonkids @uwaresearch @PerkinsComms

Talks:

First joint CAB – Institute of Data joint meeting

Wednesday 14th September 3pm at Forrest Hall followed by drinks and nibbles, and online,

Presenters:

> Philipp Bayer (Mindaroo): OceanOmics at Minderoo – bioinformatics for healthier oceans
> Eric Alves (UWA): Applied bioinformatics for immune cell profiling
> Nicola Armstrong (Curtin): Identifying short tandem repeats and their impact on disease.

In person attendance is limited so reserve your place early by email:
dave.edwards@uwa.edu.au

COMBINE Fireside Chats with Industry

It is our pleasure to announce that our next speaker for September will be Rowland Mosbergen from the WEHI Research Computing Platform sharing with us about life as a research software engineer. This program series is an excellent opportunity for upcoming student bioinformaticians to learn more about industry-related career pathways and from the successes of industry leaders in the field. Sign up to our mailing list to receive updates about upcoming Fireside Chats!

Date and time: Wednesday 7th September, 1.30-2.30pm (AEST)
Please register via zoom for this free event:
https://monash.zoom.us/meeting/register/tZEpcOiqqTosGtad0NoQ63bmfzOSbCPY7pRM

Conferences:

COMBINE 2022 Symposium

The COMBINE Symposium is a student-run, non-profit conference that aims to gather a diverse group of students and ECRs who are curious, passionate and eager to learn more about bioinformatics and computational biology. COMBINE Symposium 2022 will be held as a hybrid virtual/in-person event on the 28th of November, in conjunction with the ABACBS/VCBS/BioCAsia conferences. Abstract submissions are now open and will close on 12/09/2022 [registration will remain open after this date]. Check out: https://pheedloop.com/ABACBS2022/site/

Infrastructure:

NCMAS is open:

The National Computational Merit Allocation Scheme call for 2023 is open.

Key dates:

15 August – Applications Open
18 September – Applications Close
30 November-2 December – Merit Allocation Meeting
Week of 12 December – Allocations Announced

The NCMAS Secretariat will be running weekly information sessions from the 9th of August to the 13th of September. Register here. https://anu.zoom.us/meeting/register/tZwtc-CtrjsiG9ZNd2VCi_hBmBVSAnSVx8KX

Pawsey partner scheme is open:

In contrast to previous years where the Pawsey partner scheme was linked to the NCMAS application, Pawsey now have a separate application in a different format. Details are available here:

https://support.pawsey.org.au/documentation/display/US/The+Pawsey+Partner+Merit+Allocation+Scheme

Nimbus servers:
Did you know that you can request Linux servers with up to 16 cores and 64 GB RAM through Pawsey? 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, please contact Dave.Edwards@uwa.edu.au for details.

Training:

ResBaz Perth 2022:

6 - 8 September (this week) I Curtin University

The Perth Research Bazaar is a 3-day conference where researchers come together to up-skill in 'next generation digital research tools and skills', including bioinformatics.

Places are limited, register here: https://curtinic.github.io/ResBazPerth2022/

Australian BioCommons Webinar: Portable, reproducible and scalable bioinformatics workflows using Nextflow and Pawsey Nimbus Cloud

Nandan Deshpande from the Sydney Informatics Hub, University of Sydney, tells us how you can deploy freely a available nf-co.re bioinformatics workflows with a single command and will also show you how to can use Nextflow to build your own workflows that save you time and support reproducible, portable and scalable analysis.

In the latter half of the webinar, Sarah Beecroft from the Pawsey Supercomputing Research Centre will talk about their Nimbus Cloud systems. She'll describe why using Nimbus with Nextflow is a brilliant option for many bioinformatics projects.

When: 20 September 2022, 12pm AEST / 11:30am ACST / 10am AWST

More details and to register: https://www.biocommons.org.au/events/nextflow-nimbus

Australian BioCommons Workshop: RNA-Seq: reads to differential genes and pathways

The BioCommons has a workshop coming up on RNAseq analysis in partnership with the Sydney Informatics Hub and Pawsey Supercomputing Research Centre.

You'll learn about the fundamental concepts of RNA sequencing experiments and how to take the data from reads to functional analysis and pathway enrichment. You will get hands-on using nf-core/rnaseq - a portable, scalable, reproducible and publicly available workflow on Pawsey Nimbus Cloud. In the second part of the workshop you will use the count data you created to identify differential genes and pathways using R/Rstudio. By the end of the workshop, you should be able to perform your own RNA-seq analysis for differential gene expression and pathway analysis!

When: 27 & 28 September 2022

More details and to apply: https://www.biocommons.org.au/events/rnaseq-2022

[Expression of interest] Free introductory machine learning workshop:

COMBINE is collecting expressions of interest for a machine learning workshop and will launch one in mid-September if demand is high enough. To register your expression of interest and be put on the waiting list if it happens, please fill in this form.
https://docs.google.com/forms/d/e/1FAIpQLScRzd5htp8PVjlct2dbKP-hMHP41TQ_ktHJsVg6Mf-yPV3TWg/closedform

NCI Training:

NCI, Pawsey, and NeSI CUDA GPU Bootcamp on 7-9 September (https://www.openhackathons.org/s/siteevent/a0C5e000005UNudEAG/se000140)

NCI-NSCC Introduction to MPI course on 21-22 September (https://opus.nci.org.au/display/Help/Introduction+to+MPI)

HPC and Data in Drug Design and Delivery course from 6 September to 1 December (https://intersect.org.au/education/collaborative-graduate-courses/2nd-collaborative-course/)

HPC-AI Hackathon in early November (https://opus.nci.org.au/display/Help/NCI-NVIDIA+HPC-AI+Hackathon)

PhD Scholarship:

Advertise your PhD scholarships here

Jobs:
Advertise your bioinformatics job vacancies here