SEFARI 3D RNA-seq App Workshop

12th and 19th November 2020

# Summary

**Owing to the ongoing situation with covid-19, this event will be organised as a virtual workshop**.

RNA-seq has been widely used for differential gene expression (DE) and alternative splicing (DAS) analysis. Researchers at the James Hutton Institute and the University of Dundee-Plant Sciences have developed the 3D RNA-seq App (https://3drnaseq.hutton.ac.uk) for biologists to implement complex DE and DAS analysis only with “clicking mouse”. 1) The 3D App includes both DE and DAS analysis. It works for RNA-seq data from plant, animals, human, etc. 2) It is very accurate and has good controls of false positives. 3) It is very flexible for complex experimental design, such as time-series and developmental-series. 4) The entire analysis only takes 1-2 hours to generate publication-quality figures, tables and reports. 3D RNA-seq App can be applied universally to all species and has been used for Arabidopsis, rice, potato, barley, human, mouse, Drosophila, plant nematodes, Phytophthora, water flea, etc. It will be highly relevant to plant and food health and animal disease and treatment studies across the SRP/Portfolio.

# Workshop login

When it's time, join your Webex meeting here.

**Meeting link:** <https://hutton.webex.com/hutton/j.php?MTID=mf232509bf184526135ef1bfed1ac4452>

**Meeting number (access code):** 175 308 4786

**Meeting password:** VrCSskjU832

# Schedule

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| Day1: 12 November, Thursday | Lecture  (Wenbin & Runxuan) |
| 9:30 | Welcome |
| 09:35-10:05 | Reference transcriptome and transcript quantification (Runxuan Zhang) |
| 10:05-10:30 | Demo: Galaxy transcript quantification (Wenbin Guo) |
| 10:30-10:40 | Break |
| 10:40-11:10 | 3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists (Wenbin Guo) |
| 11:10-11:30 | Demo: 3D RNA-seq analysis (Wenbin Guo) |
| 11:30-12:00 | Q&A and wrap up |

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| Day 2: 19 November, Friday | One-to-one session, reservation required  (Wenbin & Runxuan) |
| 9:00-9:25 | One-to-one session 1 |
| 9:30-9:55 | One-to-one session 2 |
| 10:00-10:25 | One-to-one session 3 |
| 10:30-10:55 | One-to-one session 4 |
| 11:00-11:25 | One-to-one session 5 |
| 11:30-11:55 | One-to-one session 6 |
| 13:00-13:25 | One-to-one session 7 |
| 13:30-13:55 | One-to-one session 8 |

Please contact Linda Milne ([linda.milne@hutton.ac.uk](mailto:linda.milne@hutton.ac.uk)) to reserve a place for one-to-one session.

# Workshop organiser

Wenbin Guo, Linda Milne, Runxuan Zhang and Iain Milne from Information & Computational Sciences at the James Hutton Institute.

# Sponsors

With thanks to funding form SEFARI Gateway.

# Meeting recording – Privacy notice

* Please note that this workshop is being filmed and the recording will be made available online for you to revise.
* We cannot guarantee that your image will not be recorded during the workshop. If you do not want to be filmed, you could turn-off your video. We will mask all the personal images before making the video publicly available.
* To minimise the background noise, we will mute your microphone during the presentations.

# Q & A

* We will leave time for Q & A after each presentation.
* You can also leave your questions in the chat box, start with Q: xxxx. We will answer questions from the beginning to the end.
* If time doesn't permit, we will make summary of the Q & A in the chat box and make it available online after the workshop.
* You can also post your question on the google groups: <https://groups.google.com/g/3d-rna-seq-app-user-group>

# User guides

Don’t worry if you get lost in the workshop

* Recording will be made available online
* Github: <https://github.com/wyguo/ThreeDRNAseq>
* User manual : <https://github.com/wyguo/ThreeDRNAseq/tree/master/vignettes/user_manuals>
* YouTube video: <https://www.youtube.com/watch?v=rqeXECX1-T4>
* Google groups: <https://groups.google.com/g/3d-rna-seq-app-user-group>