Scottish Phylogeny Discussion Group

The James Hutton Institute, Dundee 18 February 2013



Programme

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The meeting is in the **NEW SEMINAR ROOM** at The James Hutton Institute in Invergowrie, on the edge of Dundee. For venue information, see http://www.hutton.ac.uk/sites/default/files/files/About/Directions_Dundee.pdf

<u>Arrival at reception (The James Hutton Institute, Invergowrie)</u> For those visiting the institute, please sign in at reception and collect a badge. We will come and collect you from reception and take you to the New Seminar Room (as entry to buildings requires a swipe card).

<u>1 PM</u>

Buffet lunch (New Seminar Room – same room as the meeting)

<u>2 PM</u>

Introduction and Welcome: Frank Wright (BioSS) and Daniel Barker (University of St Andrews)

<u>2:10 PM</u>

Creation, curation and analysis of Protein and RNA alignments with Jalview **Jim Procter, University of Dundee**

Abstract: Jalview (www.jalview.org) is a BBSRC funded open source tool for the visualisation and analysis of protein and nucleic acid sequence alignments that is widely used in teaching and research. Available as a web based applet, or Desktop application, version 2.8 incorporates Jmol, a molecular structure viewer, and the RNA structure viewer VARNA. The Jalview Desktop supports figure generation, and provides access to a range of sequence, alignment, 3D structure and annotation databases, and analysis services provided by the University of Dundee and Free University of Amsterdam. It also acts as a graphical client for the alignment, protein disorder prediction and amino acid conservation analysis programs made available as Java Bioinformatics Analysis Web Services (http://www.compbio.dundee.ac.uk/jabaws).

In this talk, I will highlight the key developments in Jalview that have made it possible to create, curate and analyse protein and RNA sequence alignments in the context of structure, biological knowledge and evolutionary analyses. I'll also discuss some of the current challenges with regard to the creation, curation and analysis of alignments, and how they fit with Jalview's development roadmap.

<u>3:10 PM</u>

Independent evolution of β -lactam hydrolysis in the metallo- β -lactamase superfamily **Rosanna Alderson, University of St.Andrews**

<u>3:30 PM</u> Tea/Coffee.

<u>4 PM</u>

Identification and expression analysis of barley clock genes **Cristiane Calixto, University of Dundee**

<u>4:20 PM</u>

Phylogenetics in Practice **Frank Wright, BioSS**

<u>5.00 PM,</u>

Meeting ends.

The meeting will be followed by dinner at a restaurant in Dundee. Dinner is open to anyone registered for the meeting, but **requires separate booking in advance**. If you would like dinner, pleaseemail Frank Wright (frank@bioss.ac.uk) before noon on Monday. Dinner will be charged at cost.

Speakers

Jim Procter

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Organizer

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Further Information

The Scottish Phylogeny Discussion Group is funded by a grant from the Scottish Bioinformatics Forum and by the former Centre for Evolution, Genes and Genomics at the University of St Andrews. For information on the Scottish Phylogeny Discussion Group and its activities, please see:

http://biology.st-andrews.ac.uk/cegg/spdg