

SIROCCO

Silencing RNAs: organizers and coordinators of complexity in eukaryotic organisms

DEC 2009 Newsletter 35

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SIROCCO BIOINFORMATICS—

a bioinformatics service for SIROCCO members

A SIROCCO pipeline has been developed for analysing the results of high throughput sequencing experiments. It is currently used most often for Illumina reads but can be used to process 454 reads as well.

So far, it has been successfully used for the processing of

- sRNA reads
- ChIP-Seq
- genomic DNA

Current analyses include:

- adaptor removal
- de-multiplexing of multiplex sequencing runs
- alignment against genomes, transcripts or other datasets
- generation of statistics/counts at each stage of the process

The group would like to offer this as a service to SIROCCO laboratories, particularly to those that do not yet have the infrastructure to perform the analysis themselves.

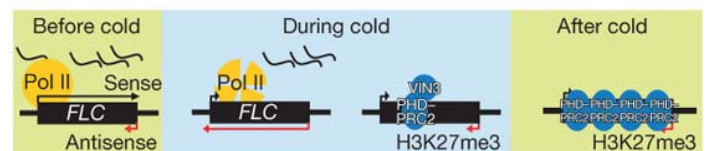
Interested groups that have (or plan to have) samples for analysis can contact bioinformatics@plantsci.cam.ac.uk

The bioinformatics group is also happy to help with general bioinformatics problems.

SIROCCO Partner Caroline Dean has published two papers describing the link between non-coding RNA and gene regulation. In the first, the link between non-coding RNA and chromatin regulation is investigated through analysis of *FLC* — a regulator of flowering time in *Arabidopsis* and a target of several chromatin pathways. *FLC* is silenced by prolonged cold in the Polycomb-mediated process vernalization. Upregulation of long non-coding antisense transcripts covering the entire *FLC* locus are now suggested to have an early role in the cold-induced silencing mechanism.

[Cold-induced silencing by long antisense transcripts of an Arabidopsis Polycomb target.](#)

Swiezewski S, Liu F, Magusin A, Dean C. Nature. 2009 Dec 10;462(7274):799-802.



In the second paper, two conserved RNA 3'-end processing factors CstF64 and CstF77 were shown to be required for RNA-mediated chromatin silencing of the *Arabidopsis* major floral repressor gene, *FLC*. CstF64 and CstF77 are required for 3' processing of *FLC* antisense transcripts. A specific RNA-binding protein directs their activity to a proximal antisense polyadenylation site. This targeted processing triggers localized histone demethylase activity and results in reduced *FLC* sense transcription. [Targeted 3' Processing of Antisense Transcripts Triggers Arabidopsis FLC Chromatin Silencing.](#) Liu F, Marquardt S, Lister C, Swiezewski S, Dean C. Science. 2009 Dec 3. [Epub ahead of print]



RESEARCH SPOTLIGHT



[An emerging player in the adaptive immune response: microRNA-146a is a modulator of IL-2 expression and AICD in T lymphocytes.](#)

Curtale G, Citarella F, Carissimi C, Goldoni M, Carucci N, Fulci V, Franceschini D, Meloni F, Barnaba V, Macino G.

Blood. 2009 Nov 12. [Epub ahead of print]

[miRNA processing turned upside down.](#)

Schwab R, Voinnet O.

EMBO J. 2009 Dec 2;28(23):3633-4.

[TRIMming microRNA function in mouse stem cells.](#)

Dueck A, Meister G.

Nat Cell Biol. 2009 Dec;11(12):1392-3.

[Tandem affinity purification of miRNA target mRNAs \(TAP-Tar\).](#)

Nonne N, Ameyar-Zazoua M, Souidi M, Harel-Bellan A.

Nucleic Acids Res. 2009 Dec 2. [Epub ahead of print]

Reporting Update

Financial reports for the third period (2009) are due by [31st January 2010](#)

Reports should include:

- Form C financial statement
- Audit Certificate if necessary
- Major costs tables
- Justification of Major Costs table

Please email Aileen fah37@cam.ac.uk
with any questions regarding financial reporting



Happy Holidays
to all members of
the SIROCCO consortium