



This site provides online material for the www.cosmoss.org 3rd Physcomitrella Genome Workshop that will be held

on

September 13th-15th 2010

at

University of Freiburg, Germany



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Sponsors



FRIAS
FREIBURG INSTITUTE FOR ADVANCED STUDIES
ALBERT-LUDWIGS-UNIVERSITÄT FREIBURG



Organization is in cooperation with Kongress & Kommunikation GmbH,
<http://www.kongress-und-kommunikation.de>

Information

- [Have a look at previous workshops](#)
- Spread the news: [Workshop Announcement Poster](#)

Cosmoss accounts

You have to be a registered cosmoss user in order to access some of linked material.

For the workshop participants, accounts have been created (unless you already had one) with an initial password handed out at the registration desk. Please change it as soon you [log in](#).

Everyone else is also invited to register! Please contact helpdesk-cosmoss@uhura.biologie.uni-freiburg.de for an account!

Registration

- **Deadline for registration:** August 29, 2010.
- **Registration fee:** 200?

Program

Learn how to work with cosmoss.org and the *Physcomitrella patens* genome. Find and annotate your gene(s) of interest. Get in touch with other people working with *Physcomitrella* and other bryophytes.

Covered topics

Tutorial sessions for the computational tools and databases available on cosmoss.org. E.g.:

- BLAST
- Sequence Retrieval
- Genome Browser
- Functional Annotation Interface *genonaut*
- Structural Annotation Interface [Apollo](#)

Annotation jamboree:

- Invited Speakers on gene annotation (see [below](#))

- Functional and structural annotation *Howto*
- Hands-on annotation session (annotate your genes of interest)

Schedule

Monday September 13

09:00 13:00 Registration

09:30 13:15 **Morning session including lunch**

09:30 Welcome

09:30 10:00 The *Physcomitrella* Genome

10:00 10:30 cosmoss.org: resources, databases and versions

10:30 13:15 Welcome reception, industry exhibits and lab tours

13:30 17:30 **Afternoon session including coffee break**

13:30 14:00 Lecture: Homology searching / BLAST

14:00 14:50 Hands-on: BLAST

14:50 15:15 Lecture: gene families

15:15 15:30 Coffee break

15:30 16:00 Hands-on: gene family tools

16:00 16:40 Lecture: sequence retrieval

16:40 17:15 Hands-on: sequence retrieval/keyword search

17:30 ? Social event: Bus trip to a typical south German locality (Strauße) including evening meal

Tuesday September 14

09:00 12:00 **Morning session including coffee break**

09:00 10:00 Lecture: Genome browser and Hands-on: genome browser basics

10:00 10:15 Lecture: Genome Browser Tracks

10:15 10:30 Coffee break

10:30 11:00 Lecture: Genome Browser hidden treasures

11:00 12:00 Hands-on: Advanced gbrowsing & Questions

12:00 13:30 Poster session & Lunch

13:30 17:30 **Afternoon session including coffee break**

13:30 14:00 Lecture: functional annotation

14:00 15:00 Hands-on: genonaut

15:15 15:30 coffee break

15:30 16:00 Lecture: structural annotation (Gbrowse)/Apollo annotation editor

16:00 17:00 Hands-on: structural annotation

17:30 ? Social event: Conference dinner and industry night with talks on *Physcomitrella*/genome-specific applications

18:00 18:20 BMG

18:20 18:40 Agrisera

18:40 19:00 Genxpro

19:00 19:20 High-throughput transcriptomics in *Physcomitrella*

19:20 ? Dinner

Wednesday September 15

09:00 12:00 Morning session including coffee break

09:00 09:30 Annotating MADS-box Genes and KNOX Genes in the *Physcomitrella* Genome

09:30 10:00 Gene Annotation in Transcriptomic Analysis

10:15 10:30 Coffee break

10:30 12:00 Annotation guidelines, Evidence Codes, examples (Student Annotation Project) and discussion

12:00 13:30 Poster session & Lunch

13:30 17:00 Afternoon session (Annotation Jamboree) including coffee break

13:30 15:15 Gene family assignment (publications) / Jamboree

15:15 15:30 Coffee break

15:15 16:30 Jamboree

16:30 17:00 Concluding remarks / discussion

Poster session

Carolin Aldinger

Examination of the annotated tRNA^{Arg} GCG in *Physcomitrella patens*

Alexandra Castro

Differentially expressed genes in response to pathogens in *Physcomitrella patens* cancelled

Mahmoud Madgy

The genetic structure of the *Funaria hygrometrica* populations in Sierra Nevada (Spain) using the sequence-related amplified polymorphism (SRAP) technique

Bernadeta Kukuczka

Characterization of iron-deficiency responses and targeted knockout of the pgr11 gene in *Physcomitrella patens*

James Llyod

Can moss read nonsense? Exploring gene regulation by nonsense-mediated decay in *Physcomitrella*

Stefanie Müller

Mitochondrial proteomics in the moss *Physcomitrella patens*: Are there two subpopulations of mitochondria?

Sergio Pisa

Genetic diversity of *Bryum argenteum* Hedw. along an altitudinal gradient in Sierra Nevada, Spain

Cecilia Ruibal

Search for genes involved in abiotic stress tolerance in *Physcomitrella patens* cancelled

Venue

University of Freiburg, Germany

Biology I

- Campus, Hauptstr. 1, Computer Pool & Lounge
- main workshop location

[Google map of the location](#)

Biology II

- Campus, Schänzlestr. 1, Main Entrance, Small Lecture Hall & Lecture Hall Foyer
- morning session on the first day
- the registration desk is located in the Lecture Hall Foyer

[Google map of the location](#)

Speakers

- Elizabeth Barker (Invited talk: [Annotating MADS-box genes and KNOX genes in the *Physcomitrella* genome](#))
- Andrew C. Cuming (Invited talk: [Gene annotation in transcriptomic analysis](#))
- [Stefan Rensing](#)
- Andreas Zimmer
- [Daniel Lang](#)

Workshop Content

First Day

Morning Session

location

[Biology II Small Lecture Hall](#)

The *Physcomitrella* Genome

speaker

Stefan

slides

[Genome.pptx](#)

cosmoss.org: resources, databases and versions

speaker

Daniel

slides

[cosmoss_resources_databases_versions.pdf](#)

Afternoon Session

location

[Biology I Computer Lab](#)

Lecture: Homology searching / BLAST

speaker

Stefan

slides

[BLAST.pptx](#)

Hands-on: BLAST

speaker

Stefan

slides

[BLAST_hands-on.pptx](#)

Lecture: gene families

speaker

Stefan

slides

[GeneFamilies.pptx](#)

Hands-on: gene family tools

speaker

Stefan

slides

[GeneFamiliesHands-On.pptx](#)

Lecture: sequence retrieval and genome browser

speaker

Andreas

slides

[Sequence Retrieval 2010.pptx](#)

Hands-on: sequence retrieval/keyword search

speaker

Andreas

Sequence Retrieval

documentation

[Sequence Retrieval](#)

Familiarize yourself with the Cosmoss Retrieval system:

Tasks

Try to retrieve the following sequences:

Pp1s1_770V6.1
Pp1s1_128V6.2
Phypa_430365

You can access the sequence retrieval via the transcriptome and genome menu.

Hint: These accession numbers above are from the annotated V1.6 P.patens transcripts database. You can retrieve multiple sequences by providing their accession numbers as a comma- or space-separated

Have a look at the receiving FASTA files.

What are the first five bases of Phypa_430365 transcript sequence? *mark text from here --> ACTA
What is the description of Pp1s1_128V6.2 ? *mark text from here --> patatin t5<-- to here for the
What is the CGI (cosmoss gene id) of Phypa_430365 ? *mark text from here --> Pp1s33_278V6.1<-- t

As you may have already noticed, you could retrieve your P.patens sequence (V1.1, V1.2, V1.6) of interest using the Phypa_id or CGI. e.g. Phypa_430390 or Pp1s33_43V6.1

Batch retrieval

For a vast number of sequences you could upload your request in a text file.

File format: text
Provide accession number per line.

Select the following accession numbers and copy them into a new text file (e.g. notepad) and save it.

Pp1s459_1V2.1

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Pp1s7_181V2.1
Pp1s204_88V2.1
Pp1s204_91V2.1
Pp1s352_13V2.1
Pp1s312_46V2.1
Pp1s56_169V2.1
Phypa_125839
Pp1s56_166V2.1
Phypa_125903
Pp1s188_40V2.1
Pp1s545_4V2.2
Pp1s109_143V2.1
Pp1s352_57V2.1
Pp1s66_46V2.1
Pp1s12_223V2.1
Pp1s46_41V2.1
Phypa_146969
Phypa_87740
Phypa_87752
Phypa_151552
Phypa_8310
estExt_fgenesht1_pg.C_330027
EDQ76486
XM_001758564

Goto the cosmoss.org sequence retrieval:

Select database: P.patens_all_models_transcripts

This all models database contains all P.patens gene predictions (V1.0 V1.1 V1.2 V1.6) proteins.

The *Physcomitrella patens* genome accession numbers work for both transcripts and proteins databases. Just change the database to change to your favored sequence type.

Browse for the previously created file and submit your request

Save the sequences in a new file in FASTA format

Select only a subset of the sequences and save it to a new file

Keyword search

documentation

Keyword search

How many *geranyl geranyl pyrophosphate synth(et)ases* (GGPS) are in the virtual transcriptome?

Try to find the corresponding pp0304 virtual transcripts by keyword search!

Tasks

1. Read the documentation
2. Use the simple search menu to find the GGPS's in pp0304
3. Play around with the advanced search option.

4. How many geranyl geranyl pyrophosphate synthase hits to you find with the keyword search in the V1.6 transcripts?

Hits in pp0304

mark text from here --> 3 Hits in the pp0304 transcripts <-- to here for a possible query

Hits in V1.6 transcripts

mark text from here --> 5 Hits on 4 loci<-- to here for a possible query

This is the advanced query that works:

*mark text from here --> "geranyl geranyl"[DESC] AND "phosphate"[DESC] AND "synth"[DESC] <-- to h

Finally, here are the four loci in the genome:

- Pp1s167_155V6.1
- Pp1s3_343V6.1
- Pp1s55_266V6.1
- Pp1s8_131V6.1 Pp1s8_131V6.2

Second Day

Morning Session

Lecture: Genome Browser Basics

speaker

Andreas

slides

Zimmer GenomeBrowser 10.pptx

Hands-on: Genome Browser Basics

speaker

Andreas

slides

Hands_on_gbrowse_basics.pptx

Lecture: Genome Browser hidden treasures

speaker

Daniel

slides

[cosmoss_gbrowse_treasures.pdf](#)

Hands-on experience

Genome browser: customization and special features

prepared by


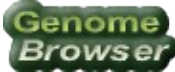
Daniel

BLAST gbrowse integration

documentation

[BLAST gbrowse integration](#)

Tasks

1. BLAST with an arbitrary transcript/EST vs the scaffolds and follow the  link.
2. Compare results when BLASTing w/o low complexity filtering!
3. Compare the BLAST to the spliced-alignment results. Are there lonely exons?
4. BLAST with the *Arabidopsis* protein AT5G13930.1 vs the v1.2 gene models and follow the  link.
5. Compare one of the hit *Physcomitrella* loci vs the *Arabidopsis* locus [AT5G13930](#)

Advanced navigation and zooming

Tasks

1. Find out the definition of a *gene* in [SO](#) by using the *Ontology_term* cross-link in a gene feature's mouse-over window
2. Zoom into a CDS exon and back again to the region of its *mommy* mRNA or gene
3. Play around with the zoom function to inspect EST and cDNA spliced alignments!

Exporting sequence annotations and publication quality images

Tasks

1. Export the upstream 10kbp your most favorite region to [FASTA](#) format and reverse it when necessary to reflect the gene's orientation.
2. *OPTIONAL*: Get another upstream region and try to find shared putative promoter elements using e.g. [AlignACE](#)
3. Save your most favorite region as a [png](#) image.

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4. Check out the exemplary PDF created with Inkscape from the SVG of a region:
www.cosmoss.org/inkscape_example.pdf

Highlighting

example locus

[scaffold_29:573541..579040](#)

documentation

[available colors](#) (scroll down to *Colors*)

Tasks

1. Let gbrowse highlight a feature and zoom out again, in order to see whether it overlaps with another feature in another track (*highlight and zoom to the region of this feature* link in the mouse-over)
2. Highlight your favorite gene model for the locus using the *Highlight feature* box in the *Display panel*.
3. Visualize an PCR experiment on the genomic locus! You've just amplified and sequenced a genomic PCR product for the locus using the primer coordinates below. Highlight the genomic region using the *Highlight regions* box in the *Display panel*.

forward primer mapping

[scaffold_29:575397..575417](#)

reverse primer mapping

[scaffold_29:577964..577950](#)

The screenshot shows the gbrowse web interface. At the top, there are several tracks with checkboxes: 'MIPS ANGELA long_terminal_repeat', 'TE related PFAM domains', and 'Helitrons Bennetzen lab'. Below these tracks are buttons for 'Configure tracks...' and 'Update'. A section titled 'Display Settings' is expanded, showing three input fields: 'Highlight feature(s) (feature1 feature2...)' with the value 'all_Phypa_205678@yellow', 'Highlight regions (region1:start..end region2:start..end)' with the value 'scaffold_29:577964-577950', and 'Region Size (bp)' with a dropdown menu set to '10 kbp'. There is an 'Update' button at the bottom right of this section. Below the 'Display Settings' section is another section titled 'Add your own tracks'.

Displaying custom annotation

You can draw your own features and have your own custom track in the browser!

documentation

[gbrowse custom annotation help](#)

Exporting sequence annotations and publication quality images

example locus

[scaffold_29:573541..579040](#)

Tasks

1. Go through the documentation
2. Visualize an RT-PCR experiment on the genomic locus! You've just amplified and sequenced an RT-PCR product for the locus below. Display it as custom annotation using the coordinates:

```
RT-exon1 scaffold_29:575397..575570
RT-exon1 scaffold_29:576849..576875
RT-exon1 scaffold_29:577042..577335
RT-exon1 scaffold_29:577629..577692
```

See the [example file](#) which combines everything. Adjust it, if you like!

Lecture: functional annotation

speaker

Daniel

slides

[cosmoss_genonaut.pdf](#)

Live presentation: Upcoming structural annotation at cosmoss.org using gbrowse and Apollo

speaker

Daniel

Third Day

Morning Session

Invited talk: Annotating MADS-box Genes and KNOX Genes in the *Physcomitrella* Genome

speaker

Elizabeth Barker

abstract

[Talk.Elizabeth_Barker.abstract.pdf](#)

slides

[Barker_Cosmoss_Workshop_2010.ppt](#)

Invited talk: Gene Annotation in Transcriptomic Analysis

speaker

Andrew Cuming

Displaying custom annotation

abstract

[Talk.Andrew.Cuming.abstract.pdf](#)

slides

[Cuming_Freiburg_2010.ppt](#)

Lecture: Annotation Guidelines, Student Annotation Project and Moss Ontology

speaker

Daniel

slides

[Annotation.pdf](#)

Lecture: Annotation examples

speaker

Stefan

slides

[AnnotationExamples.pptx](#)