Using electronic laboratory notebooks to promote student research mentoring and monitoring

Dr Dave Lunt
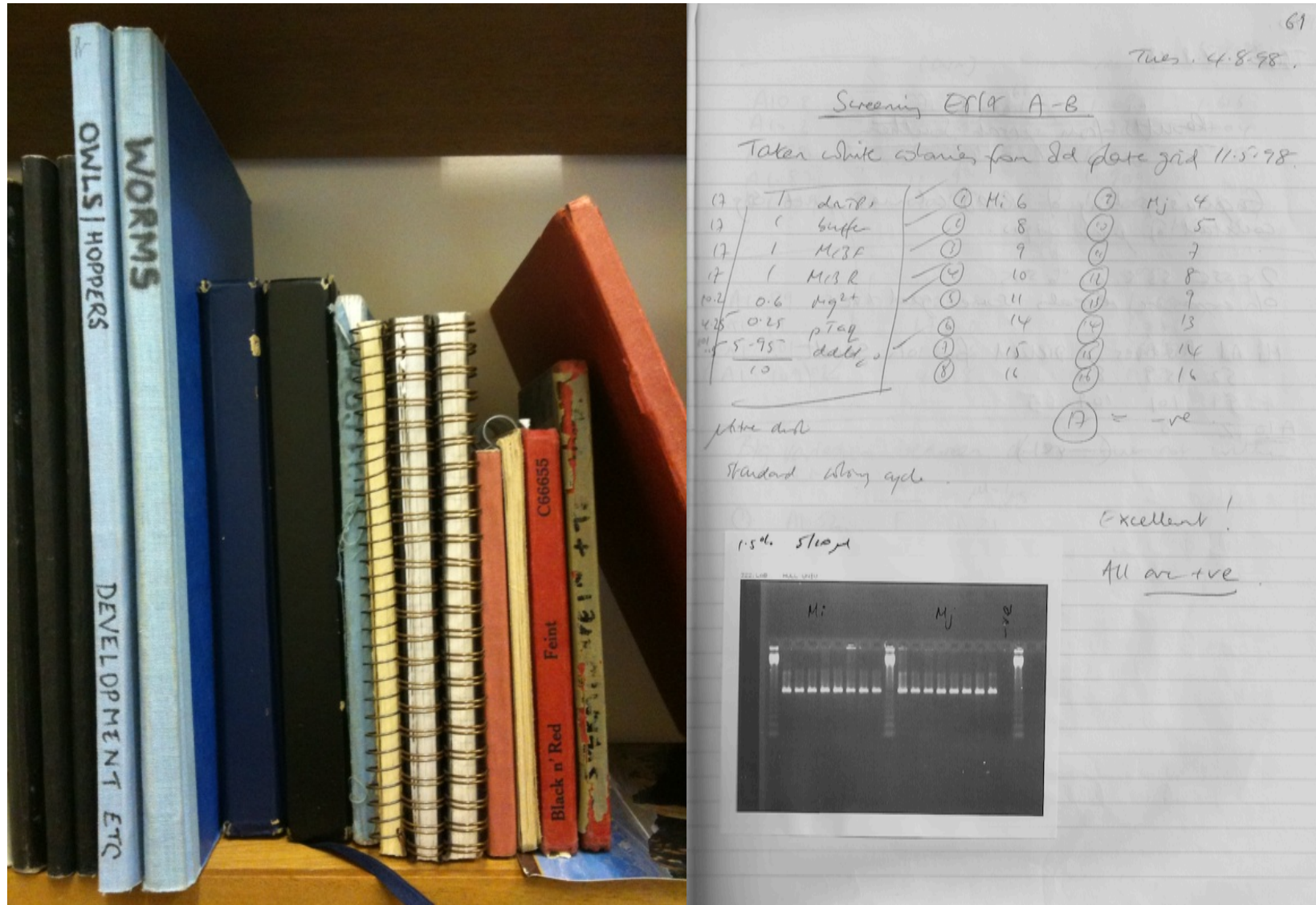
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Undergraduate Research Projects

- Biological Sciences 3rd year research projects
  - 20 or 40 credit module
  - Almost all students and staff are involved

- Keeping a laboratory experimental record is required and assessed

- Are there any advantages for teaching or learning of Electronic Laboratory Notebooks (ELN)?
  - ELN= Any computer-based method of experiment-recording

Traditional (paper) lab books

Traditional lab books

- Successful, but…

- Source, not method, of student-supervisor interaction

- Social Web (Web2.0)
  - Twitter, Facebook, Blogs, RSS

- Can Social Web research project interactions benefit supervisor or student?

Quick tour of the ELN basics

- Goals for a Student ELN…

- Simple to use for students of mixed ability
  - Yet expandable with powerful Social Web tools

- Should improve supervisor-student interaction
  - Better access to student work
  - Better opportunities for commenting and interaction

- My chosen ELN is WordPress blog software
  - Free, open-source, very well tested by millions, active development

- Quick tour….

A Student ELN (editable web site)

Steve's Lab Notebook

Ramblings and status updates from my ventures into computational biology research; otherwise known as my project's electronic lab notebook

Posts Comments

« Upgrading...   Upgrade »

CleanUP

I just had a quick play with CleanUP on the Ubuntu machine in the lab and received this output:

    root@Bioinformatics4:/home/steve/Downloads/CleanUP/Linux# ./CleanUP

Cleanup (2.0) generates a non redundant sequence data library from any set of sequences.

For more info contact the authors:
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Sandra Brunetta – areasb16@area.ba.cnr.it

CLEANUP of what sequences ? out3.fas
What should I call the output searching file (* out3.fas.s *) ?
What should I call the file listing erased sequences (* out3.fas.e *) ?
What should I call the file of cleaned sequences (* out3.fas.nr *) ?

Sequence pre-processing...
Sequences format is: FASTA/Pearson

_____

Sequences   = 80000   Nucleotides   = 91890000

C.P.U. time [17.65 sec.]

Searching...

Meta

- Site Admin
- Log out
- Entries RSS
- Comments RSS
- WordPress.org

Links

- Align Sequences using ClustalW2 | EBI
- ATGC: PhyML
- Bayesian Evolutionary Analysis Sampling Trees – BEAST Software
- BioJava
- BioPerl
- BioWeka
- BLAST: Basic Local Alignment Search Tool
- CD-HIT Paper
- genome.gov | National Human Genome Research Institute
- MAFFT – a multiple sequence alignment program
- Molecular evolution,

Tags

algorithm aptitude automation Bio::SeqIO **bioinformatics** BioPerl **BLAST** boot-loader CD-HIT CleanUP **CLUSTAL-W** ClustDB code configuration download dual-boot efi greengenes grub information Linux MOTU **multiple-alignment** NAST **OSX** partition **perl** phylogenetics phylogeny PHYML **pipeline redundancy** refit source-code ss-rRNA ssh **STAP** taxonomy Time::HiRes tree Ubuntu upgrade welcome wordpress XCode

Recent Posts

- Taxonomy Code and XML Parsing
- Speed and efficiency...
- Upgrading...
- CleanUP
- Upgrade
- Literature review
- Ubuntu Linux

Each Piece of work is a 'Post'

Search RNase A family 1

Title

Date

📅 November 12, 2009   👤 samchambers09   💬 Leave a comment   ✏️ Edit

#4	Search **"RNase A" AND homo [orgn]**	10:00:32	246
#18	Search **"RNase A family* 1"[TITL] AND homo [orgn]**	09:56:28	0
#17	Search **"RNase A family* 1" AND homo [orgn]**	09:54:42	0
#16	Search **RNase A family* 1 AND homo [orgn]**	09:54:27	153
#15	Search **RNase A family, 1 AND homo [orgn]**	09:53:16	142
#14	Search **RNase A family, 1**	09:52:59	820
#13	Search **"RNase A family, 1"**	09:52:37	0
#12	Search **"RNase A family, 1" AND homo[orgn]**	09:49:32	0
#11	Search **"RNase A family 1" AND homo[orgn]**	09:49:26	0
#10	Search **"RNase A family 1" AND homo [orgn]**	09:43:34	0
#9	Search **RNase A family 1 AND homo [orgn]**	09:43:19	142
#8	Search **RNase A 1 AND homo [orgn]**	09:42:58	144
#7	Search **RNase A 1**	09:42:41	833
#6	Search **"RNase A 1"**	09:42:31	0
#5	Search **"RNase A 1" AND homo [orgn]**	09:42:22	0

Data

despite searching for RNase A family 1 in a variety of ways as seen above, search results were mixed. Was not able to search with quotation marks as no results were found and when searching without quotation marks got a series of results including results for RNase A family 9 isoform 1.

Searched with asterisk instead of comma to try and see whether this would alter the search results which it did and increased the search results from 142 to 153 however still did not prevent the search from being uncontaminated with other families of RNase A

Discussion

Searched with [TITL] to see whether the search engine was searching through the search term in a different way and trying to associated RNase A with the [ORGN] search term however this resulted in no results

Think about this later as to why no specific search results could be obtained for just RNase A family 1

📁 Uncategorized 🏷️ outstanding

Posting is word processor like

Title

Insert images etc

Body of Post

Text formatting toolbar

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RSS Notification- student monitoring

■ RSS will notify me every time a post is made

RSS Notification- student monitoring

■ RSS feeds of student's work appears in my own ELN

ul	reagent	concentration	5x
3	DNA		
2.5	dNTP	[2mM]	12.5
2.5	NH4 buffer	10x	12.5
1.5	MgCl2	[25mM]	7.5
0.5	RPolF3	[10uM]	2.5
0.5	RPol3R	[10uM]	2.5
0.5	Taq		2.5
12.5	ultrapure H20		62.5
=25	**FINAL VOLUME**		

NB volume of H2O wrong by 1.5ul.

Reaction Tubes, with mineral oil.

1. M.flor-3
2. M.flor-5
3. +ve control, MjNCSU7-2 10-3
4. -ve control H2O

Cycle Conditions (ABI machine 3 DaveSSU program)

1	94	3 mins	
2	94	45 secs		
3	50	1 min		x35
4	72	3 mins		
5	72	10 mins	

Repeat 2-4 35 times (36 in total)

Started at 5pm 13.10.09 machine 3.

| Tags: PCR, RNApol2 | Category: 2:Research, Meloidogyne | Comment | Edit

February 2009
January 2009
December 2008

November 2009

M	T	W	T	F	S	S
						1
2	3	4	5	6	7	8
9	10	11	12	13	14	15
16	17	18	19	20	21	22
23	24	25	26	27	28	29
30						

« Oct

Moss ELN
Speed and efficiency…
Upgrading…
CleanUP
Upgrade
Literature review

Brandwood ELN
SOX Genes and SRY List – Humans.
Third Booklet Task.
Second Booklet Task.
First Booklet Task.
First genbank search!

Chambers ELN
k6 family
Searches into K6 family
k6 families?
RNase A family table
RNase A families

Smith ELN

10

Simple Comments (Feedback)

Comments and Feedback

Student Post

My Comment

➡ Home > Uncategorized > Search RNase A in protein

Search RNase A in protein

📅 November 10, 2009   👤 samchambers09   💬 Go to comments   💬 Leave a comment   ✏ Edit

search RNase A and homosapiens gives 263 results

Results gained from this contain all the results for RNase A in homo sapiens as there are 13 different types

First Result -

```
" LOCUS       P07998                    156 aa           linear   PRI 03-NOV-200!
  DEFINITION  RecName: Full=Ribonuclease pancreatic; AltName: Full=RNase 1;
              AltName: Full=RNase A; AltName: Full=RNase UpI-1; AltName:
              Full=RIB-1; AltName: Full=HP-RNase; Flags: Precursor.
  ACCESSION   P07998
```

📁 Uncategorized

💬 Leave a comment   💬 Trackback   Trackbacks (0)   Comments (1)

Dave Lunt

November 12, 2009 at 1:57 pm | #1   Reply | Quote | Edit

Good. Maybe you could expand a little on this post? It would be better to paste in your EXACT search phrase, and do comparisons with other spellings and searches limited by fields. How is a *Homo sapiens* search different if you add [ORGN] with it? Maybe you could comment on whether the search results look OK, or whether they are full of odd sequences that look wrong.

Comments become conversations

2 comments to Speed and efficiency…

dave
November 21st, 2009 at 20:34 · Reply · Edit

I agree about the taxonomy issue. This is the majority of the time. Maybe you could have a look at what this section is actually doing. Try to see whether the slowness comes from poor decisions in how to parse the information or a general struggle with a large computational task. If the second then C++ could be a good choice. If the former then doing it right in any language is the priority.

Steve
November 22nd, 2009 at 12:06 · Reply · Edit

Hi, yeah I'm looking into a few options with this, as the speed there is a real issue and let down overall for the total runtime! I think optimally, having the whole pipeline running in C++ would be beneficial, as any speed increase is undoubtedly a bonus, when we take into account the volume of sequences we are likely to process. This would be a bit of a task however, but not completely impossible. Perhaps if I have time left towards the end of the project, or even over xmas/holidays, I will have a look at this?

ELN Advantages

- Advantages for Students
  - Easier to enter complex data
  - They prefer web-based nature

- Advantages for Supervisors
  - Comments and feedback are better
  - Problems can be identified earlier
    - I am alerted to new student work
    - Students cannot fib about progress
      - "I forgot my book"
  - I can work from home (student too)
  - Scales well- I can deal with a greater volume of student work more easily

ELN Conclusions

- Realism is needed
  - Weak students have bad lab-books no matter what format

- Social Web has many tools useful for teaching

- Monitoring; tracking student work is much easier

- Mentoring; commenting and feedback is MUCH better

- 'Extras' may become valuable
  - Archiving, publishing, distance learning

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Tags & categories for organization

- ## Posts can be filed in categories
  - Experiment 1
  - Experiment 2
  - Meta analysis

- ## Posts are labeled "tagged"
  - To-do
  - Gene X

- ## Tag-clouds allow easy navigation