

Using electronic laboratory notebooks to promote student research mentoring and monitoring

Dr Dave Lunt

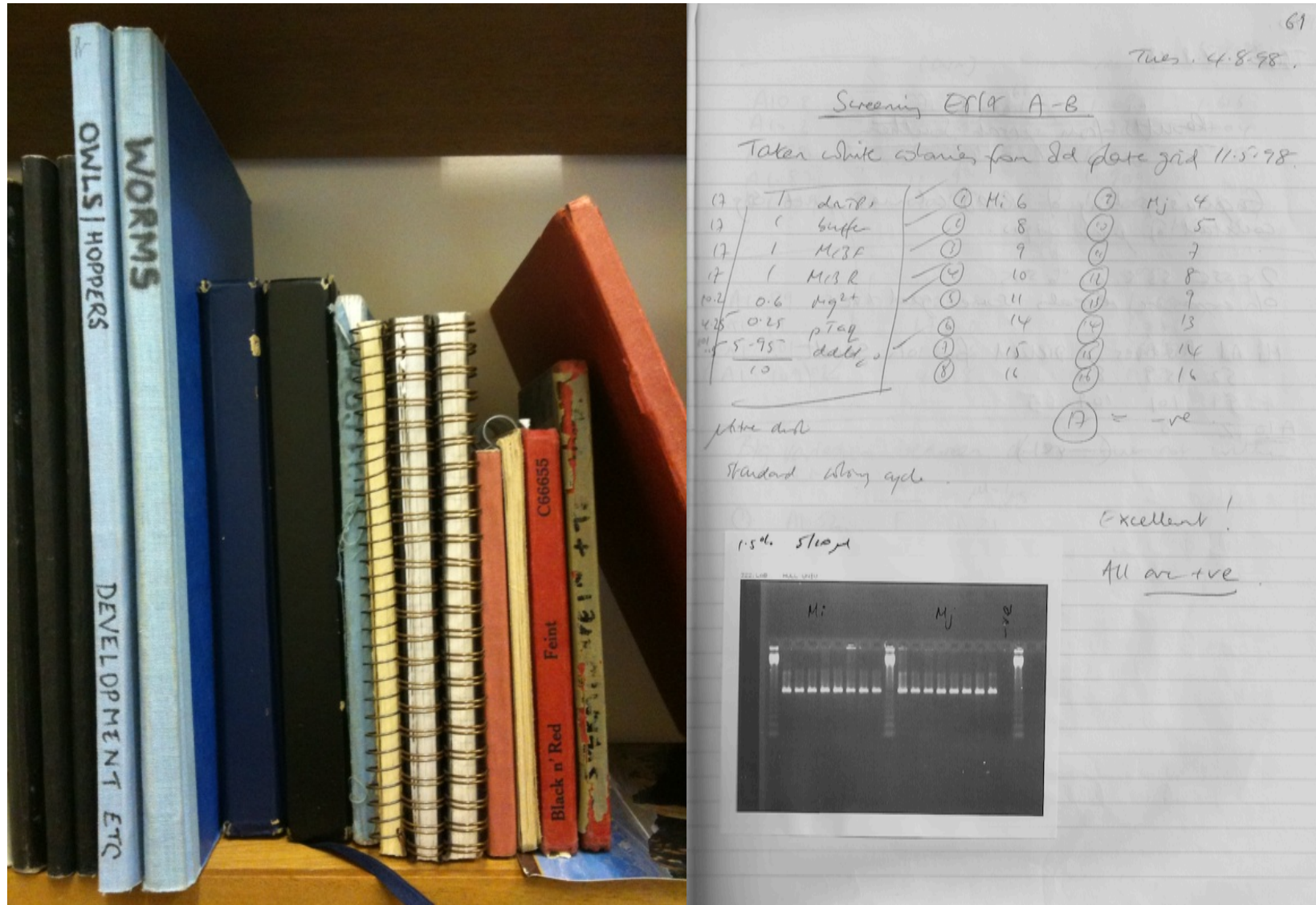
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Undergraduate Research Projects

- 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



WORMS
OWLS | HOPPERS
DEVELOPMENT ETC


- 
- A photograph showing an older man with white hair and a younger man with dark, curly hair. Both are wearing light-colored, button-down shirts. They are standing in front of a green chalkboard. The older man is holding a pen and pointing at an open book held by the younger man. The younger man has his hand to his chin, looking thoughtful. The scene suggests a teaching or mentoring interaction.





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 decision is actually doing. Try to see whether the slowest 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 best.



Steve
November 22nd, 2009 at 10:06 - Reply - Edit

Hi, yeah I'm taking into a few options with this, as the speed there is a real issue and let down overall for the total runtime! I think optimising, while 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 the data and the processing process. This would be a bit of a task however, but not impossible. Perhaps if I have time left towards the end of the project, or even over summer holidays, I'll have a look at it.


On a slightly different note, Petafishs be working now? I've changed to a different members-only plug-in for the site, that has better support for works. You may need to refresh the feed, or delete it and set it up again in your reader for it to work?

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)


[HOME](#) [ABOUT](#) [WRITE-UP](#) [TODO](#)



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](#)



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, phylogenetics and](#)

« [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:
Giorgio Grillo – giorgio@area.ba.cnr.it
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...

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'

Title

Date

Data

Discussion

Search RNase A family 1

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

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

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

The image shows the 'Add New Post' interface in WordPress, which is designed to be word processor-like. The interface includes a title field at the top, a large text area for the post body, and a rich text editor toolbar. The toolbar has two tabs: 'Visual' and 'HTML'. The 'Visual' tab is active, showing various formatting options like bold, italic, underline, link, unlink, list, and more. There are also icons for inserting images, media, and other elements. At the bottom, there is a 'Path' field and a 'Word count' display.

Title

Body of Post

Insert images etc

Text formatting toolbar

RSS Notification- student monitoring

- RSS will notify me every time a post is made

The screenshot shows the Google Reader interface. On the left is a sidebar with navigation options: Home, All items (86), Starred items, Your stuff, Shared items, Notes, Trends, Browse for stuff, People you follow, Explore (Popular items, Recommended sources), and Subscriptions. The main content area displays an RSS feed titled 'ELN'. The feed shows a list of items with their titles, authors, and dates. The items are as follows:

Author	Title	Date
Dan Brandwood's ELN	SOX Genes and SRY List – Humans. - SOX Genes and SRY in Humans as currently listed in Genbank. SOX1 SOX2 SOX3 SOX4	Nov 25, 2009
Steve's Lab Notebook	Speed and efficiency... - I've been considering, although not much of a priority, attempting to upgrade STAP to C or preferably	Nov 22, 2009
Steve's Lab Notebook	Upgrading... - Trying to get the libssh2 module installed as an Apache extension on the Freeside server at uni, so I can	Nov 22, 2009
Steve's Lab Notebook	CleanUP - I just had a quick play with CleanUP on the Ubuntu machine in the lab and received this output:	Nov 22, 2009
Steve's Lab Notebook	Upgrade - Just upgraded to Wordpress 2.8.5! All seems to be in order!	Nov 22, 2009
Steve's Lab Notebook	Literature review - My literature review seems to be coming along well! To help with organising my review and also with citation	Nov 22, 2009
Steve's Lab Notebook	Ubuntu Linux - I've just managed to finish the configuration of a dual-boot installation of Mac OS X Leopard 10.5.8 and Ubuntu	Nov 22, 2009
Steve's Lab Notebook	Preparation++ - One of the main issues with running the large dataset through STAP, would be the number of redundant	Nov 22, 2009
Steve's Lab Notebook	Benchmarking and preparation - Now that we had tested the functionality of the pipeline. It was time to focus on preparing it for	Nov 22, 2009
Steve's Lab Notebook	Critical thinking and planning - We are going to be using STAP to process a large set of genetic data and attempt to process it into	Nov 22, 2009
Steve's Lab Notebook	How STAP works - STAP as the name suggests (ss-rRNA Taxonomy Assigning Pipeline) uses the publicly available programs	Nov 22, 2009
Steve's Lab Notebook	No Feed Key Found - You need to use a Feed Key to access feeds on this site. Please login to obtain yours.	Nov 22, 2009
Will Smith's ELN	To do: uncategorised - Unkown protiens: AAP21892 ORIGIN 1 mipiqtlvff miyivieslt iivqssliiva vlgrewlqvr rimpvdmili slgisrfclq 61	Nov 19, 2009
Will Smith's ELN	Human T2R Genes - TAS2R1 NM_019599, BC101729 TAS2R2 NG_005302, NG_004702 TAS2R3 BC069337, NM_016943	Nov 18, 2009
Sam Chambers- ELN	k6 family - on search for k6 family within genbank came across this paper which clearly shows where RNase family 6 is present	Nov 18, 2009
Sam Chambers- ELN	Searches into K6 family - Search in nucleotide section of genbank for k6 This search in Gene shows 4 results, including: RNASE6	Nov 18, 2009
Sam Chambers- ELN	k6 families? - when searching for families within RNase A, genbank came across some results which did not say they were part of	Nov 18, 2009
Sam Chambers- ELN	RNase A family table - table to show size, accession number and definition of each of the families of RNase A only family with no	Nov 18, 2009
Will Smith's ELN	Key term TAS2R/T2R - Nucleotide search: ' T2R; 527 hits- Not specific to humans. Use of Top Organisms tab 'Homo sapien': (t2r	Nov 16, 2009
Sam Chambers- ELN	RNase A families - From research into papers and journals it is expected that there will be a total of 13 families of RNase A in	Nov 12, 2009
Sam Chambers- ELN	Search RNase A family 1 - #4 Search "RNase A" AND homo [orgn] 10:00:32 246 #18 Search "RNase A family" 1*[TITL] AND	Nov 12, 2009
Sam Chambers- ELN	Square brackets for homo - Search in Protein Section of genbank website. Search "RNase A" and homo sapiens - gave 263	Nov 12, 2009
Sam Chambers- ELN	Search RNase A in protein - search RNase A and homosapiens gives 263 results Results gained from this contain all the results	Nov 10, 2009
Sam Chambers- ELN	Search RNase A - Searched RNase A in genes and got 161 results When searching RNase A and human in genes and got just 1	Nov 10, 2009
Will Smith's ELN	blastx and blastn. - ATTCATCAGTAAGCAGGCGCAAGAAAATGCCACAATTCTGATGAACATTTTACTGTC	Nov 2, 2009
Will Smith's ELN	BLAST search 2 - GTTCGACGACAAGCACACCTACTACATGAAGGTGAATTTTTTTTATCTTTT	Nov 2, 2009
Will Smith's ELN	BLAST identification task. - CACTAATCGCTTACTCATCAGTAAGCCACATAGGACTAGTCATCACCGCATGCCTAA	Nov 2, 2009

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 H2O		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

Simple Comments (Feedback)

Leave a Reply

Name (required)

Mail (will not be published) (required)

Website

You can use these HTML tags

Submit Comment

Comments and Feedback

Student Post



[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.

My Comment



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.



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

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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

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3	DNA		
2.5	dNTP	[2mM]	12.5
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- Realism is needed

- 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

HOME ABOUT WRITE-UP TOOLS

Steve's Lab Notebook

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

Meta

- Site Admin
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Sequences format is: FASTA/Pearson*

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------------------	----------------	--------------------	-------------------

CPU time [17:55 sec.]

Searching...

Tags

Alphabetical alphabet substitution
Bio:neuro bioinformatics
BioPerl BLAST
BioPerl last-trader
CD-HIT CleanUP
CLUSTAL-W ClustalC code
configuration download
dot-dot-all dot programs grab
information Linux NCBI
multiple-alignment rust
OSX perl
phylogenetic phylogeny python
pipeline redundancy nets
sequence-to-sequence tool

STAP

Taxonomy
Taxonomic tree library
update genome sequences
XCode

Recent Posts

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Dr Dave Lunt

Department of Biological Sciences, University of Hull, UK

d.h.lunt@hull.ac.uk

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

