





TUO REVOLUTIONS

CANADA'S MICHAEL SMITH SENAME SCIENCES CENTRE Martin Krzywinski Gustrestud Nare Paran Gustrester

Acknowledgements

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JOMES T. KIAK IO "MIAA¢A, MIAA¢A"



two revolutions

revolution [n.]

- drastic and far-reaching way of thinking and behaving
- paradigm shift
- promise beneficial change
 - increased quality of life for under-represented
 - independence, broader rights, protection from predatory elements
- who are the (a) under-represented, and (b) predatory elements?
 - in computers
 - under-represented: the OS user
 - predators: corporate bodies with monopolies, marketing, FUD
 - my ability to meaningfully participate in development of close-source software is negligible
 - in science

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- under-represented: individuals
- predators: restrictive patents/licenses, large privately-funded centers bereft of public accountability, academic cliques isolated from social context
- my ability to grasp new findings, evaluate their impact and foresee implications is negligible

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NO, THE NHOLE POINT OF LINUX ISN'T THAT IT'S FABE, AND NEVER Has been.

THE POINT WITH LINUX IS THET I DION'T HAVE D 9000 05 00 My Machine ... So I whote one.

LINUZ TORVALDZ COMP.OZ.MINIX, 20 DEC 1992

revolution 1 | linux

UNIX on Intel CPU

- free OS on cheap hardware
 - performance per unit cost is steadily dropping
 - "free" vs "absolutely free" what is the real cost?
 - in our lab, computer hardware costs are negligible compared to personnel and laboratory equipment
 - my workstation costs ~ 1/50th of my salary
- line between user and developer base blurred
- "Beowulf" clusters are ubiquitous
 - cheap, limitless potential, free toolkits
- community encourages users to experiment
 - communities, not cliques
 - anyone can contribute
 - code, document, test, mirror
- rewards innovation and sharing
 - does not rely on scarcity tokens to drive its economy
 - skill and meaningful contribution is rewarded independent of socioeconomic status, reputation, or charisma

and all can all

Ten years out, in terms of actual hardware costs you can **almost** think of hardware as being free – I'm **not saying it will be absolutely free**.

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B. Gates emphasis is mine

revolution 2 genomics

- genomics, [n.]
 - study of organisms in terms of their genomes
- offers insight to fundamental building blocks of living systems
 - structure, biochemistry, evolution
 - organism as network system biology
 - understand basic processes in a living cell
- genomics is the branch of golden era of biology
 - less classification, more integrated descriptive and predictive models
 - periodic table of elements, quantum mechanics
- applications are the fruits
 - accelerate drug development by identifying target pathways
 - recognize variants contributing to health and resistance to disease

- generate diagnostics for early detection of cancer
- understand reasons for individual drug resistance

It should be possible to understand the difference between a "bag of molecules" and a biological system.

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F. Collins et al. Nature (2003) 422: 835-847

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common philosophy



Timo Hannay, Thought Experiment: Science as an Open Source Project www.oreillynet.com/pub/a/network/2002/07/17/timo.html



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common process

programming science new conclusions backwards-compatible new code should not crash system with existing knowledge increase range power of explanation and prediction; reduce complexity of add features or elegance fundamental laws robust and logical in accordance to observed data reproducible properly documented extraordinary claims require major rewrites require damn good code extraordinary evidence advancement

Timo Hannay, Thought Experiment: Science as an Open Source Project www.oreillynet.com/pub/a/network/2002/07/17/timo.html



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embracing openness

- success in science requires open source principles
 - examine, verify and extend knowledge
 - knowledge must be publicly accessible to promote discovery
 - many eyes make all bugs shallow
 - scientists have created many open source tools
 - communication and collaboration
 - manipulate, munge, analyze large data sets
 - agree, adopt and improve
- integration of science into society requires open source principles
 - scientific process is not suitable for handling emergent ethical, legal and social issues (ELSI)
 - it is impossible to "test" wide-scale social models
 - social harm caused by misguided policies cannot be reversed
 - keeping science and its products open allows everyone to participate in ELSI discussions
 - experts from social sciences, law, humanities, cultural anthropology

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• public forums

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public effort triumphs

- public assembly of human genome done on UCSC centicluster
 - June 2000
 - 100 800-MHz P3 Linux boxes



I thought it would help to get as much information about genes and the genome into the public domain to help discourage people from patenting it wholesale.

Jim Kent



Venter, Collins TIME July 3 2000



Venter, Clinton, Collins

www.cbse.ucsc.edu/UCSC_Kilokluster.html, biomedical.ucsc.edu/Computation.html



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ACTGs of genomics





proteins

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proteins participate in biochemical pathways and mediate processes

- > alter molecules
- > transport molecules
 > catalyze reactions

phe 508

membrane transporter

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FRANCIS COLLINS In Vision for the future of Benomics Research, Nature (2003) 422: 835-847





genomics data is public

- the net started at CERN
 - physicists needed to share documents and large datasets
 - genome centers and scientists have been networked from the start
- public data release is a mandate of sequencing centers
 - data is submitted to Genbank, a public repository of sequence information, as soon as it is collected
 - "Bermuda Principles" ratified during a 1996 sequencing conference, call for automatic and rapid release of primary sequence data to the public domain

• internet is the natural forum

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www.ncbi.nlm.nih.gov/ www.ebi.ac.uk/embl

www.gene.ucl.ac.uk/hugo/bermuda.htm



data viewers are public

- openly available genome browsers
 - permit public mining of information
 - visualization of annotations
- Ensembl and UCSC browsers run on MySQL
 - entire data set can be downloaded freely
 - you can become an Ensembl mirror
 - ~100 Gb, MySQL/Perl

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develop a software system which produces and maintains automatic

annotation on metazoan genomes.

Ensembl is primarily funded by the

Wellcome Trust.

This site provides free access to all the data and software

from the Ensembl project. Click on the species buttons to the

Access to all the data produced by the project, and to the software used to analyse and present it, is provided free and

For all enquiries, please contact the Ensembl HelpDesk

without constraints. Some data and software may be subject

Help and documentation

Help

News

DAS

Apollo

Help Desk

Documentation

Take the Ensemblitour, go through a step-by-step worked

There is also an index of help pages, and a set of guided



Sequence similarity searches Batch data/sequence retrieval Vertebrate Genome Annotation (VEGA) Access to whole genome shotgun data (includes additional species) Download Ensembl data via FTP

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Ensembl Assembly Pre	view Browser
For early access to genomes undergoing annotation visit the Pre-Ensembl website www.pre.ensembl.org	Pre!
Click for more info	rmation



right to browse the data.

(helpdesk@ensembl.org).

How do I....? trails. Recent Ensembl news

Apollo genome browser

to third-party constraints [details].

example, or read these papers.

For help on any web page click:

Display your own data in Ensembl

Questions or suggestions? Try the

Documentation (includes tutorial on direct

data access & instructions for installing Ensembl on your own site)



genomics community is online

- Lincoln Stein, CSHL (NY, USA)
 - CGI.pm, GD.pm
 - generic genome browser
 - genome knowledge base
 - generic model organism database construction set
 - modular and extensible framework for storing biological information
 - distributed sequence annotation system (DAS)
 - XML web service for contributing sequence information
 - "How Perl Saved The Human Genome Project"
- Jim Kent, UCSF (CA, USA)
 - Gigassembler algorithm assembly algorithm
 - open source, Linux cluster
 - public effort beat Celera by 3 days
- Ewan Birney, Wellcome Trust (UK)
 - Ensembl browser
 - BioPerl bundle

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SARS – linux called to action

- sudden acute respiratory syndrome
 - first case in 1999
 - 8,100 cases, 800 deaths since Nov 2002
- our center was the first to publicly release the full coronavirus sequence assembly
 - 30kb ~ 1/100,000 size of human genome
 - assembled on 8-way Linux machine
 - published on Zope/Apache web server
 - sequence data used to characterize virus and search for potential therapies



SARS affects everyone www.stileproject.com



sockeye 3D genome browser



www.who.int/csr/sars/country/table2004_04_21/en/

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open data - SARS genomes in Genbank

- complete genomic sequence was immediately submitted to Genbank
- 293 sequences from 151 different strains of SARS in Genbank database
- currently >1,600 SARS-related publications indexed by Pubmed

Bioterrorism and emerging infectious disease - antimicrobials, therapeutics and

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www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&val=30271926 www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=227859

Planning for epidemics--the lessons of SARS.

immune-modulators. SARS coronavirus.

PMID: 15057645 [PubMed - indexed for MEDLINE]

PMID: 15175434 [PubMed - in process]

IDrugs. 2004 Feb;7(2):91-5.

N Engl J Med. 2004 Jun 3;350(23):2332-4. No abstract available.

2: Weinstein RA.

□ 139: Shurtleff AC.

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Related Articles, Links



News for Nerds. Stuff that matters.

Open-Source Desktop Publishing: Scribus

How we sequenced the SARS virus in five days

itable cluster management with OSL

and support

obr 10 servers

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Canadian Lab Unravels SARS With A Beowulf Cluster

Posted by timothy on Sunday April 13, @03:21PM from the you-knew-they'd-come-in-handy dept.

Amad writes "A Canadian Genetics Research Lab in BC, Canada has used a Liv sequence the genetic code of the virus linked to SARS. This lab is the first to cra the public. You can read an article about the discovery, or check out the lab."

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SAR52-12

INTERNET DATE

SARS2-6

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SARS2 -

equickly developed, but that Vancouver has a ab that could unravel a lethal mystery virus in ecord time, a comforting thought in an age that's

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TOP STORY

SARS BUSTERS the virus crackers oot started

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Smith Genome Sciences Centro, and Yaron Butterfield, assistant co-clect at the B.C. Cancer Agency.

ARS cases

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public feedback

Subject: transcription starting position of genes in TOR2

Dear BCGSC:

I downloaded your sequences of TOR2. Thank you very much for your great work about this.

JZ, Palo Alto, CA

Subject: SARS draft sequence

To all involved, CONGRATULATIONS! We will have a PCR-based SARS diagnostic up and running by next week thanks to YOU.

MJM, Madison, WI

Subject: You have to be NUTS!

My daughter doesn't think its such a good idea to have the gene sequencing for the new coronavirus on the internet. I don't either! There should have been a better way! You must be crazy!











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TID

ALL STATES

Zebra S600 ZPL printer

- wireless interface to ZPL printers for on-demand barcodes
 - Perl/Apache, Compaq IPAQ, Zebra S600
- MySQL database stores all events, objects and data

Zebra Z4Mplus ZPL printer

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MySQL LIMS





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---MOKE LIS PLOOS.

DANIEL GUANHAM Aachitect

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