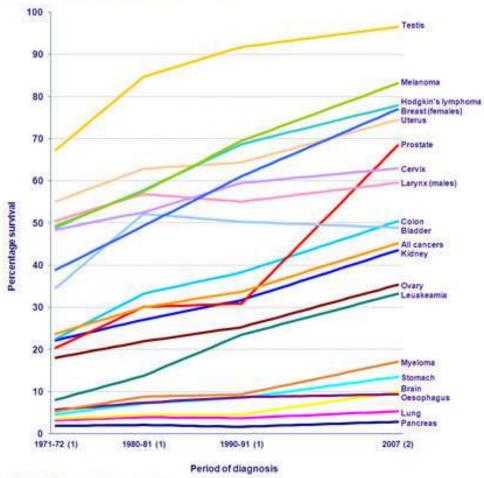


Cancer and Computers

John Pearson
QUESTnet 2016, RACV Royal Pines Resort, Gold Coast
6 July 2016

Cancer - cancer types we work on:

Figure 1.2: Relative survival (%), adults (15-99 years), selected cancers, England and Wales: survival trends for selected cancers 1971-2007



Pancreatic

Brain metastases

Oesophageal

Mesothelioma

Ovarian

Melanoma

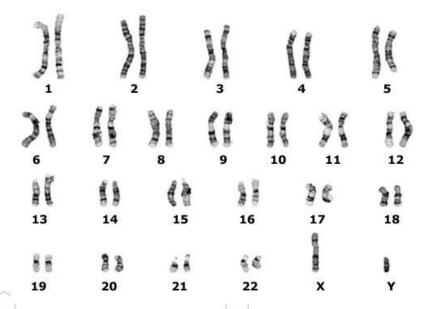
Breast

(1) 1971-1991 Cohort analysis - actual survival (2) 2007 Hybrid analysis - predicted survival



The Human Genome

- Every cell in the human body starts with a copy of the human genome
- The human genome is a set of 23 chromosomes (2 copies of each)
- Each chromosome is a long molecule of a type called DNA
- A DNA molecule is a string of chemicals called nucleic acids
- There are 4 nucleic acids A, C, G, T
- The 23 human chromosomes contain 3 billion nucleic acids





Next-generation Sequencing (NGS)

Smash DNA genome into small pieces



Sequence the fragments and create lists of base-sequences as strings



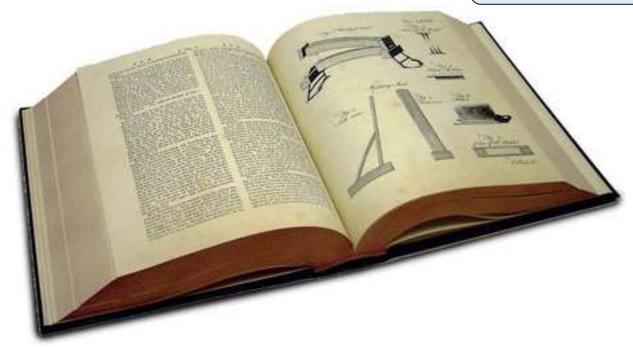
Use HPC to align strings to genome to recreate genome



A volume of the Encyclopedia Britannica: 500 double-sided pages, 8 million characters



megabytes

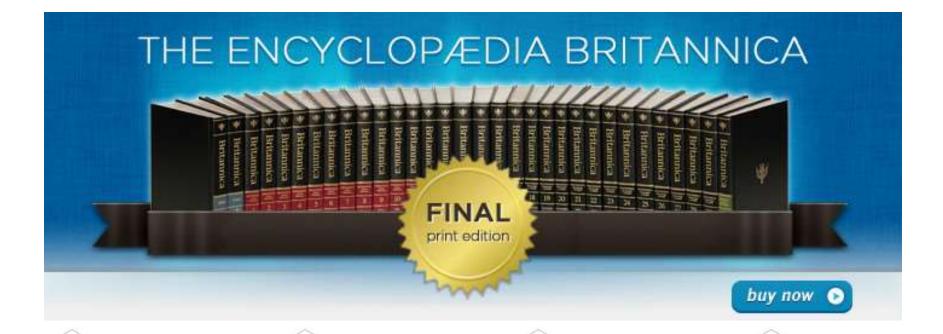




A set of the Encyclopedia Britannica: 40,000 articles, 44 million words



250 megabytes



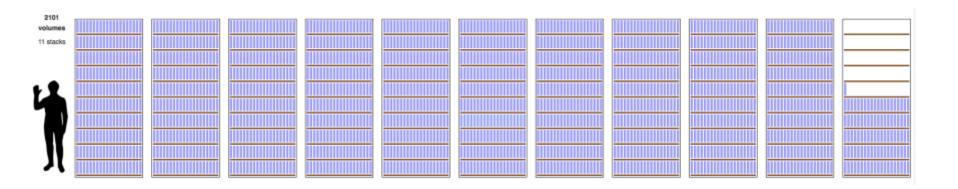


A printed copy of the English version of Wikipedia: 4.7 million articles, 2.7 billion words.



x 2,100

17
gigabytes

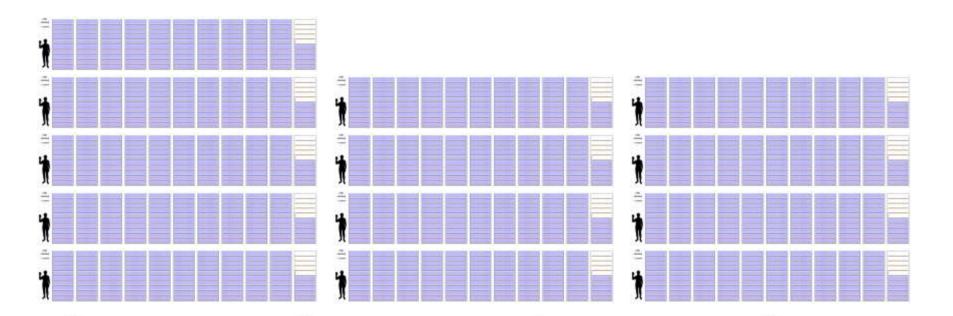


A single patient's cancer genome data: tumour sample @60x, normal sample @30x



x 37,500

300 gigabytes



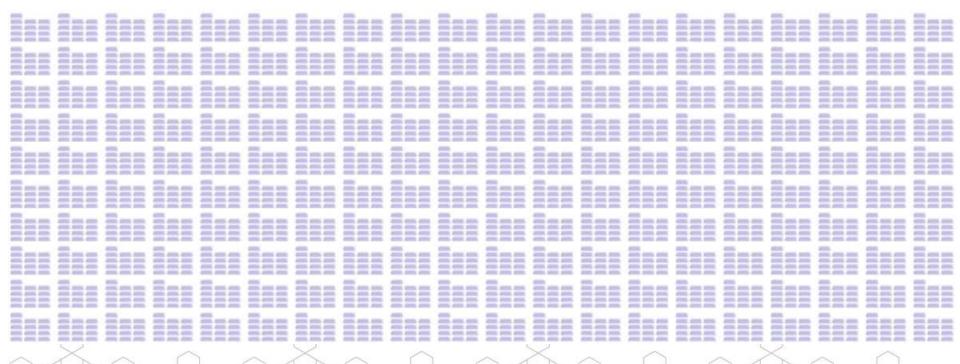


A study of 200 cancer patients using whole genome sequencing: tumour sample @60x, normal sample @30x



x 750,000

60 terabytes

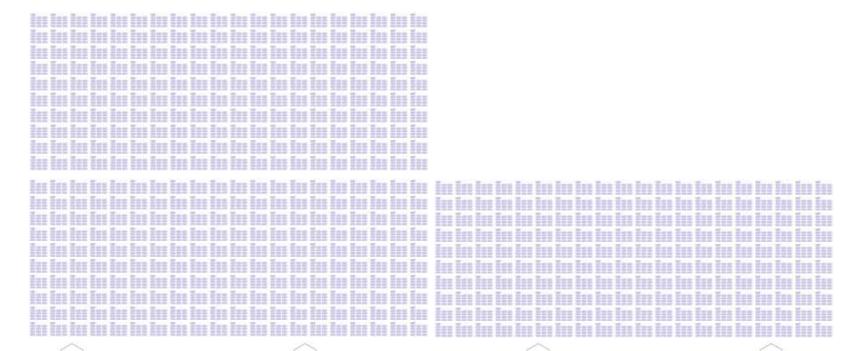


During analysis we need triple the space so we have room for intermediate and temporary files



x 2,250,000

180 terabytes



Ideally we'd do 1000 patients per cancer instead of 200 and what happens if we decide to do more cancer types ...



x ???????







Cancer is a story of good cells gone bad

Skin (good):

- Keratin armour waterproof, airtight, puncture resistant, self healing
- Continually being renewed complete replacement every fortnight
- DNA copy fidelity "10 9's quality"
- Repair injuries cells copy themselves but just enough

Cancer (bad):

- Moves, makes blood vessels, stops listening to cellular signals, copies
- DNA repair is broken so DNA copy mistakes get made
- Mistakes accumulate
- To spot a mistake you need to be able to compare the "broken" cancer genome AND the "normal" genome



Detecting broken genes in a cancer sample

Human Reference Genome (Pete)

ACGTAGTCTCAATTTAATGCACTAGAACGG

Bob's Cancer Genome

A G G T A G C C T C A T A T T A A T G C A C T A A A G G G

Bob's Normal Genome

A G G T A G C C T C A A A T T A A T G C A C T A A A A G G G



Hardware:

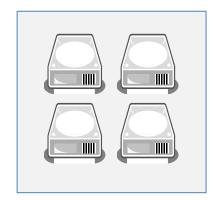
Compute



40 nodes

- 2 x 12 core Intel
- 256 GB RAM
- 4 x 1TB disks striped
- 1 x 10 GigE

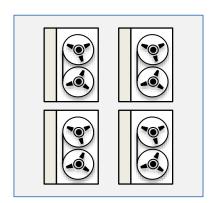
Disk



1.4 PB Lustre

- 4 x OSS pairs
- 8 x 10 GigE per pair

Tape

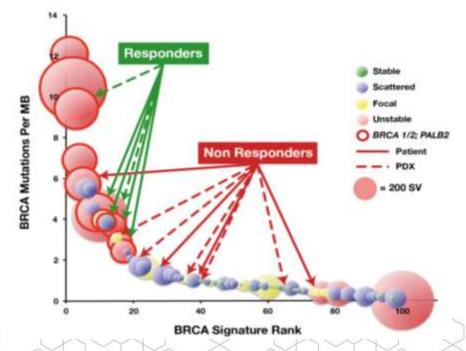


2 redundant sites

- 30 kms apart
- 2.5 PB per site
- 10 GigE connection
- Nightly updates

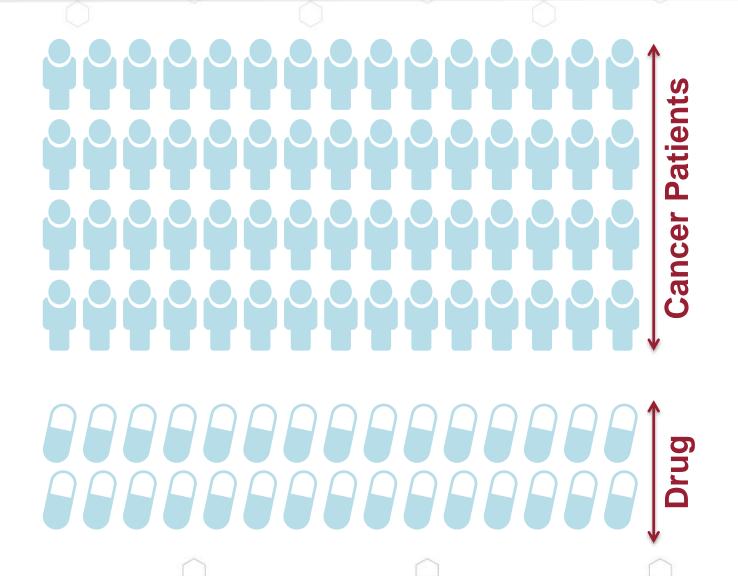
What can we do with cancer genome sequencing:

- Increase our understanding of what cancer is
- Better classification of patients into cancer subtypes
- Identification of potential new targets for drugs
- Can improve diagnosis for patients



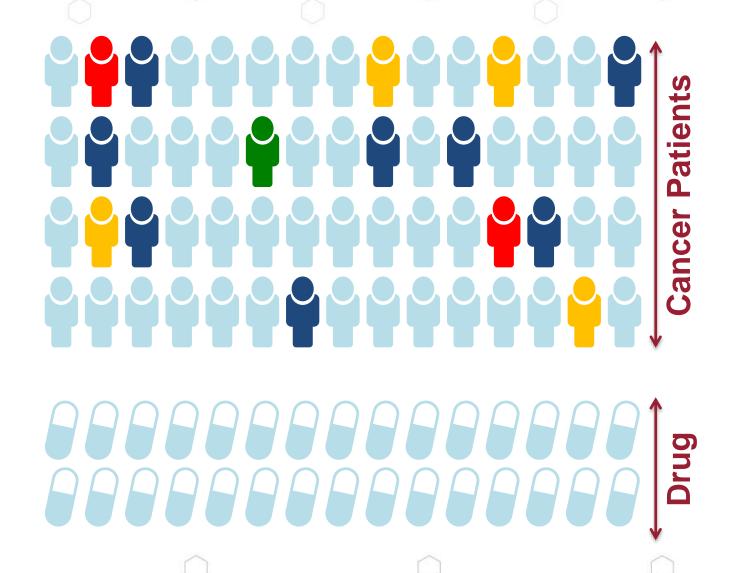


The current way we treat cancer:



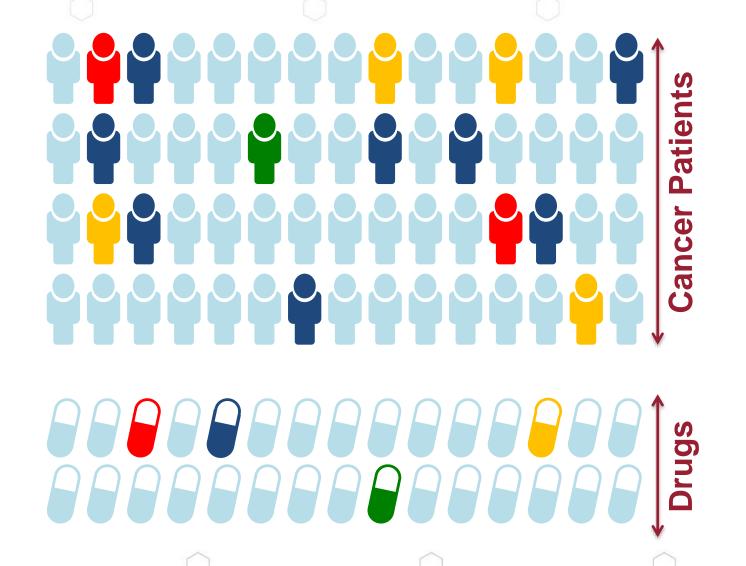


But we know cancer patients are different:





We need to match patients to drugs – Precision Medicine:





Cancer & Computers - Summary

- Cancer research is hard and expensive
- New technologies are reshaping our knowledge of cancer
- Progress is being made in diagnosis and treatment
- Modern cancer research needs:
 - labcoats and laptops
 - bunsen burners and broadband
 - freezers and fiber-optics



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