Les NGS en pratique

Quelques slides sur les NGS et leur utilisation ...

Laurent (travail avec Marta, toujours en cours ...)
THE SEQUENCE EXPLOSION

At the time of the announcement of the first drafts of the human genome in 2000, there were 8 billion base pairs of sequence in the three main databases for finished sequence: GenBank, run by the US National Center for Biotechnology Information; the DNA Databank of Japan; and the European Molecular Biology Laboratory (EMBL) Nucleotide Sequence Database. The databases share their data regularly as part of the International Nucleotide Sequence Database Collaboration (INSDC). In the subsequent first post-genome decade, they have added another 270 billion bases to the collection of finished sequence, doubling the size of the database roughly every 18 months. But this number is dwarfed by the amount of raw sequence that has been created and stored by researchers around the world in the Trace archive and Sequence Read Archive (SRA).

DNA SEQUENCES BY TAXONOMY

International Nucleotide Sequence Database Collaboration: The main repositories of ‘finished’ sequence span a wide range of organisms, representing the many priorities of scientists worldwide.

DNA SEQUENCES BY TAXONOMY

INSDC databases

Human

Trace

DNA Sequences

Non-human

SRA

How many human genomes?

The graphic shows all published, fully sequenced human genomes since 2000, including nine from the first quarter of 2010. Some are resequencing efforts on the same person and the list does not include unpublished completed genomes.

Quelques infos
Equipement des “ménages”

Laurent (travail avec Marta, toujours en cours ...)

source: http://pathogenomics.bham.ac.uk/hts/
Quelques infos
Marché concurrent, nombreuses nouveautés

Quelques infos
nouvelles versions "scale down" (plus accessibles)

Laurent (travail avec Marta, toujours en cours ...)
Les NGS en pratique
Quelques infos

le SMS arrive sur le marché

Laurent (travail avec Marta, toujours en cours ...)

Les NGS en pratique
Quelques infos
un “SMRTbell”
Quelques infos
des nouveautés surprenantes (à suivre donc ...)

"the world’s smallest solid-state pH meter."
Prix de 50,000$ et coût des réagents faible (puce à changer ≈ 500$)
source : http://www.iontorrent.com
Quelques infos des nouveautés surprenantes (à suivre donc ...)

source : http://www.iontorrent.com
Quelques infos
des nouveautés surprenantes (à suivre donc ...)

source : http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1458907
Quelques infos

des nouveautés surprenantes (à suivre donc ...)

source : http://www.nanoporettech.com/
video : http://www.youtube.com/watch?v=HbjAMJehS1g
Quelques infos

des nouveautés surprenantes (à suivre donc ...)

Laurent (travail avec Marta, toujours en cours ...)

Les NGS en pratique
Quelques infos
des nouveautés surprenantes (à suivre donc ...)

Life Technologies’ approach involves tethering a nanocrystal semiconductor called a quantum dot to a DNA polymerase. A laser excites the dot, which then transfers energy to fluorescent dye-tagged bases, but only when the polymerase adds a base to the DNA chain being built from the template being sequenced.

source : http://www.sciencemag.org/cgi/content/full/327/5970/1190
Cas pratiques
Neanderthals & Homo sapiens

Genome comparisons suggest that the two groups mated an estimated 45,000–80,000 years ago in the eastern Mediterranean area. The sequencing study, from a consortium led by Svante Pääbo of the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, found that the genomes of non-African H. sapiens today contain around 1–4% of sequence inherited from Neanderthals.

Cas pratiques
Désamination C -> U (fréquent sur de l’ADN ancien)

Laurent (travail avec Marta, toujours en cours ...)

Les NGS en pratique
Most of these studies used tiling microarray technology, in which thousands of probes are used to assess the presence of RNA transcripts. But this method is known to suffer from limitations — some probes can become attached to inappropriate sequences, for example. More recent research, however, in which RNA transcripts are sequenced directly using a technique called RNA-Seq, have hinted that the amount of the mammalian genome transcribed might not be as great as the earlier work suggested. ... The team found that whereas the microarrays reported many mysterious transcripts, the RNA-Seq technology found few transcripts other than those linked to genes coding for proteins. ... But Philipp Kapranov of Helicos BioSciences ... is seeing quite different results. He says that he and his colleagues continue to find a high percentage of a cell’s RNA originating from regions between genes.


article original: http://view.ncbi.nlm.nih.gov/pubmed/20502517
Quelques liens

pour suivre “ceux” qui suivent l’actualité NGS (blogs):

- Dan Koboldt: http://www.massgenomics.org
- Nick Loman: http://pathogenomics.bham.ac.uk/blog
- Daniel Macarthur: http://scienceblogs.com/geneticfuture

un papier récent résumant les technos commercialisés:
http://www.nature.com/nrg/journal/v11/n1/abs/nrg2626.html