GENETICS

ILLUMINA 1G SOLEXA ROADSHOW

3.05.2007 3 COMMENTS

I attended today a seminar organized by Illumina here at Mariott in Munich covering their new sequencing technology after the recent acquistion of Solexa. Maybe it is easy to impress me but it seems that also the rest of the audience shared my amazement. Courtney Brady (who came with Solexa this January to Illumina) gave the introductory lecture. Following DNA sample preparation (denature into single strands, fragment and ligate adapters), DNA is attached in clusters to so called “flow cells” precoated with a dense lawn of primers (I skip a briding step). The next step is repeated again and again as “sequencing by synthesis”. After adding polymerase and all four labeled dNTPs the field is laser excitated and photographed – wash – add+wait – click – wash …. Images are processed, the colors translated into bases and aligned to the reference sequence. Hopefully, all my notes are correct: 40 million clusters per flow cell – each run 1 billion bp or 1Gb – max 35 bp /read – 20,000 clusters / tile, 200 tiles / channel, ultimately 1 billion bp for ~ 3000€. There are already service labs who can do that for you. With the small read lengths, there might be problems with repeats; resequencing with paired ends might be a solution; sequencing multiple individuals is possible by sacrifying the first 4 bases to start with unique sequence.
Finally, Chris Clee from the Wellcome Sanger Center was talking about his early access experience. Many years they used the ABI 373/377, then the 3700 and now the 3730xl. They are interested in low costs, paired end data and/or long ready lengths, fast throughput with low hands-on time. The new 1G can be handled by a single person that can do all steps, process is very “hands off”, does not need much extra equipment, with little contamination risk as there is no cloning step. No more errors seen already at 3x fold coverage in bacterial DNA. Will check my notes with the slides as soon as they are available. It will be interesting to see , how the Illumina/Solexa system scales to the Genome Sequencer 20 of 454/Roche and the forthcoming SOLiD System of Agencourt/Applied.
My Conflicts of interest: free dinner. Yea, yea.

Addendum

I am trying here a very first comparison of the technologies, please correct me if I am wrong:

	Time per run	read length bp	reads per run	MB	€$ / run
Illumina / Solexa 1G	? 2-3d	25	60,000,000	1,500	? 6,000
ABI SOLiD	? 2-3 d	25	80,000	2	? 12,000
Roche 454 GS 20	? 8 h	100	200,000	20	? 6,000
Roche 454 GS FLX	? 8 h	250	400,000	100	? 12,000

3 THOUGHTS ON “ILLUMINA 1G SOLEXA ROADSHOW”

cgb

14.09.2007 AT 21:04

your table – is out by orders of magnitude.

illumina 1 G = 40 million reads per run – closer to 60 million now.

1.4 GBases not megabases per run.

I dont know about the solid.

admin

17.12.2007 AT 16:14

thanks, corrected

zuj

18.02.2008 AT 12:42

hi, thanks for putting up all the information, just want to point out, ABI SOLiD is capable of producing almost 3GB per run. =)

COMMENTS ARE CLOSED.