Genome - the new intimacy.

Once scanned (sequenced), your genome brings extraordinary amount of information about you, your predecessors and your successors. All that in a file of size between ~700MB and ~3GB.

That it is something different than privacy like your home address or your router's temporary IP. Can you feel the difference?

What if file will not be deleted right after analysis were made? What if it would expose much more than is needed to perform analysis? What if it would leak to the Internet? What then if it would be found by insurance companies and/or your future employer? There are many risks and they are really huge.

Genome(s) will become new intimacy.

Is it just about human genomes? Of course not. Today expensive racing horses are sequenced and analysed (it is not a surprise that owners would like to know everything about horse's health and potential). Third part of the market are plants.

Next generation sequencing (NGS [https://en.wikipedia.org/wiki/DNA_sequencing#Next-generation_methods]) gets cheaper each half of the year. Once price will reach magic point masses will want to have their own scan. What then? It is not hard to predict that market for analysis services will explode. People will send genomes for this-or-that analysis on a mass scale. Companies will try to overuse current lack of awareness about safety and risks - they will collect extremely pricey data that they will never ever delete.

In a series of blog posts tagged ideas-for-genomics-project [http://scalaakka.blogspot.com/search/label/ideas-for-genomics-project] I am describing ideas that will allow scanning & analysis market to growth by addition of genome safety, reduction, signing and anonymity.

Let me also add this sentence to my predictions [http://scalaakka.blogspot.com/search/label/prediction] : soon we will see dozens of new companies that will provide services over genome files. Part of them will be about "genome safety [http://scalaakka.blogspot.com/search/label/SafeGenome]".

Posted 21st November 2015 by Artur Stanek (kermitas)

Labels: bioinformatics, GenomeBank, genomics, ideas-for-genomics-project, NGS, non web find, prediction, SafeGenome

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