

GENETICS, SOFTWARE

GENOME EXPLAINED

12.12.2007 1 COMMENT

You may want to read the full story at Public [Rambling](#) (fiction), the [NYT article](#) of Amy Harmon (fact) or the [“Peepshow” article](#) of Marco Evers (fact) and come back here afterwards. The recent advances in genome sequencing (and typing) has left us with an enormous amount of data. Although technology has been available for a couple of years knowledge [exploded only recently](#), where people now may decide to participate in a genome study or even have their genes tested on their own costs at DeCodeMe, 23andme, Navigenics or other personal genome service provider.

The main question is, what do these data really mean for us? Should we start an Open Source Project Genome Explained to collect the necessary annotation rules and provide a platform to apply these rules to local data? The data mode may be quite simple: a multi-line FASTA flatfile where each sequence is associated with one or more disease risks.

My Genome Explained

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| | |
|--------------------------|--|
| 12.12.07 RSS User XXX | Your genome data file d:\affx\20303.txt <input type="button" value="Durchsuchen..."/> |
| | Data description: Enter any text 500K data from me |
| | obtained on YYYY-MM-DD 2007-12-03 |
| | produced by Decode 23andMe Navigenics |
| | Is this an anonymous set? <input checked="" type="radio"/> yes <input type="radio"/> no |
| | Data Format FASTA multiline DBSNP_RSnames ILLUMINA_IDs |
| | <input type="button" value="send >>"/> |

For individual advice, however, we need to take into account also the interaction with risk lowering sequences which is impossible. So this is not a technical question: there are so many ethical questions that need to be answered first. “Do not harm” is a longstanding principle in the medical field.

NACHTRAG

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