東北大学グローバルCOE

Network Medicine 創生拠点

NM高等教育セミナー

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Comparison of sequencing platforms for single nucleotide variant calls in a human Sample

2012年9月14日(金) 16時-17時30分
医学部5号館201号室

Next-generation sequencings platforms coupled with advanced bioinformatic tools enable re-sequencing of the human genome at high-speed and large cost savings. We compare sequencing platforms from Roche/454, Illumina/HiSeq, and Life Technologies/SOLiD for their ability to identify single nucleotide substitutions in whole genome sequences from the same human sample. The differences in the variant calls were investigated with regards to coverage, GC content and sequencing error. Some of the variants called by only one or two of the platforms were experimentally tested using mass spectrometry; a method that is independent of DNA sequencing. We establish several causes why variants remained unreported, specific to each platform. We report the indel called using the three sequencing technologies and from the obtained results we conclude that sequencing human genomes with more than a single platform and multiple libraries is beneficial when high level of accuracy is required.

本セミナーは医学履修課程特別セミナー等を兼ねています。受講学生は履修簿を持参し、セミナー修了後にサインを受けること。聴講は自由大歓迎です。学部生の皆さんもぜひどうぞ。

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