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International Human Epigenome Collaboration and DNA Methylation Data Analysis

国際ヒトエピゲノム連携の現状と DNA メチル化情報解析の手法

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IHEC (International Human Epigenome Consortium) is an international research collaboration of epigenome projects around the world to jointly provide a human reference epigenome dataset. The 2nd IHEC meeting is held in Berlin, Germany in this November. The up-to-date status report of IHEC activity will be given in this seminar.

Also, an introduction to Bisulfighter will be given. Bisulfighter is a software package for detecting methylated cytosines (mCs) and differentially-methylated regions (DMRs) from bisulfite sequencing data. The mC calling part utilizes LAST aligner which provide highly sensitive mapping of bisulfite treated short reads. Based on the LAST alignment results, Bisulfighter provides highly accurate mC rate estimation. The DMR detection part of Bisulfighter uses a novel hidden Markov model (HMM)-based framework that captures probability distributions of distances among neighboring mCs. Compared to other published tools, Bisulfighter provides better sensitivity on mC calling with lower false discovery rate, more precise mC level estimation, and more exact DMR identification.

Keywords: Epigenome, DNA methylation, International Human Epigenome Consortium