HLAscan v2.0

1. Updates

(1) HLAscan v2.0 is compatible with human reference (hg19 (v37) and v38).

(2) Bam file and Fastq files can get to as an HLAscan v2.0 input.

(3) Increase the ease of use.

(4) Optimizations

HLAscan v2.0 uses Suffix Array (SA) method instead of BWA-mem for alignment with IMGT/HLA Database.

  - Time efficiency: about 10 times faster than previous version (ex: under a minute for HLA-typing (<100dp))

  - Space efficiency: < 20MB disk (no create intermediate files)

2. Contents

(1) DB

   HLA-ALL.IMGT : IMGT/HLA database

(2) Tool

   hla_scan_r_v2.0

3. Usage

(1) Download the DB & Tool

(2) Read Manual

   ./hla_scan

(3) Execute the tool

   • Bam Input

     - ./hla_scan –b [Bam file] –v [37/38] –d [DB] –g [Gene Symbol] –t [# of threads]

   • Fastq Input

     - ./hla_scan –l [fastq file] (-r [fastq file2]) –v [37/38] –d [DB] –g [Gene Symbol] –t [# of threads]

4. Commands

(1) HLA typing (input: bam file)

     ./hla_scan_v5.0 -b [bam] -d [IMGT/HLA DB] -v [version (37 or 38)]

(2) HLA typing (input: fastq files)

      ./hla_scan_v5.0 -l [fastq] (-r [fastq2]) -d [IMGT/HLA DB]

5. Options

(1) Gene List -g [string], default=HLA-A

    HLA-A, HLA-B, HLA-C, HLA-E, HLA-F, HLA-G, MICA, MICB,

    HLA-DMA, HLA-DMB, HLA-DOA, HLA-DOB, HLA-DPA1, HLA-DPB1, HLA-DQA1,

    HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, TAP1, TAP2

(2) Score Cutoff -s [int], default=50

(3) Constant using ScoreFunc -c [int], default=30

(4) # of threads -t [int], default=32