1   Purpose

Generate a .bbl file from a list of citations, so that references can be included within a document. Simply copy the reference list from the .bbl file that Bib-TeX generates and paste it into the main .tex file (and delete the associated \bibliography and \bibliographystyle commands).

2   Example

Once bibtex is run, the .bbl file will contain the following:

```
\begin{thebibliography}{1}
\bibitem{snpsift}
P.~Cingolani, V.~M. Patel, M.~Coon, T.~Nguyen, S.~J. Land
    , D.~M. Ruden, and
  X.~Lu.
\newblock {{U}sing {D}rosophila melanogaster as a {M}odel
    for {G}enotoxic
  {C}hemical {M}utational {S}tudies with a {N}ew {P}
    rogram, {S}np{S}ift}.
\newblock {\em Front Genet}, 3:35, 2012.
\end{thebibliography}
```

Simply copy and paste this code into the main document.

3   Citing bioinformatic tools

1. SnpSift[6]

2. BWA-MEM[10]

3. FastQC[2]

4. SAMtools and BCFtools[11]

5. Trimmomatic[4]

6. bam.iobio[13]

7. Bpipe[19]

8. BEDTools[18]

9. PLINK2[5]

We sequenced 10 samples on 10 lanes on an Illumina HiSeq 2000, aligned the resulting reads to the hg19 reference genome with BWA-MEM[10], applied GATK[12] base quality score recalibration, indel realignment, duplicate removal, and performed SNP and INDEL discovery and genotyping across all 10 samples simultaneously using standard hard filtering parameters or variant quality score recalibration according to GATK Best Practices recommendations [8, 21].

4 Other citations

1. GWAS on Australian aboriginal population [1]

2. The Mardu aborigines : living the dream in Australia's desert[20]

3. Cleared out : first contact in the Western Desert[7]

4. Exome sequencing as a tool for Mendelian disease gene discovery[3]

5. Exome sequencing identifies MLL2 mutations as a cause of Kabuki syndrome[15]

6. Exome sequencing identifies the cause of a Mendelian disorder[16]

7. Mimura et al.[14]

8. Inoue et al.[9]

9. Papantonis et al.[17]

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