The Journal of Open Source Software

Xenomapper: Mapping reads in a mixed species context

Matthew J. Wakefield[1]

1 The Walter and Eliza Hall Institute, The University of Melbourne

DOI: 10.21105/joss.00018

Software

- Review
- Repository
- Archive

Summary

Xenomapper is a utility for post processing mapped DNA sequencing reads that have been aligned to a primary genome and a secondary genome, and binning reads into species specific, multimapping in each species, unmapped and unassigned categories. It can be used on single end or paired end sequencing data across a wide range of genomics methods including RNAseq. In paired end data evidence of sequence specificity for either read will be used to assign both reads.

Use cases include xenografts of human cancers and host pathogen interactions.

Xenomapper is most effective with mapped reads that include an XS or ZS score that gives the mapping score of the next best read. These include Bowtie2 (Langmead and Salzberg 2012) and HISAT (Kim, Langmead, and Salzberg 2015).

This work builds upon a similar approach by Rossello et. al. (Rossello et al. 2013) with a more rigorous implementation and extensions for paired end data and exon aware aligners.

References

Kim, D., B. Langmead, and S. L. Salzberg. 2015. "HISAT: A Fast Spliced Aligner with Low Memory Requirements." Journal Article. *Nat Methods* 12 (4): 357–60. doi:10.1038/nmeth.3317.

Langmead, B., and S. L. Salzberg. 2012. "Fast Gapped-Read Alignment with Bowtie 2." Journal Article. *Nat Methods* 9 (4): 357–9. doi:10.1038/nmeth.1923.

Rossello, F. J., R. W. Tothill, K. Britt, K. D. Marini, J. Falzon, D. M. Thomas, C. D. Peacock, et al. 2013. "Next-Generation Sequence Analysis of Cancer Xenograft Models." Journal Article. *PLoS One* 8 (9): e74432. doi:10.1371/journal.pone.0074432.