

LOLA: Locus overlap analysis for enrichment of genomic ranges

Nathan C. Sheffield^{1, 2}

¹Center for Public Health Genomics, University of Virginia

²Departments of Public Health Sciences, Biomedical Engineering, and Biochemistry and Molecular Genetics, University of Virginia

We're pleased to announce the release of a new Bioconductor package, [LOLA](#) (Locus Overlap Analysis). LOLA is a package for genomic locus overlap enrichment. Roughly analogous to what GSEA does for gene sets, LOLA does for genomic regions, which can be defined however you like, including experiments like ChIP-seq, BS-seq, DNase-seq, etc. LOLA lets you test your genomic ranges of interest against a database of other genomic range sets to identify enrichment of overlap, tying external annotation to your regions of interest. A complete enrichment analysis against a database of thousands of region sets requires just 3 lines of R code and completes in minutes.

Along with LOLA, we provide [LOLA Region Databases](#), which include region sets from ENCODE, Roadmap Epigenomics, Cistrome, CODEX, UCSC, and other public databases. We intend to build, maintain, and curate this database in the future. You can also use LOLA for custom analysis by creating custom databases following instructions in the LOLA readme.

You can find more information, vignettes, and downloads at [LOLA's website](#), or follow our development at the [LOLA GitHub repository](#). We would be eager to hear any suggestions or feedback!

We originally developed the method in Tomazou *et al.* (2015). The LOLA paper is published in bioinformatics (Sheffield and Bock, 2016).

References

- Sheffield, N.C. and Bock, C. (2016) LOLA: Enrichment analysis for genomic region sets and regulatory elements in R and bioconductor. *Bioinformatics*, **32**, 587–589.
- Tomazou, E.M. *et al.* (2015) Epigenome mapping reveals distinct modes of gene regulation and widespread enhancer reprogramming by the oncogenic fusion protein EWS-FLI1. *Cell Reports*, **10**, 1082–1095.