

# Logolas: New Frontiers in Logo Visualization

Enrichment Depletion Logos (EDLogo) | String Logos | Adaptive Scaling of Logos

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# Project Page

https://kkdey.github.io/Logolas-pages

## Gallery

https://kkdey.github.io/Logolas-pages/Gallery.html

# R package

### Github Version

https://github.com/kkdey/Logolas

#### Bioconductor

https://bioconductor.org/packages/releas e/bioc/html/Logolas.html

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## **Logo Universe - Softwares**

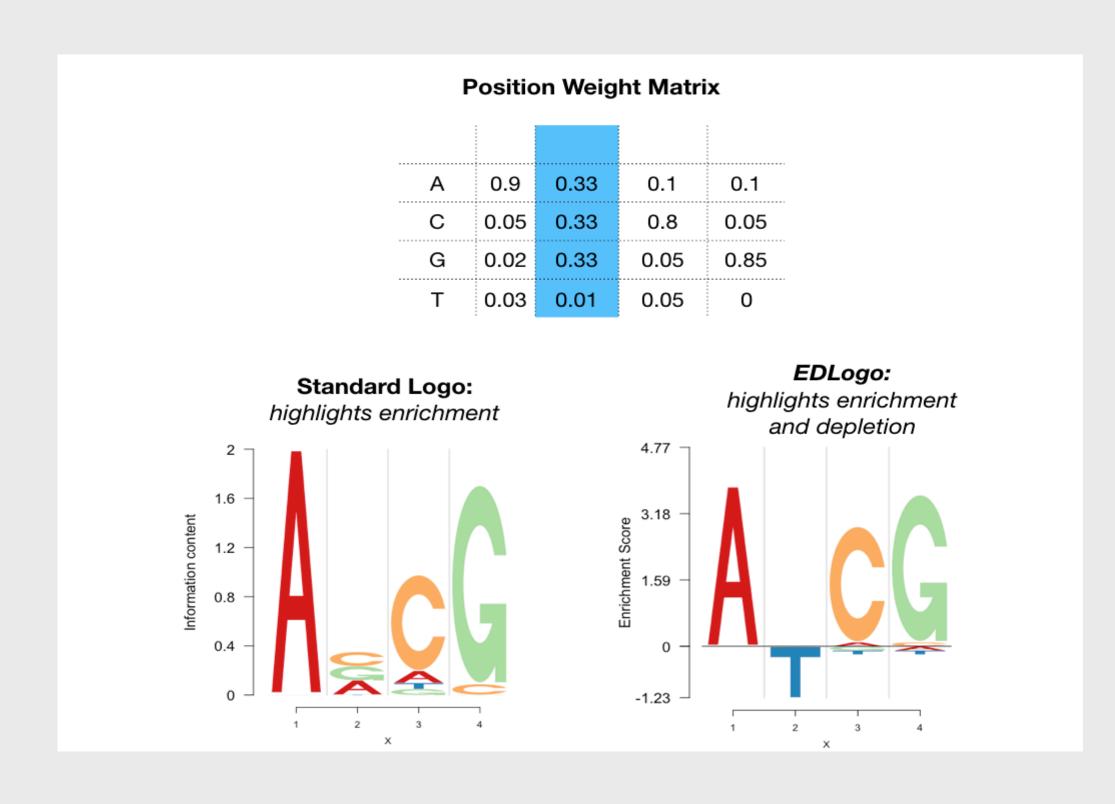
seqLogo, seq2Logo, motifStack, iceLogo, kmer Logo, TFBStools, atSNP, DiffLogo, WebLogo, Rweblogo, ggseqLogo

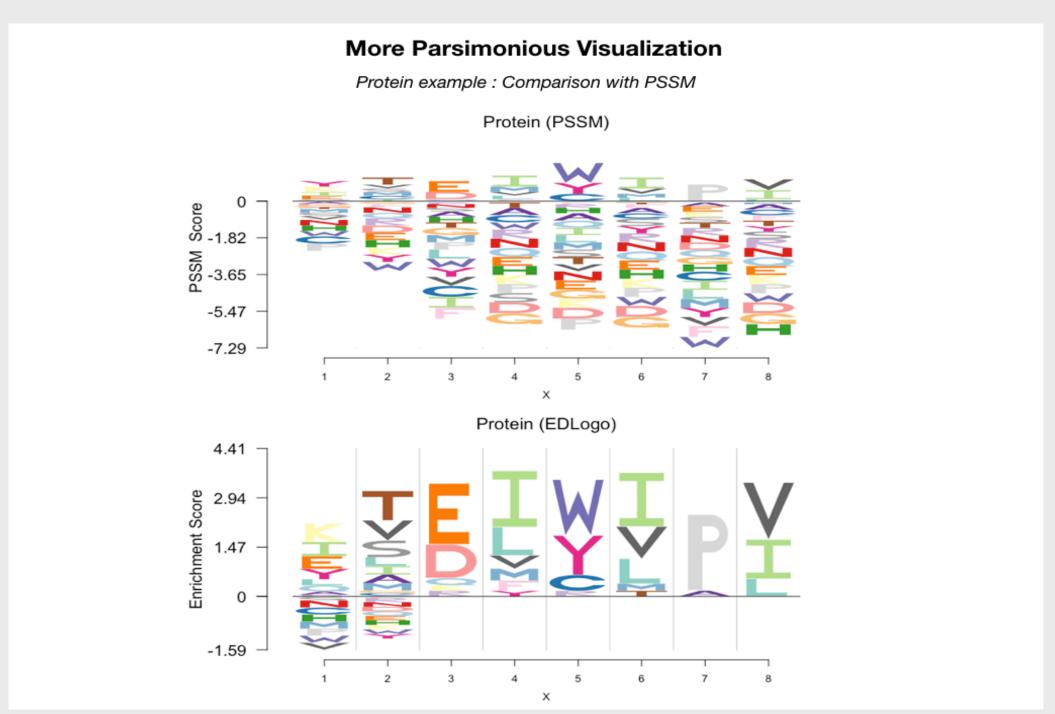
#### References

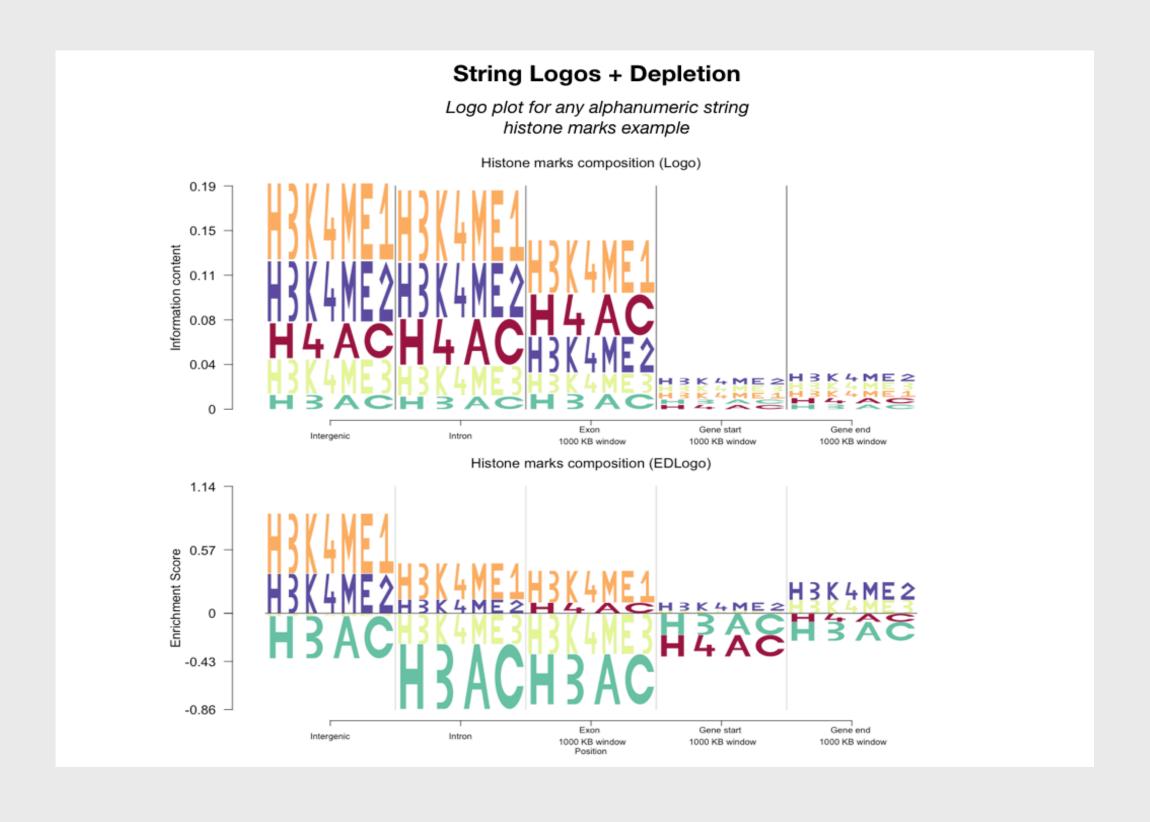
Stephens, M.: False discovery rates: a new deal. Biostatistics 18 (2), 275–294 (2016) Koch, C.M., et al.: The landscape of histone modifications across 1in five human cell lines. Genome Research 17(6), 691–707 (2007)

Alexandrov, L., Nik-Zainal, G., Wedge, D., Campbell, P., Stratton, M.: Deciphering signatures of mutational processes operative in human cancer. Cell Reports 3(1), 246–259 (2013) Kheradpour, P., Kellis, M.: Systematic discovery and characterization of regulatory motifs in encode tf binding experiments. Nucleic Acids Research, 1–12 (2013)

Joseph, A.P., Shingate, P., Upadhyay, A.K., Sowdhamini, R.: 3pfdb+: improved search protocol and update for the identification of representatives of protein sequence domain families. Database (Oxford) bau026 (2014)







## Other Features of Logolas

