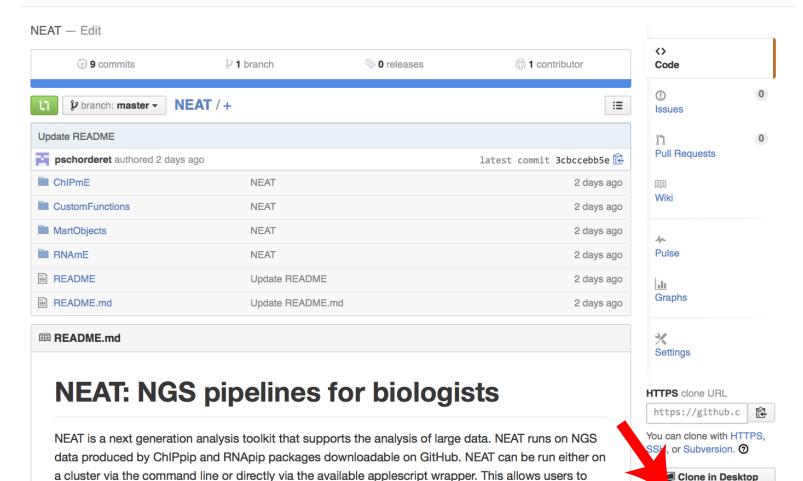




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generate metagene analysis (for ChIPseq data) as well as differentially regulated gene calling (for

RNAseq data) using a simple double click approach. All files including count tables, RPKM values, DEG, venn diagrams, feature-centered enrichment plots, smear plots, etc are automatically saved and