

**Peak tool:** A tool to report detailed promoter / intragenic / enhancer / super-enhancer / intergenic occupancy of multiple bed files.

An often asked biological question in cancer genomics is: “Does a list of de-regulated genes (e.g. BMI1) have co-occurring transcription factors like (**AR**, **ERG**) as well as co-occurring histone marks like (**H3K4me3**, **H3K27Ac**) in its promoter / enhancer”?

To solve this, I developed a tool in C++ to parse the human/mice gene annotation and annotate multiple lists of ChIP-Seq peaks or genomic regions in bed format.

The software tool will find co-occurring peaks, and then produce a list of detailed **promoter / gene-body / intergenic / enhancer occupancy** in human or mouse.

Co-occupied regions are used to elicit putative co-acting transcription factors and helps with better understanding of the biology of aberrant genes in cancer.

The tool also allows correlation of a new ChIP-Seq dataset with ENCODE originated or other published data sets. For e.g. this tool was instrumental in showing that **ERG** and **EZH2** co-occupy promoters of several de-regulated genes in prostate cancer and the histone modification landscape.



Fig: Co-occupying ERG, EZH2 and histone modification landscape of BMI1. The co-occupancy was reported by **peak tool**.

Link to software: <https://github.com/goxed/peak-tool/>