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## **FuncSNPi - FLOWCHART**

Provide a list of riskSNP for a disease Provide Biological Features (e.g. Breast or Prostate Cancer) (e.g. FAIRE, ChIPseq (AR) peaks for cell type) riskSNP.n Make a region of interest (ROI) centered on each riskSNP (e.g. 1MB on either side: total 2MB) BioFeature.n ROI.riskSNP.n For each ROI.riskSNPn, extract all known SNPs from 1000genomes database For each ROI.riskSNP.n and for each BioFeature.n, compare the overlap. For each overlap riskSNP to BioFeature, extract frequency and location info from 1000genomes database 1) Generate correlation values for all identified SNPs to riskSNP 2) Filter list by r^2 value. 3) Generate Haploview Plots for all overlapping SNPs and associated riskSNP

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