This github website is about a statistical method to test for dependence between nonhomogeneous Poisson processes, which can be applied to detect interactions between transcription factors based on ChIP-seq data. The website contains the complete source code (including both simulation and real data analysis) and datasets (including all simulated and demo data), as listed in the following table:

Content	Code	Data
Demo (for Figure 1 and Figure 2)	drawfig1&2.R	demo_arrtime.RData demo_intensity.RData demo_intensityestimate.RData demo_intarrtime.RData demo_cdfintarrtime.RData
Simulation 1 (for Table 1 and Table 2)	maketab1&2.R	simu1_arrtime_scenI_npath1.RData simu1_arrtime_scenII_npath1.RData simu1_arrtime_scenIII_npath1.RData simu1_arrtime_scenI_npath5.RData simu1_arrtime_scenII_npath5.RData simu1_arrtime_scenIII_npath5.RData
Simulation 2 under H0 (for Table 3)	simu2h0sever.R maketab3.R	simu2h0_scenIV.RData simu2h0_scenV.RData simu2h0_scenVI.RData
Simulation 2 under Ha (for Table 4)	simu2hasever.R maketab4.R	simu2ha_arrtimes_scenI_rho_-1.RData simu2ha_arrtimes_scenI_rho_-0.5.RData simu2ha_arrtimes_scenI_rho_-0.3.RData simu2ha_arrtimes_scenI_rho_0.RData simu2ha_arrtimes_scenI_rho_0.1.RData simu2ha_arrtimes_scenI_rho_1.RData simu2ha_arrtimes_scenII_rho_-1.RData simu2ha_arrtimes_scenII_rho_-0.5.RData simu2ha_arrtimes_scenII_rho_-0.3.RData simu2ha_arrtimes_scenII_rho_0.RData simu2ha_arrtimes_scenII_rho_0.1.RData simu2ha_arrtimes_scenII_rho_1.RData simu2ha_arrtimes_scenIII_rho_-1.RData simu2ha_arrtimes_scenIII_rho_-0.5.RData simu2ha_arrtimes_scenIII_rho_-0.3.RData simu2ha_arrtimes_scenIII_rho_0.RData simu2ha_arrtimes_scenIII_rho_0.1.RData simu2ha_arrtimes_scenIII_rho_1.RData
Real Data Application (for Figure 3)	drawfig3.R	mmc2.xls [2] mmc3.xls [1] mES_OCT4_SOX2_NANOG_TCF3.WIG [3]

Brief explanations to the R script files:

"nhppfun.R" contains all functions for (1) simulating NHPP sample paths, (2) estimating NHPP intensity, and (3) evaluating GoF of estimated NHPP.

"drawfig1&2.R" is a demo for simulation results for true/estimated NHPP intensity functions and CDFs of interarrival times of true/estimated NHPPs.

"maketab1&2.R" (simulation 1) calculates MISE/PNP for evaluating intensity estimation and GoF test based on single and five sample paths.

"simu2h0server.R" (simulation 2) calculates FPR for testing dependence between NHPPs.

"maketab3.R" (simulation 2) summarizes FPR results for Scenarios IV, V, and VI.

"simu2haserver.R" (simulation 2) calculates TPR for testing dependence between NHPPs.

 "maketab4.R" (simulation 2) summarizes TPR results for Scenarios I, II, and III at different correlation levels -1, -0.5, -0.3, 0, 0.1, 1.

"drawfig3.R" (real data application) calculates a summary matrix for the average pairwise dependence among TFs across chromosome 1 using ChIP-seq data for 14 TFs in mouse ESCs.