This Repository saves raw data for a research project entitled "Testing dependence among transcription factors based on a nonhomogeneous Poisson process model". The project 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 Repository contains 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.txt demo_intensity.txt demo_intensityestimate.txt demo_intarrtime.txt demo_cdfintarrtime.txt
Simulation 1 (for Table 1 and Table 2)	maketab1&2.R	simu1_arrtime_scenI_npath1.txt simu1_arrtime_scenII_npath1.txt simu1_arrtime_scenIII_npath1.txt simu1_arrtime_scenI_npath5.txt simu1_arrtime_scenII_npath5.txt simu1_arrtime_scenIII_npath5.txt
Simulation 2 under H0 (for Table 3)	simu2h0sever.R maketab3.R	simu2h0_scenIV.txt simu2h0_scenV.txt simu2h0_scenVI.txt
Simulation 2 under Ha (for Table 4)	simu2hasever.R maketab4.R	simu2ha_scenI_rho_-1.txt simu2ha_scenI_rho_-0.5.txt simu2ha_scenI_rho_-0.3.txt simu2ha_scenI_rho_0.txt simu2ha_scenI_rho_0.1.txt simu2ha_scenI_rho_1.txt simu2ha_scenII_rho_-1.txt simu2ha_scenII_rho_-0.5.txt simu2ha_scenII_rho_-0.3.txt simu2ha_scenII_rho_0.txt simu2ha_scenII_rho_0.1.txt simu2ha_scenII_rho_1.txt simu2ha_scenIII_rho_-1.txt simu2ha_scenIII_rho_-0.5.txt simu2ha_scenIII_rho_-0.3.txt simu2ha_scenIII_rho_0.txt simu2ha_scenIII_rho_0.1.txt simu2ha_scenIII_rho_1.txt
Real Data Application (for Figure 3)	drawfig3.R	mmc2.xlsx [2] mmc3.xlsx [1] mES_OCT4_SOX2_NANOG_TCF3.txt [3]

References:

[1] Chen, X., Xu, H., Yuan, P., al.: Integration of external signaling pathways with the core transcriptional network in embryonic stem cells. Cell 133(6), 1106–1117 (2008).

[2] Heng, J.C., Feng, B., Han, J., al.: The nuclear receptor Nr5a2 can replace Oct4 in the reprogramming of murine somatic cells to pluripotent cells. Cell Stem Cell 6(2), 167–174 (2010).

[3] Marson, A., Levine, S.S., Cole, M.F., al.: Connecting microRNA genes to the core transcriptional regulatory circuitry of embryonic stem cells. Cell 134(3), 521–533 (2008).

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.