Software

**hichelix**: inferring spatial organizations of chromosomes via helix models. Available at: [https://sourceforge.net/projects/hichelix/](https://sourceforge.net/projects/hichelix/)

**HiView**: a genome browser for the integrative analysis of Hi-C data, SNP data and epigenetic data. Available at: [http://www.unc.edu/~xuzheng/HiCBrowser/Part6_HiC_Browser/](http://www.unc.edu/~xuzheng/HiCBrowser/Part6_HiC_Browser/)

**HMRFBayesHiC**: A hidden Markov random field based Bayesian method for the detection of long-range chromosomal interactions in Hi-C data. Available at: [http://www.unc.edu/~xuzheng/HMRFBayesHiC/](http://www.unc.edu/~xuzheng/HMRFBayesHiC/)

**Bayesian 3D constructor for Hi-C data (BACH)**: infer chromosome 3D structures and characterize chromatin structural variations. Available at: [http://www.people.fas.harvard.edu/~junliu/BACH/](http://www.people.fas.harvard.edu/~junliu/BACH/)

**HiCNorm**: removing biases in Hi-C data via Poisson regression: Available at: [http://www.people.fas.harvard.edu/~junliu/HiCNorm/](http://www.people.fas.harvard.edu/~junliu/HiCNorm/) ([HiCNorm has been included in the HiTC Bioconductor package](http://www.people.fas.harvard.edu/~junliu/HiCNorm/))

**GPUmotif**: An ultra-fast and energy-efficient motif analysis program using graphics processing units. Available at: [http://sourceforge.net/projects/gpumotif/](http://sourceforge.net/projects/gpumotif/)

**Poisson Mixed-Effects Regression for RNA-Seq Data (POME)**: quantifying exon-level gene expression in RNA-Seq. Available at: [http://www.stat.purdue.edu/~yuzhu/pome.html](http://www.stat.purdue.edu/~yuzhu/pome.html)

**Hybrid Motif Sampler (HMS)**: de novo motif discovery using ChIP-Seq data. Available at: [http://www.sph.umich.edu/csg/qin/HMS/](http://www.sph.umich.edu/csg/qin/HMS/)

**Bayesian Expression Search Tool (BEST)**: query large scale microarray compendium datasets. Available at: [http://www.sph.umich.edu/csg/qin/BEST/](http://www.sph.umich.edu/csg/qin/BEST/)