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Zooming in on genome organization. Zhou, X. J., & Alber, F. Nature Methods (2012)

Iterative correction of Hi-C data reveals hallmarks of chromosome organization. Imakaev et al. Nature Methods (2012)



















Imakaev et al. Nature Methods (2012)

Many alternatives

Tool	Short-read aligner(s)	Mapping improvement	Read filtering	Read-pair filtering	Normalization	Visualization	Confidence estimation	Implementation language(s)
HiCUP [46]	Bowtie/Bowtie2	Pre-truncation	✓	✓	_	-	_	Perl, R
Hiclib [47]	Bowtie2	Iterative	√°	\checkmark	Matrix balancing	✓	-	Python
HiC-inspector [131]	Bowtie	-	\checkmark	\checkmark	_	\checkmark	_	Perl, R
HIPPIE [132]	STAR	√ ^b	\checkmark	\checkmark	-	-	-	Python, Perl, R
HiC-Box [133]	Bowtie2	_	\checkmark	✓	Matrix balancing	✓	-	Python
HiCdat [122]	Subread	_c	\checkmark	✓	Three options ^d	✓	_	C++, R
HiC-Pro [134]	Bowtie2	Trimming	\checkmark	✓	Matrix balancing	_	_	Python, R
TADbit [120]	GEM	Iterative	\checkmark	\checkmark	Matrix balancing	\checkmark	-	Python
HOMER [62]	_	-	\checkmark	✓	Two options ^e	\checkmark	\checkmark	Perl, R, Java
Hicpipe [54]	_	-	_	_	Explicit-factor	-	_	Perl, R, C++
HiBrowse [69]	_	-	_	_	-	✓	\checkmark	Web-based
Hi-Corrector [57]	_	-	_	_	Matrix balancing	_	_	ANSI C
GOTHIC [135]	_	-	\checkmark	✓	-	_	✓	R
HiTC [121]	_	-	_	_	Two options ^f	✓	\checkmark	R
chromoR [59]	_	-	_	_	Variance stabilization	_	_	R
HiFive [136]	_	-	\checkmark	✓	Three options ^g	✓	_	Python
Fit-Hi-C [20]	-	-	-	-	_	\checkmark	\checkmark	Python

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Hicup [46]	Bowtie/Bowtie2	Pre-truncation	✓	✓	_	-	_	Perl, R	
Hiclib [47]	Bowtie2	Iterative	\checkmark^{a}	\checkmark	Matrix balancing	✓	– Python		
HiC-inspector [131]	Bowtie	_	\checkmark	\checkmark	_	\checkmark	_	Perl, R	
HIPPIE [132]	STAR	√ ^b	\checkmark	\checkmark	-	-	-	Python, Perl, R	
HiC-Box [133]	Bowtie2	-	\checkmark	\checkmark	Matrix balancing	✓	-	Python	
HiCdat [122]	Subread	_c	\checkmark	\checkmark	Three options ^d	\checkmark	-	C++, R	
HiC-Pro [134]	Bowtie2	Trimming	\checkmark	\checkmark	Matrix balancing	_	-	Python, R	
TADbit [120]	GEM	Iterative	\checkmark	\checkmark	Matrix balancing	\checkmark	_	Python	
HOMER [62]	_	-	✓	✓	Two options ^e	✓	\checkmark	Perl, R, Java	
Hicpipe [54]	_	_	_	_	Explicit-factor	_	 Perl, R, C++ 		
HiBrowse [69]	_	_	_	-	_	✓	\checkmark	Web-based	
Hi-Corrector [57]	_	_	_	-	Matrix balancing	-	_	ANSI C	
GOTHIC [135]	_	_	\checkmark	\checkmark	-	-	\checkmark	R	
HiTC [121]	_	_	_	_	Two options ^f	✓	\checkmark	R	
chromoR [59]	_	_	_	-	Variance stabilization	-	_	R	
HiFive [136]	_	-	\checkmark	\checkmark	Three options ^g	✓	-	Python	
Fit-Hi-C [20]	_	-	_	-	_	✓	\checkmark	Python	

Many alternatives

Method *available	Representation	Scoring	Sampling	Models			
onnie		U _{3C}	UBiol	UPhys			
		$F_{ij} \rightarrow D_{ij}$ conversion Functional form					
ChromSDE [*] [37]	Points	$D_{ij} = \begin{cases} \left(\frac{1}{F_{ij}}\right)^{\alpha} \text{ if } F_{ij} > 0\\ \infty \text{ if } F_{ij} = 0 \end{cases} \alpha \text{ is optimized}$	$\frac{\sum_{(ij)D_{\parallel}<\infty)} \frac{\langle r_{ij}^2 - D_{ij}^2 \rangle}{D_{\parallel}} - \lambda \sum_{(ij)} r_{ij}^2 \text{ where } \lambda \text{ is set to } 0.01$	N/A	N/A	Deterministic semidefinite programming to find the coordinates	Consensus
ShRec3D* [38]	Points	$D_{ij} = \begin{cases} \left(\frac{1}{F_{ij}}\right)^{\alpha} & \text{if } F_{ij}' > 0\\ \frac{N^2}{\sum_{j \in F_{ij}'}} & \text{if } F_{ij}' = 0 \end{cases} F_{ij}' \text{ is the original } F_{ij} \text{ corrected to} \\ \text{satisfy all triangular inequalities with the shortest path} \\ \text{reconstruction} \end{cases}$	N/A	N/A	N/A	Deterministic transformations of D _{ij} into coordinates	Consensus
TADbit [*] [43]	Spheres	$D_{ij} \propto \begin{cases} \alpha F_{ij} + \beta & \text{if } F_{ij} < \gamma' \text{ or } F_{ij} > \gamma \\ \frac{S_i + S_j}{2} & \text{if } i - j = 1 \end{cases} \alpha \text{ and } \beta \text{ are estimated} \\ \text{from the max and the min } F_{ij}, \text{ from the optimized max} \\ \text{distance and from the resolution. } \gamma' < \gamma \text{ are optimized too. } s_i \\ \text{is the radius of particle } i \end{cases}$	$\sum_{(i,j)} k_{ij} (r_{ij} - D_{ij})^2$ where $k_{ij} = 5$ if $ i - j = 1$ or proportional to F_{ij} otherwise	Yes	U _{exct} and U _{bond} have harmonic forms	Monte Carlo (MC) sampling with Simulated annealing and Metropolis scheme	Resampling
BACH [*] [45]	Points	$D_{ij} \propto \frac{B_i B_j}{F_{ij}^2}$. The biases B_i and B_j and α are optimized	$b_{ij}D_{ij}^{1/2} + c_{ij} \log(D_{ij})$ where b_{ij} and c_{ij} are optimized parameters	No	No	Sequential importance and Gibbs sampling with hybrid MC and adaptive rejection	Population
Giorgetti et al. [40]	Spheres	Particles interact with pair-wise well potentials of depths B_{ij} a hard-core radius and smaller than a maximum contact radiu the population of models	No	N/A	MC sampling with metropolis scheme	Population	
Duan et al. [41]	Spheres	$\overline{F_{[i-j]}} = \frac{\sum_{k=0}^{N-1-1} F_{[i,k+i-j]}}{N-[i-j]} \text{ is the average of } F_{ij} \text{ at genomic distance} \\ i-j \text{ expressed in kb. } D_{ij} = \overline{F_{[i-j]}} \times 7.7 \times i-j \text{ assuming that} \\ \alpha \text{ 1 kb maps onto } 7.7 \text{ nm}$	$\sum_{(i,j)} (r_{ij} - D_{ij})^2$	Yes	U _{excl} and U _{bond} have harmonic forms	Interior-point gradient- based method	Resampling
MCMC5C* [49]	Points	$D_{ij} \propto \frac{1}{F_{ij}^{2}}$ where is optimized	$\sum_{(i,j)} (F_{ij} - r_{ij}^{-1/2})^2$	N/A	N/A	MC sampling with Markov chain based algorithm	Resampling
PASTIS [*] [47]	Points	$D_{ij} \propto \frac{1}{F_{ij}^{\alpha}}$ where α is optimized	$b_{ij}D_{ij}^{1/2} + c_{ij}\log(D_{ij})$ where b_{ij} and c_{ij} are optimized parameters	No	No	Interior point and isotonic regression algorithms	Resampling
Meluzzi and Arya [48]	Spheres	$\sum_{(l,l))}k_{ij}r_{ij}^2$ where k_{ij} are adjusted such that the contact probab F_{ij}	pilities computed on the models match the	No	U _{exct} is a pure repulsive LJ potential. U _{bond} and U _{bend} have harmonic forms	Brownian dynamics	Resampling
AutoChrom3D* [44]	Points	$ \begin{array}{l} D_{ij} \propto \begin{cases} \alpha F_{ij} + \beta & \text{if } F_{\min} < F_{ij} < F_{\gamma} \\ \alpha' F_{ij} + \beta' & \text{if } F_{\gamma} < F_{ij} < F_{\max} \end{cases} \text{ where } F_{\min} \left(F_{\max} \right) \text{ are } \\ \text{the min(max) of } F_{ij}. \text{ The parameters } (\alpha, \beta), (\alpha', \beta') \text{ and } F_{\gamma} \text{ are } \\ \text{found using the nuclear size, the resolution and the decay of } \\ F_{ij} \text{ with } i-j \end{cases} $	$\sum_{(ij)} \frac{(r_{\theta} - D_{\theta})^2}{D_{\theta}^2}$	Yes	N/A	Non-linear constrained	Consensus
Kalhor et al. [14]	Spheres	$D_{ij} = R_{contact}$ to enforce the pair contact, if the normalized contact frequency F_{ij} is higher than 0.25. Otherwise the contact is not enforced	$\sum_{\text{models}} \sum_{(i,j)} k_{ij} (r_{ij} - D_{ij})^2$ where k_{ij} is different for pairs of particles, on different chromosomes, on the same chromosome, or connected	Yes	U _{exct} and U _{bond} have harmonic forms	Conjugate gradients sampling with Simulated annealing scheme	Population

* These methods are publicly available.

Restraint-based three-dimensional modeling of genomes and genomic domains.

Serra F, Di Stefano M, Spill YG, Cuartero Y, Goodstadt M, Baù D, Marti-Renom MA. FEBS Lett 589: 2987–2995 (2015)