

Detection of colinear blocks and synteny and evolutionary analyses based on utilization of MCScanX

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Supplementary Table 1. Detailed comparisons with other methods

Tools	Abstract	Extension	Pros	Cons	Limitation	Link	Year	Publication
DAGchainer	The DAGchainer software computes chains of syntenic genes found within complete genome sequences. This algorithm can be used to mine large evolutionary conserved regions of genomes between two organisms.	Alternatively, by examining colinear sets of homologous genes found within a single genome, segmental genome duplications can be revealed.	This software distribution includes a Java-based graphical interface that allows the inputs and outputs to be navigated and interrogated dynamically.	The single input file, which contains a list of homologous gene pairs, their genome locations, and their E-value resulting from a BLAST search, needs to be retrieved before the executive.	1:1 correspondence comparison. No additional downstream analyses are provided.	https://dagchainer.sourceforge.net	2004	https://academic.oup.com/bioinformatics/article/20/18/3643/202025?login=false
ColinearScan	Implement a statistical approach in the software package ColinearScan to detect putative colinear regions using a dynamic programming algorithm.	NA	Statistical inference, high computational efficiency, and flexibility of input data type.	Focus on statistical algorithm improvement.	1:1 correspondence comparison. No additional downstream analyses are provided.	http://colinear.cbi.pku.edu.cn	2006	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1626491/
SyMAP	SyMAP (Synteny Mapping and Analysis Program) is a software package for detecting, displaying, and querying syntenic relationships between sequenced genomes. SyMAP provides both synteny computing algorithms and a Web-based graphical display.	SyMAP can align a draft genome to a fully sequenced genome and perform self-synteny. It also can align with FPC physical maps.	Align an FPC-based physical map to a genomic sequence and align two FPC maps to one another.	Focus on sequence-FPC synteny detection.	No additional downstream analyses are provided.	http://www.agcol.arizona.edu/software/syemap/	2006	https://genome.cshlp.org/content/16/9/1159
MCScan	MCScan provides a clustering module for viewing the relationship of colinear segments in multiple genomes (or heavily redundant genomes).	NA	MCscan condenses the combinatorial matches between multiple chromosomal segments resulting from divergence and recursive duplication events, creating a view of the multiply-aligned segments.	MCscan reads in at least two sources of data: .blast file and .bed file that need to be retrieved before the executive.	No additional downstream analyses are provided.	https://github.com/tanhaibao/mcscan	2008	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593578/
SynChro	SynChro is a tool that reconstructs synteny blocks between pairwise comparisons of multiple genomes based on a simple algorithm that computes Reciprocal Best-Hits (RBH) to reconstruct the backbones of the synteny blocks and then automatically completes these blocks with non-RBH syntenic homologs.	Provide scripts to generate a summarizing table, plot some block properties, and reconstruct families of syntenic homologs.	Synteny block reconstruction is fast and straightforward as all steps are integrated, and there is only one parameter to set up. It also provides the user with a set of three graphical outputs.	Users have minimal control for analysis as well as customized plot ability.	No additional downstream analyses are provided.	http://www.lcqb.upmc.fr/CHRONicle/SynChro.html	2014	https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0092621
VGSC	VGSC is A web-based Vector Graph toolkit of genome Synteny and Collinearity, which provides all kinds of visual representation automatically for synteny and Collinearity data.	Provide a java-based bytecode binary to enable the command-line execution.	Accept multiple genomes collinearity result.	Users need to upload sequence alignments from blast and collinearity relationship from the synteny analysis tools. Due to performance limit, VGSConline only accept files that LESS THAN 50M.	For visualization only.	https://dvb.ac.cn/vgs-c2/service/home.php	2016	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4783527/
JAX Synteny Browser	The JAX Synteny Browser is a web-based synteny viewer application preloaded with human and laboratory mouse data to allow researchers to highlight or selectively display genome features according to the biological attributes of the features.	The JAX Synteny Browser software can be deployed for any two genomes.	Preloaded, and no extra work needs to be done.	For any non-preloaded genomes, users need to provide input files where genome coordinates for syntenic blocks are defined and for which biological attributes of the features in one or both genomes are available.	1:1 correspondence comparison. No additional downstream analyses are provided.	https://syntenybrowser.jax.org/browser	2019	https://link.springer.com/article/10.1007/s00335-019-09821-4
halSynteny	halSynteny performs efficient processing of pairwise alignment blocks for any pair of genomes in the alignment and enables accurate and rapid identification of synteny in multiple full-genome alignments.	halSynteny is implemented in C++11 as a component of the halTools software and released under MIT license.	halSynteny requires only the alignment input.	halSynteny implements a DAG-based algorithm for identifying synteny blocks directly from HAL alignment and reporting synteny blocks in PSL format.	Users need to find a way to visualize the result.	https://github.com/ComparativeGenomicsToolkit/hal/tree/master/synteny	2020	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7254927/