

Figure 1. (a) An interval list sorted by the Start and augmented with MaxE, the maximum End counting from the first interval. (b) Intervals in the above list with End value larger than that of the three following intervals are put into a separated list. The two split interval lists L1 and L2 are both 'smoothed'. (c) Optional structure can be used to obtain the two location indexes of a query in L1 and L2 with a single binary search. Two queries [9,12) and [17,21) are discussed in the text.

Table 1: Genomic interval datasets used as database for performance evaluation. The query dataset is chainRn4 with 2,351 thousand intervals. Datasets fBrain-DS14718 and exons are from BedTools site, and others are from UCSC site.

Genomic Dataset Name	fBrain- DS14718	exons	chainOrnAna1	chainVicPac2	chainXenTro3 Link	chainMonDo m5Link
No. of intervals (x1000)	199	439	1,957	7,684	50,981	128,187
No. of total overlaps (x1000)	321	2,633	1,086,692	3,892,116	18,432,255	27,741,145

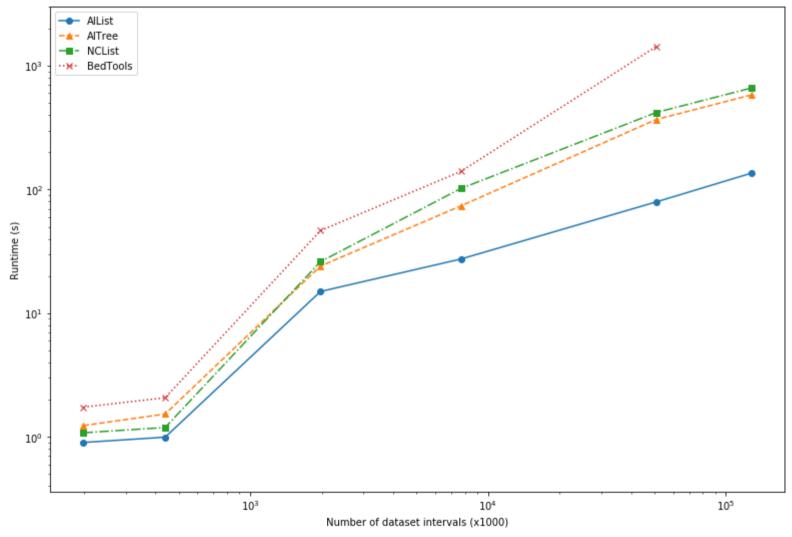


Figure 2. Performance comparison of AIList with AITree, NCList and BEDTools. Six datasets of size  $\sim$ 200K to 128M are used (see Table 1). The time is the wall time including dataset loading, data structure construction and searching. The query dataset is chainRn4 with size of 2,351 thousand. No result for BEDTools for the largest dataset since it took nearly all of the machine memory (16GB) and was terminated.