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ACT: aggregation and correlation toolbox for analyses of genome tracks

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Comments
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There is now an abundance of genome-sized data from high-signal tracks that describe a genomic landscape or distinct region. In most cases, the representations of these data take the form of either ChIP-chip or ChIP-seq signal profiles from dbSNP (Sharry et al., 2001) and the 1000 genomes project. In general, this type of aggregation analyses helps identify proximity correlations and functional relationships between the signals and anchors. In the ENCODE pilot study (ENCODE Project Consortium, 2007), it has been used to demonstrate positional relationships between chromatin features and TSSs.

ACT facilitates three main types of analysis:

Aggregation: in many scenarios, it is useful to determine the distribution of signals in a signal track relative to certain genomic anchors (Fig. 1, aggregation). For example, it has recently been reported that the contribution of each transcription factor binding site to tissue-specific gene expression depends on its position relative to the transcription start site (TSS) (MacIssac et al., 2010). It is thus useful to aggregate binding signals of transcription factors at a certain distance from the TSSs of all genes (the anchors). In general, this type of aggregation analyses helps identify proximity correlations and functional relationships between the signals and anchors.

Correlation: it is also useful to consider how multiple-related signal tracks are correlated with each other. For example, a previous study (Zhang et al., 2007) demonstrated, using whole-track correlation methods, that there was a consistent relationship among transcription factors as judged by their signal profiles across several ChIP-chip experiments. By providing a means of correlating signal tracks with each other, ACT allows for initial comparison of different experiments to see which are more similar or related than others (Fig. 1, correlation).

Saturation: another important type of analysis is determining the number of experimental conditions required to achieve a high genomic coverage of the biological phenomenon under study. For example, using ChIP-chip or ChIP-seq experiments, one could identify a set of transcription factor binding sites from a human cell line. When the experiment is repeated using another cell line, some additional binding sites could be identified. How many cell lines need to be considered in order to reach the point of saturation, so can be applied to any experiments producing data in these formats. The ability to analyze multiple genomic datasets is important, as demonstrated by tools like Galaxy (Giardine et al., 2005). ACT provides a unique set of functionality that complements existing methods of analysis.
ACT is available as a suite of downloadable scripts corresponding to the aggregation, correlation and saturation components of the toolbox. The tool is intended for Linux/Unix users with Java and Python. In addition, it is useful to have R for output visualization for the aggregation and correlation tools. There is also a compendium of other versions of the tool components written in different languages and with varied functionality. For some types of analysis, there are web components for demonstration purposes on small datasets with built-in visualization features. However, because most whole-genome signal tracks are too large to upload via standard Internet connections, users are recommended to download the toolbox and run it locally. As performing these calculations on whole-genome data can be especially time intensive, the version of the tools presented here has been designed to run efficiently on large datasets.

**Aggregation:** the aggregation component is designed to take a signal track (.sgr or .wig) and an annotation track (.bed) as input, and compute the average signal over a certain number of base pairs upstream and downstream of (i.e. a fixed radius around) the annotations. In other words, signal values are taken from the region surrounding each annotation, and averaged over the number of annotation anchors provided. The base pair resolution of the aggregation can be specified by the number of bins (narrower bins give more data points and therefore finer granularity). Results of such calculation can be plotted as in Figure 1 (aggregation). ACT also provides features such as computing the standard deviation, median and quartiles that can be viewed as a boxplot, as well as scaling aggregation over regions such as areas between transcription start and end sites or within exons so that all of the aggregate signals within those regions fall into a fixed number of bins. In this case, bin size is dynamically computed for each region so that the same number of bins cover regions of different sizes.

**Correlation:** the correlation analysis takes a set of active genomic regions (.bed) such as a SNP track or a genomic signal track (.wig). It then divides genomic coordinates into bins and gives each bin a value corresponding to the mean or maximum signal values which fall within the bin, or assigns value based on the number of ‘active regions’ which fall within the bin. A final correlation matrix is created based on either the Spearman’s, Pearson’s or normal score correlation between each pair of binned datasets. The results can be visualized as a heatmap or as a phylogenetic tree using programs such as PHYLIP (Felsenstein, 1996). One version of the correlation tool uses parallelization to decrease the pro-gram’s overall running time. This component was written largely in Java. Examples of correlation output based on SNP tracks and ChiP-chip data are shown in Figure 1 (correlation).

**Saturation:** we provide an efficient implementation of saturation plot generator. Each input file corresponds to one dataset (e.g. one new individual, in .bed format), and each line in a file specifies a genomic location that has the biological phenomenon under study (e.g. tagged SNPs). The saturation plot shows, with each new dataset (x-axis), what percentage of genome base pairs are covered (y-axis). The program considers the various combinations in which tracks can be added so that the increase in base pair coverage is a range of values based on all the files in the input. The resulting plot is output in PDF format (Fig. 1, saturation), in which a series of boxplots depicts increasing base pair coverage, where the boxplot at each position m on the x-axis shows the coverage values of all combinations of m conditions. Boxplots that approach a horizontal asymptote indicate that the coverage has reached saturation. Our implementation makes use of special data structures to avoid redundant counting. It normally takes less than a minute to generate the plot for up to 30 input files each with a few thousand lines. To handle more files and files with more lines, the tool also provides an option to compute the coverage of a random sample of the input file combinations.

### 3 DETAILS AND USE CASES

ACT is available as a suite of downloadable scripts corresponding to the aggregation, correlation and saturation components of the toolbox. The tool is intended for Linux/Unix users with Java and Python. In addition, it is useful to have R for output visualization for the aggregation and correlation tools. There is also a compendium of other versions of the tool components written in different languages and with varied functionality. For some types of analysis, there are web components for demonstration purposes on small datasets with built-in visualization features. However, because most whole-genome signal tracks are too large to upload via standard Internet connections, users are recommended to download the toolbox and run it locally. As performing these calculations on whole-genome data can be especially time intensive, the version of the tools presented here has been designed to run efficiently on large datasets.

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### 4 DISCUSSION

There are number of additional analyses that can be done to fine-tune the output of ACT. For instance, it is possible to use the online genomic signal aggregator (GSA), which assigns each genomic position to the nearest anchor in order to reduce the artifacts caused...
by the subsets of anchors clustering together, to handle tightly clustered anchors. Also, aggregation can be used in conjunction with genome structure correction to determine if the enrichments of a given signal with respect to anchor points are significantly relative to the non-random positioning of the anchors (ENCODE Project Consortium, 2007). This correction takes into account the fact that a ‘random’ distribution of anchors on the genome arises from a distinctly non-uniform distribution. Practically, this could be carried out through ACT by comparing the aggregation over anchors (e.g. TSSs) to that from ‘randomized anchors’, where the latter is generated by shifting anchor coordinates along the chromosome or transferring anchor coordinates from a second chromosome to the one of interest.

Finally, ACT can be used as a starting point for other downstream analyses. In the instance of RNA-seq data tracks, further analysis can be conducted with RseqTools (Habegger et al., 2011) to, for example, determine additional similarities between two or more highly correlated tracks. The results of correlation analysis, for instance, can also be fed into downstream principal component analysis, allowing for grouping of coregulating factors with their coregulated sites. This would simply involve diagonalization of the output correlation matrix from ACT. Saturation analysis can also be used to inform future experimental design.

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