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AnnotateGenomicRegions: a web application

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Abstract

Background: Modern genomic technologies produce large amounts of data that can be mapped to specific regions in the genome. Among the first steps in interpreting the results is annotation of genomic regions with known features such as genes, promoters, CpG islands etc. Several tools have been published to perform this task. However, using these tools often requires a significant amount of bioinformatics skills and/or downloading and installing dedicated software.

Results: Here we present AnnotateGenomicRegions, a web application that accepts genomic regions as input and outputs a selection of overlapping and/or neighboring genome annotations. Supported organisms include human (hg18, hg19), mouse (mm8, mm9, mm10), zebrafish (danRer7), and Saccharomyces cerevisiae (sacCer2, sacCer3). AnnotateGenomicRegions is accessible online on a public server or can be installed locally. Some frequently used annotations and genomes are embedded in the application while custom annotations may be added by the user.

Conclusions: The increasing spread of genomic technologies generates the need for a simple-to-use annotation tool for genomic regions that can be used by biologists and bioinformaticians alike. AnnotateGenomicRegions meets this demand. AnnotateGenomicRegions is an open-source web application that can be installed on any personal computer or institute server. AnnotateGenomicRegions is available at: http://cru.genomics.iit.it/AnnotateGenomicRegions.

Background

A common denominator for all applications of Next Generation Sequencing technology is the need to annotate genomic regions of interest. This task is usually performed by bioinformaticians who prepare the data as custom tracks for genome browsers and use a set of additional tools to produce tabular annotations to be scrutinized by biologists. Using these tools often requires a significant amount of bioinformatics skills and/or downloading and installing dedicated software. Tools have been developed that comprise functional annotation, for example CisGenome, W-ChIPeaks, Sole-Search, or CASSys [1-4]. These tools focus on the identification of enriched regions in chromatin immunoprecipitation sequencing (ChIP-seq) experiments and annotation of genomic regions is provided as a side-aspect. Therefore, using these tools for annotation purposes only is cumbersome. Command-line tools such as BEDTools [5] are very powerful at identifying overlapping regions in two files provided in browser extensible data (BED) format. Details on this format can be found at https://genome.ucsc.edu/FAQ/FAQformat.html. But being command-line tools, they are hard to use for biologists. The same is true for the BioConductor ChIPpeakAnno package [6]. Tools such as the EnsEMBL Ruby API [7] require considerable programming skills, which precludes widespread use by biologists.

Galaxy [8] is a sophisticated web-based suite of genome analysis tools that can also perform annotation of genomic regions as part of the “Operate on Genomic Intervals” menu option. It is an expert tool that requires some familiarity. The option “Fetch closest non-overlapping feature” will find annotations that have been defined as “neighbors” in this work. The file defining the neighbors must be uploaded along with the query regions. No

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default annotations for neighbor fetching are provided. Only one annotation can be fetched at the time. Identification of overlapping features requires the use of a different menu option ("Intersect"). The UCSC table browser [9] has the functionalities required to annotate sets of genomic regions. However, the input is restricted to 1,000 regions, which makes this tool cumbersome to use for the annotation of large genomic experiments, for example.

A widely accepted, web-based annotation tool available to bioinformaticians and biologists with widely varying skill levels is not available. Here we present AnnotateGenomicRegions [10], a web application that accepts genomic regions as input and outputs overlapping and/or neighboring genome annotations chosen on a simple web-form.

Implementation

AnnotateGenomicRegions has been developed using Java Enterprise technology on the NetBeans 7.1 Integrated Development Environment http://netbeans.org/ and runs on a Glassfish version 3.1 web server http://glassfish.java.net/. We also successfully tested other Java Enterprise Edition servers such as Apache TomEE 1.5.2 http://tomee.apache.org, JBOSS community edition 6.1 http://www.jboss.org/, and WebSphere community edition 3.0 http://www-03.ibm.com/software/products/us/en/appserv-wasce/. Java Server Faces https://javaserverfaces.java.net/ and PrimeFaces http://primefaces.org/ frameworks have been chosen for rendering the graphical user interface. Apache Maven http://maven.apache.org/ is used as a software management tool. AnnotateGenomicRegions relies on a set of Java beans to process the annotation queries and returns the annotations as zipped, tab-delimited tables. A set of tutorials and examples are provided to allow the user to get started quickly. The annotations are kept on the server for two hours before being deleted. AnnotateGenomicRegions is a Sourceforge project and can be downloaded from http://sourceforge.net/projects/annotatelocus/ along with detailed descriptions of input and output formats.

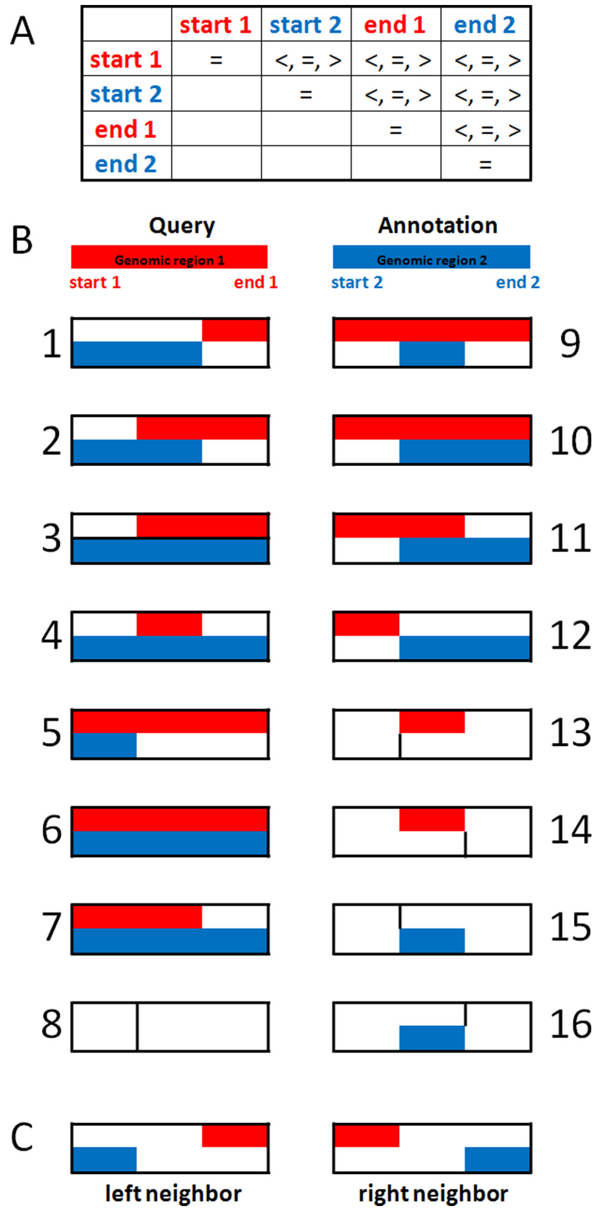
AnnotateGenomicRegions provides the annotations and genomes most frequently requested by biologists working with the developers of the tool. Currently, the annotations comprise Refseq transcripts [11], EnsEMBL transcripts [12], all_mrna transcripts [9], CpG islands, and promoter regions of transcripts. Promoter regions are defined as 1 kb regions upstream and downstream of the corresponding transcription start site. The annotations are downloaded from the UCSC genome browser [13], formatted, sorted by chromosome, start position and end position, and incorporated in the annotation pipeline. A comprehensive list of annotations and genomes for the release of October 2012 (Oct2012) is shown in Additional file 1. The users are welcome to request additional annotations or genomes that we may incorporate in the online application using the “Contact” form. Annotations will be updated on a yearly basis. AnnotateGenomicRegions doesn’t strive to provide a comprehensive list of annotations for all available genome assemblies. AnnotateGenomicRegions permits uploading customized annotations instead. Furthermore, researchers necessitating annotations not included in AnnotateGenomicRegions are encouraged to run their own local and customized installation.

Results and discussion

Conscious of the need for an easy to use application for annotating genomic regions, we have developed and made available online AnnotateGenomicRegions, a fast web application that allows submitting a list of genomic regions and displays the corresponding annotations in a web page that can be exported in a tab delimited format recognized by spreadsheet programs.

AnnotateGenomicRegions annotates sets of genomic regions of interest with overlapping and/or neighboring features that are mapped to the genome. Genomic regions of interest can be derived from experiments such as ChIP-seq, DNase I hypersensitive sites sequencing (DNase-seq), methylation profiling using reduced representation bisulfite sequencing (Methyl RRBS), quantitation of small RNAs by massively parallel sequencing (Small RNA-seq), resequencing etc., or might be derived from in-silico screens such as regions harboring a given DNA-motif. A question that typically needs to be answered early in the analysis regards the relation of the experimentally defined regions with known features in the genome. User provided and embedded annotations are annotated for overlapping and/or neighboring annotations by AnnotateGenomicRegions. The definitions of overlaps and neighborhood of genomic regions are described in Figure 1.

We consider two genomic regions in Figure 1: One region represents a query (shown in red) and the other region represents an annotation (shown in blue). Both regions have a start and an end position. Figure 1A lists the possible relations between the start and the end positions of the two genomic regions. We distinguish three possible relations between any two positions: larger than, equal to, and smaller than. From these relations follow all types of overlaps that can be observed during the annotation process, which are shown in Figure 1B. There are 16 possible types of overlaps between the query and the annotation regions, including overlaps of regions with length zero. Such regions are often found in data sets on genome variation and might describe insertion points, for example. Figure 1C depicts what is intended as neighboring annotations in AnnotateGenomicRegions. Neighboring annotations are not overlapping the query region as



	start 1	start 2	end 1	end 2
start 1	=	<, =, >	<, =, >	<, =, >
start 2		=	<, =, >	<, =, >
end 1			=	<, =, >
end 2				=

Figure 1 Overlap and neighbor queries. A) For two genomic regions located on the same chromosome, the possible relations (>, =, <) between start and end positions of the elements are listed. Note that not all configurations are realistic, e.g. start x > end x is forbidden by definition. B) Comprehensive overview of all overlap types between queries (red bars) and annotations (blue bars) are shown, including overlaps of genomic elements of size zero (cases 8, 13, 14, 15, 16). C) Neighbor annotations are defined as the closest annotation to the query that is not overlapping the query in the sense defined by panel B. Left neighbors are located upstream and right neighbors are located downstream of the query element. For left neighbors, the distance is measured between query start and annotation end. For right neighbors, the distance is measured between query end and annotation start.

defined in Figure 1B and are closest to the query region. Here, "closest" doesn't relate to the physical distance on the chromosome. It only means that there is no other genomic region in between the query region and the neighboring annotation.

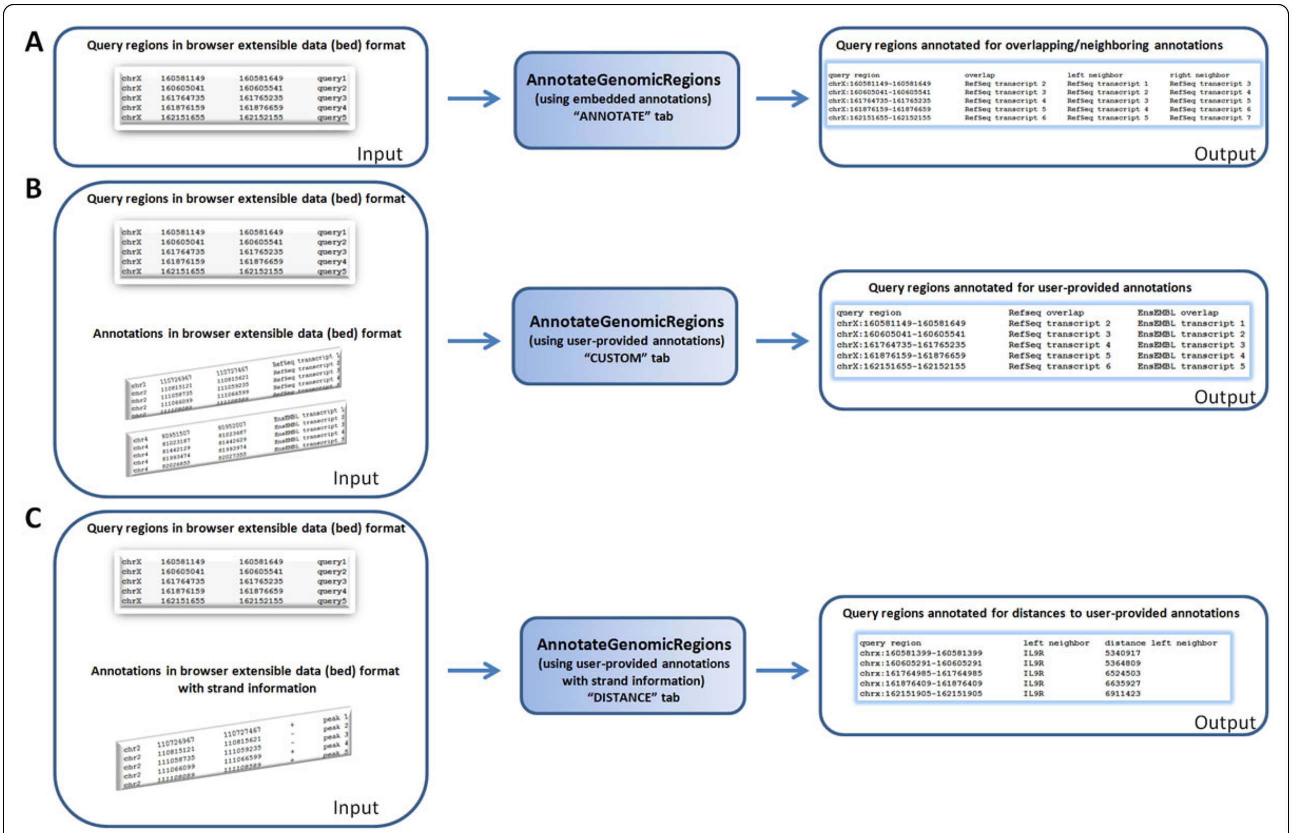
AnnotateGenomicRegions has been designed to satisfy three use-cases that are shown in Figure 2. The use-cases differ slightly in the type of input that is required from the user. In the easiest case, the user submits a set of genomic regions and annotates them for annotations that are embedded in AnnotateGenomicRegions (Figure 2A). Naturally, this mode of using the tool is limited to the embedded genome annotations. The output is a table that lists overlapping and/or neighboring annotations as chosen by the user for each query region.

In cases where the embedded annotations are not sufficient, the user may upload his/her own annotations. The uploaded files must be in BED format. As shown in Figure 2B, in this scenario the user has to upload both the query regions and all of the required annotation files. The output is represented by a table that annotates the query regions for overlaps/neighborhood of each of the uploaded annotation files.

Sometimes the user may wish to know the distance between a query region and a neighboring annotation. This often happens when transcription factors are studied and the distance to the nearest transcription start site is of interest. Figure 2C shows the input that the user must provide for obtaining distance annotations. The only difference from the use-case described in Figure 2B is that the uploaded annotation files must contain strand information. The output then lists the name of the annotation and the corresponding distance. Note that the strand information is required because distances of interest often include the 5' end or the 3' end of an annotation. By convention, the 5' end is identical to the start base of an annotation on the plus strand and the end base of the annotation on the minus strand (vice versa for 3' ends).

Figure 3 shows screenshots of AnnotateGenomicRegions. On the "**Annotate**" pane (Figure 3A) the user is invited to choose the annotation release, the genome, the desired features for annotation, and whether the annotations of the neighboring regions should be accepted. The query regions should be pasted or uploaded in BED format or position coordinates (chromosome:start-end). Upon submitting the query, the results are displayed in tabular form (Figure 3B), can be downloaded in zip format, and pasted into a spreadsheet program such as Microsoft Excel or LibreOffice. A hyperlink allows displaying each region in the UCSC genome browser [13].

For non-standard annotations, a "**CUSTOM**" menu option has been provided. Here, the user can upload an annotation file in BED format along with the queries. The user chooses the number of desired annotation files, browses to the local files containing the annotations, specifies the column indices for chromosome, start, end, and annotation name, and chooses whether


A
Query regions in browser extensible data (bed) format
Input
AnnotateGenomicRegions
(using embedded annotations)
"ANNOTATE" tab
Query regions annotated for overlapping/neighboring annotations
Output
B
Query regions in browser extensible data (bed) format
Annotations in browser extensible data (bed) format
Input
AnnotateGenomicRegions
(using user-provided annotations)
"CUSTOM" tab
Query regions annotated for user-provided annotations
Output
C
Query regions in browser extensible data (bed) format
Annotations in browser extensible data (bed) format
with strand information
Input
AnnotateGenomicRegions
(using user-provided annotations
with strand information)
"DISTANCE" tab
Query regions annotated for distances to user-provided annotations
Output

```
chrX    160581149    160581649    query1
chrX    160605041    160605541    query2
chrX    161764735    161765235    query3
chrX    161876159    161876659    query4
chrX    162151655    162152155    query5
```

```
query region                 overlap              left neighbor        right neighbor
chrX:160581149-160581649     RefSeq transcript 2  RefSeq transcript 1  RefSeq transcript 3
chrX:160605041-160605541     RefSeq transcript 3  RefSeq transcript 2  RefSeq transcript 4
chrX:161764735-161765235     RefSeq transcript 4  RefSeq transcript 3  RefSeq transcript 5
chrX:161876159-161876659     RefSeq transcript 5  RefSeq transcript 4  RefSeq transcript 6
chrX:162151655-162152155     RefSeq transcript 6  RefSeq transcript 5  RefSeq transcript 7
```

```
chr2    110726967    110727467    RefSeq transcript 1
chr2    110815121    110815621    RefSeq transcript 2
chr2    111058735    111059235    RefSeq transcript 3
chr2    111066099    111066599    RefSeq transcript 4
```

```
chr4    80951507    80952007    EnsEMBL transcript 1
chr4    81023187    81023687    EnsEMBL transcript 2
chr4    81442129    81442629    EnsEMBL transcript 3
chr4    81993474    81993974    EnsEMBL transcript 4
chr4    82026853    82027353    EnsEMBL transcript 5
```

```
query region                 Refseq overlap       EnsEMBL overlap
chrX:160581149-160581649     RefSeq transcript 2  EnsEMBL transcript 1
chrX:160605041-160605541     RefSeq transcript 3  EnsEMBL transcript 2
chrX:161764735-161765235     RefSeq transcript 4  EnsEMBL transcript 3
chrX:161876159-161876659     RefSeq transcript 5  EnsEMBL transcript 4
chrX:162151655-162152155     RefSeq transcript 6  EnsEMBL transcript 5
```

```
chr2    110726967    110727467    +    peak 1
chr2    110815121    110815621    -    peak 2
chr2    111058735    111059235    -    peak 3
chr2    111066099    111066599    +    peak 4
```

```
query region                 left neighbor   distance left neighbor
chrx:160581399-160581399     IL9R            5340917
chrx:160605291-160605291     IL9R            5364809
chrx:161764985-161764985     IL9R            6524503
chrx:161876409-161876409     IL9R            6635927
chrx:162151905-162151905     IL9R            6911423
```

Figure 2 Use cases. The three use cases are shown schematically. In all cases, the output can be downloaded and pasted into a spreadsheet. A) User provides query regions and selects desired annotations embedded in AnnotateGenomicRegions. Output lists overlapping and/or neighboring annotations as defined by the user. B) User provides query regions and annotations. Output lists overlapping and/or neighboring annotations as defined by the user. C) User provides query regions and annotations with strand information. Output lists neighboring annotations and corresponding distance.

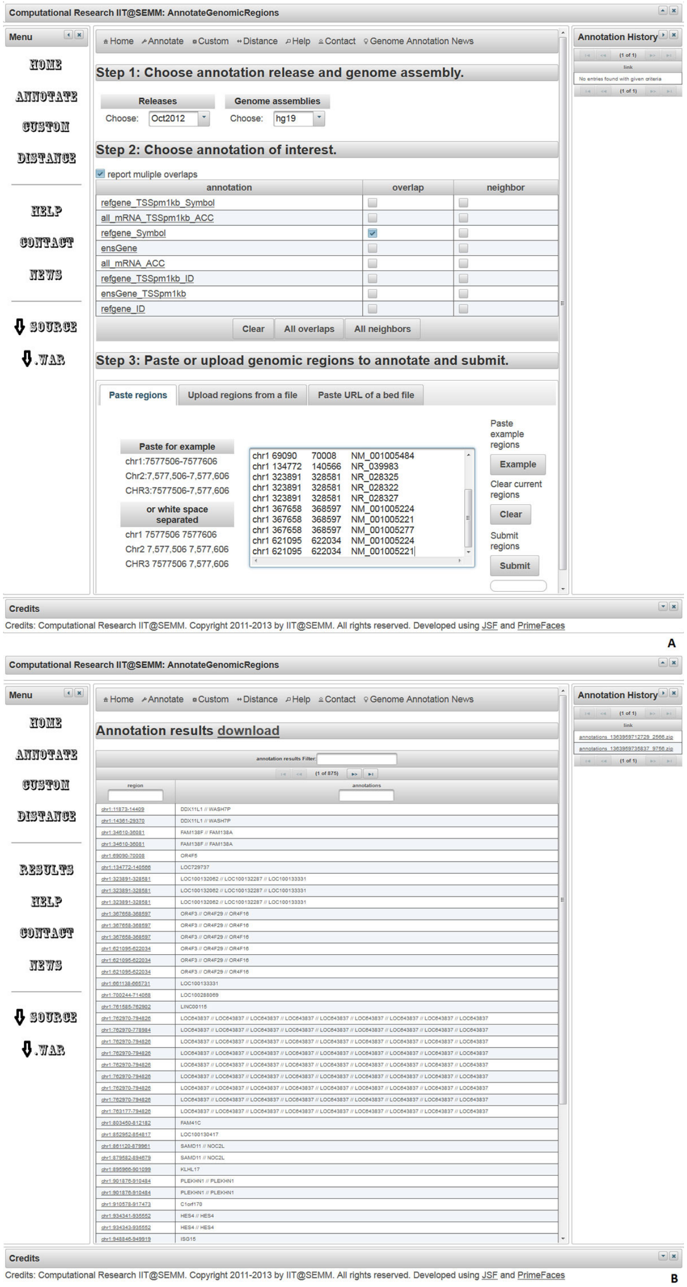
overlap or neighbors queries are desired. When submitting the queries, the annotations will be uploaded to the server, processed for fast annotation, and the annotations will be provided as a zipped output file. When the correct genome assembly is chosen on the web form, the regions may be viewed in the UCSC genome browser.

Finally, it is possible to calculate the distance between a query region and a given genome annotation. This task can be accomplished using the "**DISTANCE**" menu option. The annotations used for distance calculations must be provided by the user in the format:

″Chromosome start end strand annotation″

The user can calculate the distance to the 5' end, the 3' end, the start, the end, or the center position of the annotation. The distance is calculated either to the start, the end, or the center position of the query region, as defined by the user.

The speed of the annotation process using AnnotateGenomicRegions was compared to the speed of BEDTools [5]. BEDTools is popular in the bioinformatics community and provides command line functionality that permits annotating a set of query regions with one or more annotation files. BEDTools uses C++ libraries for annotation that were originally developed for the UCSC genome browser [5,13]. To speed up the annotation process, these libraries employ a binning scheme to the genomic regions of the annotations and build an index on the bins obtained. AnnotateGenomicRegions, on the other hand, uses hash tables for each chromosome holding the annotations sorted by start position. Auxiliary hash tables are then used that memorize the position of the last annotation found to be overlapping or neighboring a query region. Since the query regions are sorted by start position, the auxiliary hash tables help minimizing the number of times a given annotation is visited. Figure 4 shows the response times of AnnotateGenomicRegions and of BEDTools when used for annotating between 10 and 500,000 query regions with one or ten different annotations. It can be seen that AnnotateGenomicRegions is significantly faster than BEDTools, particularly for large numbers of query regions. The response times for up to 300,000 query



A

Step 1: Choose annotation release and genome assembly.

Releases — Choose: Oct2012

Genome assemblies — Choose: hg19

Step 2: Choose annotation of interest.

☑ report muliple overlaps

annotation	overlap	neighbor
refgene_TSSpm1kb_Symbol	□	□
all_mRNA_TSSpm1kb_ACC	□	□
refgene_Symbol	☑	□
ensGene	□	□
all_mRNA_ACC	□	□
refgene_TSSpm1kb_ID	□	□
ensGene_TSSpm1kb	□	□
refgene_ID	□	□

Step 3: Paste or upload genomic regions to annotate and submit.

Paste for example
chr1:7577506-7577606
Chr2:7,577,506-7,577,606
CHR3:7577506-7,577,606

or white space separated
chr1 7577506 7577606
Chr2 7,577,506 7,577,606
CHR3 7577506 7,577,606

```
chr1 69090     70008     NM_001005484
chr1 134772    140566    NR_039983
chr1 323891    328581    NR_028325
chr1 323891    328581    NR_028322
chr1 323891    328581    NR_028327
chr1 367658    368597    NM_001005224
chr1 367658    368597    NM_001005221
chr1 367658    368597    NM_001005277
chr1 621095    622034    NM_001005224
chr1 621095    622034    NM_001005221
```

Paste example regions

Clear current regions

Submit regions

link
No entries found with given criteria

(1 of 1)

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B

Annotation results download

annotation results Filter:

(1 of 875)

region	annotations
chr1:11873-14409	DDX11L1 // WASH7P
chr1:14361-29370	DDX11L1 // WASH7P
chr1:34610-36081	FAM138F // FAM138A
chr1:34610-36081	FAM138F // FAM138A
chr1:69090-70008	OR4F5
chr1:134772-140566	LOC729737
chr1:323891-328581	LOC100132062 // LOC100132287 // LOC100133331
chr1:323891-328581	LOC100132062 // LOC100132287 // LOC100133331
chr1:323891-328581	LOC100132062 // LOC100132287 // LOC100133331
chr1:367658-368597	OR4F3 // OR4F29 // OR4F16
chr1:367658-368597	OR4F3 // OR4F29 // OR4F16
chr1:367658-368597	OR4F3 // OR4F29 // OR4F16
chr1:621095-622034	OR4F3 // OR4F29 // OR4F16
chr1:621095-622034	OR4F3 // OR4F29 // OR4F16
chr1:621095-622034	OR4F3 // OR4F29 // OR4F16
chr1:661138-665731	LOC100133331
chr1:700244-714068	LOC100288069
chr1:761585-762902	LINC00115
chr1:762970-794826	LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837
chr1:762970-778984	LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837
chr1:762970-794826	LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837
chr1:762970-794826	LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837
chr1:762970-794826	LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837
chr1:762970-794826	LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837
chr1:762970-794826	LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837
chr1:762970-794826	LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837
chr1:763177-794826	LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837 // LOC643837
chr1:803450-812182	FAM41C
chr1:852952-854817	LOC100130417
chr1:861120-879961	SAMD11 // NOC2L
chr1:879582-894679	SAMD11 // NOC2L
chr1:895966-901099	KLHL17
chr1:901876-910484	PLEKHN1 // PLEKHN1
chr1:901876-910484	PLEKHN1 // PLEKHN1
chr1:910578-917473	C1orf170
chr1:934341-935552	HES4 // HES4
chr1:934343-935552	HES4 // HES4
chr1:948846-949919	ISG15

link
annotations_1363959712729_2566.zip
annotations_1363959735837_9756.zip

(1 of 1)

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Figure 3 Screenshots of AnnotateGenomicRegions. A) Annotate pane. Here, the user uploads query regions, selects desired release, the genome and embedded annotations of interest, defines if multiple hits shall be displayed, and submits the query. Query regions can be uploaded by pasting them directly, by uploading a file, or by providing a hyperlink to a file in the appropriate format. The format of the query regions can be any of the following position coordinates such as chr1:7577506-7577606 or Chr2:7,577,506-7,577,606 or CHR3:7577506-7,577,606 (case insensitive, with and without thousands separators, colon between chr and start, minus between start and end). Colon and minus characters are not compulsory and space or tabulator characters can be used instead (also called white space characters). Allowing tabulator characters as separators permits pasting query regions directly from a spreadsheet holding chromosome, start, and end positions in separate columns. Note that query regions can be duplicated. These duplications represent alternatively spliced transcripts with identical start and stop positions but with different transcript identifiers. Duplicated regions will be annotated independently from each other as if they were not duplicated. B) Output example. The output lists all the annotations found for each query region. In this example, all RefSeq Symbols for transcription units overlapping the query regions are shown, separated by two forward slash ("/") characters. A hyperlink for downloading the latest results is shown. The hyperlinks corresponding to queries executed earlier are displayed in the Annotation history. Each query region is hyperlinked for display in the UCSC genome browser. Duplicated query regions are listed independently from each other and will display identical annotations. Keeping the duplicates helps keeping the output compatible with the input so that the output can be pasted easily side-by-side to annotations obtained previously. Note that the results page contains a filter function ("annotation results filter"). Typing in the associated text field will filter out all rows that do not contain the typed word in any column. This feature is useful if a researcher is interested in a given gene, for example. Filters can be applied separately to each column by typing in the text fields labeled as “region” or “annotations”.

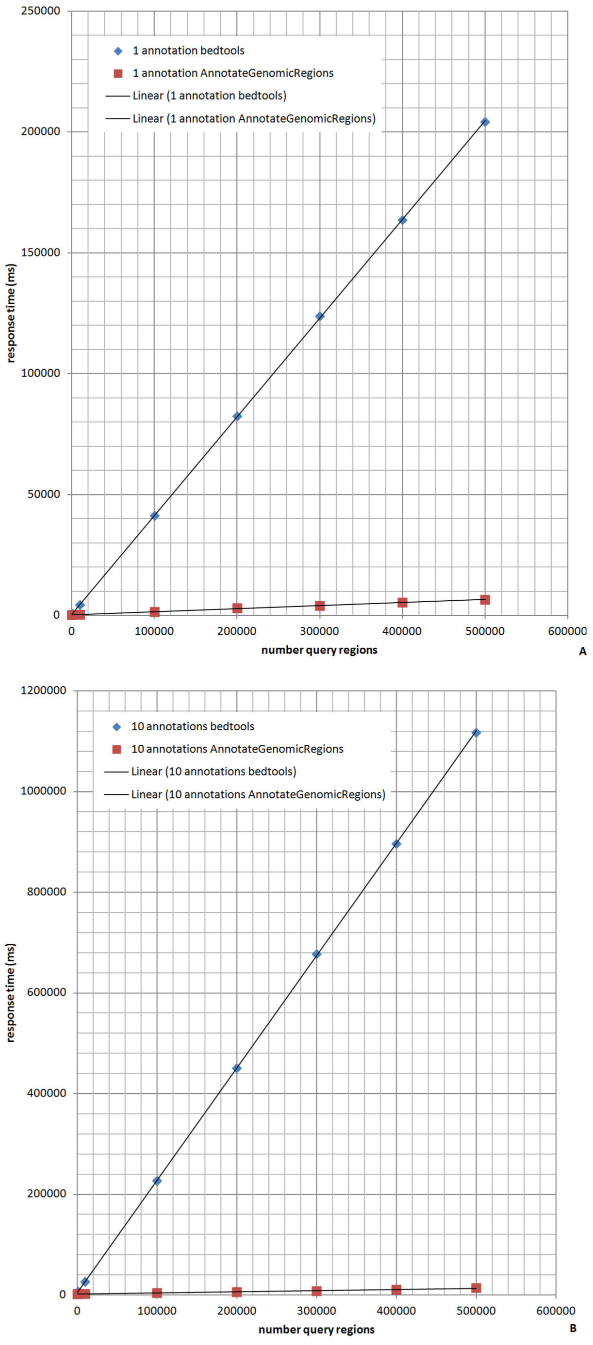

Figure 4 Comparison of AnnotateGenomicRegions and BEDTools. AnnotateGenomicRegions and BEDTools were used to annotate identical query regions with identical annotation files. The number of query regions was varied between 10 and 500,000. The response times for AnnotateGenomicRegions were found to be two times faster for up to 100 query regions. For 500,000 query regions, AnnotateGenomicRegions was found to be 30 times faster for 1 annotation (A) and 80 times faster for 10 annotations (B). The tests were performed on an Ubuntu Server Linux computer with 12 CPU's and 16 GB RAM.

regions remain below 10 seconds. This amount of query regions exceeds the number of regions to be annotated in a typical genomic experiment several fold.

Conclusions

AnnotateGenomicRegions is a web-application that allows researchers with a wide range of bioinformatics skills to annotate genomic regions of interest, e.g. ChIP-seq peaks, with overlapping or neighboring annotations. In contrast to other tools, AnnotateGenomicRegions, can be used easily by non-experts. The annotations are provided as tab-delimited text files that can be pasted into a spreadsheet. Query regions are hyperlinked for viewing them in the UCSC Genome Browser. Commonly used annotations such as Refseq transcripts [11], EnsEMBL transcripts [12], or CpG islands are downloaded regularly from the UCSC genome browser repository and made available for instant annotation of genomic regions of interest. Users are invited to leave their feedback using the contact form to improve the software or to participate in future developments of the tool.

Availability and requirements

•Project name: AnnotateGenomicRegions
•Project home page: http://cru.genomics.iit.it/AnnotateGenomicRegions
•Operating system(s): Platform independent
•Programming language: Java
•Other requirements: Java 1.6 or higher, Glassfish 3.1 or higher
•License: Apache license
•Any restrictions to use by non-academics: no restrictions

Additional material

Additional file 1: Annotations and genomes provided by AnnotateGenomicRegions. The annotation name column shows the file name that is displayed by the web application. The UCSC download file name lists the name of the file at the UCSC genome browser repository that is used as the annotation source. hg19, hg18, mm10, mm9, mm8, danRer7, sacCer3, and sacCer2 denote the genome assemblies for which annotations are embedded in the web application. The region description column holds a short description of the annotation file content. The region name example shows examples of the names associated with each genomic region.

Abbreviations

BED: browser extensible data; ChIP-seq: Chromatin Immunoprecipiation followed by massively parallel sequencing; danRer7: July 2010 zebrafish (Danio rerio) Zv9 assembly produced by The Wellcome Trust Sanger Institute; DNase-seq: DNase I hypersensitive sites sequencing; hg18: March 2006 human reference sequence (NCBI Build 36.1); hg19: February 2009 human reference sequence (Genome Reference Consortium Human Build 37); Methyl-RRBS: genome-wide methylation profiling using reduced representation bisulfite sequencing; mm10: December 2011 Mus musculus assembly (Genome Reference Consortium Mouse Build 38); mm8: February 2006 Mus musculus assembly (Genome Reference Consortium Mouse Build 36); mm9: July 2007 Mus musculus assembly (Genome Reference Consortium Mouse Build 37); Oct2012: October 2012 release of AnnotateGenomicRegions embedded annotations; sacCer2: June 2008 Saccharomyces cerevisiae genome assembly based on sequence in the Saccharomyces Genome Database; SacCer3: April 2011 Saccharomyces cerevisiae genome assembly based on sequence in the Saccharomyces Genome Database; smallRNA-seq: quantitation of small RNAs by massively parallel sequencing.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

LZ provided, formats, and maintains the annotations. RD provided the file uploads module. GB took care of application deployment and maintenance. AC maintains the project code. HM conceived the project, provided the initial implementation, and wrote the manuscript. All authors contributed to the editing of the manuscript. All authors read and approved the final manuscript.

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Declarations

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