

## **ACTG 1.10: Novel peptide mapping onto gene models**

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### **1. Requirement**

#### *1.1. Software*

ACTG requires Java Running Environment (JRE) 1.7.0\_45 or later. If JRE is not installed, please visit <http://www.oracle.com/technetwork/java/index.html>.

#### *1.2. Hardware*

ACTG's hardware requirement depends on a size of transcriptome model (GTF). If it is Ensembl transcriptome model, ACTG requires at least 8GB heap size, and 2MB stack size to construct a variant splice graph and to map on the graph.

### **2. Usage**

#### *2.1. Constructing the variant splice graph*

```
java -Xmx8G -Xss2m -jar ACTG_Construction.jar const_params.xml
```

#### *2.2. Mapping on the variant splice graph*

```
java -Xmx8G -Xss2m -jar ACTG_Mapping.jar mapping_params.xml
```

### 3. Parameters

Two parameter files (XML format) are given for construction and mapping separately.

#### 3.1. *const\_params.xml*

Tag	Type	Format	Explanation
Input	Transcriptome	GTF	Path of a folder which contains transcriptome models.
Input	Reference Genome	FASTA	Path of a folder which contains reference genome. <b>Each file name must be the same as chromosome number written in the given GTF files.</b>
Output	Graph file	Ser	Name of a constructed variant splice graph file.
TheNumber OfThreads	Setting the number of threads. A proper setting can increase the speed of construction.		

#### 3.2. *mapping\_params.xml*

Tag	Type	Format	Explanation
MappingMethod	-	-	PV: Mapping [P]rotein database first, then next [V]ariant splice graph. PS: Mapping [P]rotein database first, then next [S]ix-frame translation. VO: Mapping [V]ariant splice graph [O]nly. SO: Mapping [S]ix-frame translation [O]nly.
ILSame	-	-	Yes/No: consider isoleucine and leucine as the same.
Input	Peptide list	List	Path of a peptide list file that a user wants to map.
Output	outputPath	-	Path of a folder where the output files will be located.
Input	Protein	FASTA	If a user sets "MappingMethod" as P[V S], then the

	Database		user should provide a folder path containing protein database.
SAVs	-	-	Yes/No: automatically consider single amino-acid variant when mapping on protein database.
Input	Graph file	Ser	Serialization file path of the variant splice graph.
Junction Variation	-	-	Yes/No: consider junction variation events.
Exon Skipping	-	-	Yes/No: consider single exon skipping events.
Intron Mapping	-	-	Yes/No: consider intron mapping (exon-extension) events.
Mutation	-	-	If a user gives a VCF (variant call format), then this setting must be “yes”.
Input	Mutation	VCF	If “Mutation” tag is set as “yes”, then a user should provide the path of folder where VCF files are.  Each chromosome number must be written as 1, 2, 3, ..., X, Y.
Input	Reference Genome	FASTA	If a user sets “MappingMethod” as PS or SO, then the user should provide the path of folder where reference genome files are.
TheNumber OfThreads	A user can set the number of threads. A proper setting can increase the speed of mapping.		

## 4. Format Constraints

### 4.1. GTF

```

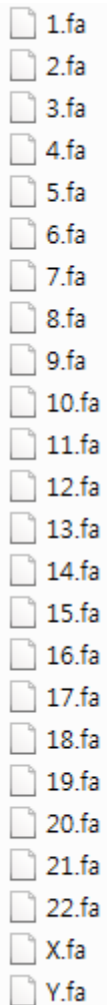
1      protein_coding  gene      30      230      .      +      .      gene_id "TESTGENE";
1      protein_coding  transcript 30      230      .      +      .      gene_id "TESTGENE";
1      protein_coding  exon      30      50      .      +      .      gene_id "TESTGENE";
1      protein_coding  CDS       40      50      .      +      0      gene_id "TESTGENE";
1      protein_coding  exon      70      130     .      +      .      gene_id "TESTGENE";
1      protein_coding  CDS       70      130     .      +      0      gene_id "TESTGENE";
1      protein_coding  exon      180     230     .      +      .      gene_id "TESTGENE";
1      protein_coding  CDS       180     210     .      +      2      gene_id "TESTGENE";

```

A chromosome number of GTF record must be number 1, 2, ..., 22, "X," or "Y."

Please include all transcriptome models of every chromosome in a single file.

#### 4.2. FASTA



All FASTA files describe reference genome must have the same file name to each chromosome number (see the left picture). If there is certain chromosome number in the GTF file, then FASTA file corresponding to the chromosome must be existed.

#### 4.3. VCF

```
1      201      rs1      A      C      1781.52 .      AC=2;
```

The chromosome number in a VCF file must be the same as chromosome number such as 1, 2, 3, ... , "X," or "Y."