

## Useful tool: annot-regs

Common problem:

- find overlaps in two sets of genomic regions (e.g. two CNV callsets)
- match records by a common column (e.g. sample name)
- transfer a field from one file to another for matching records

Requirements:

- columns can be named differently and can appear in arbitrary order
- headers may or may not be present
- can require multiple columns to match (e.g. sample name AND variant type)
- can transfer multiple fields

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Source file:

#chr	beg	end	smpl	type	qual	length	npr
5	67591246	67591246	DDDP167799	DEL	3.91	19611039	4
7	42006018	42006018	DDDP154344	DUP	64.02	19580982	29
12	14825806	14825807	DDDP123456	DEL	7.25	66506	2
16	30978217	30978217	DDDP345139	DEL	55.76	42248	3
19	42474652	42474652	DDDP114567	DUP	63.27	19581359	28

Destination file:

DDDP345139	16	30978217	30978217
DDDP123456	12	14825806	14825807
DDDP154344	7	42006018	42006018
DDDP114567	19	42474652	42474652
DDDP167799	5	67591246	67591246

annot-regs -s src.txt -d dst.txt -c chr,beg,end:2,3,4 -m smpl:1 -t qual:qual

file with source  
annotations

destination  
file

the names or  
indexes of core  
columns  
(chr,beg,end) in  
source and  
destination file

the names or  
indexes of  
columns required  
to be identical

the names or  
indexes of  
columns to  
transfer

## annot-regs usage

About: Annotate regions in DST file with texts from overlapping regions in SRC file.  
 The transfer of annotations can be conditioned on matching values in one or more columns (-m), multiple columns can be transferred (-t).  
 All indexes and coordinates are 1-based and inclusive.

Usage: annot-regs [OPTIONS] DST

Options:

--allow-dups	Add annotations multiple times
-a, --annotate list	Add special annotations:
	frac .. fraction of the destination region with an overlap
	nbp .. number of source base pairs in the overlap
-c, --core src:dst	Core columns [chr,beg,end:chr,beg,end]
-d, --dst-file file	Destination file
-m, --match src:dst	Require match in these columns
-o, --overlap float	Minimum required overlap (non-reciprocal, unless -r is given)
-r, --reciprocal	Require reciprocal overlap
-s, --src-file file	Source file
-t, --transfer src:dst	Columns to transfer. If src column does not exist, interpret as the default value to use. If the dst column does not exist, a new column is created.
--version	Print version string and exit

Examples:

```
# Header is present, match and transfer by column name
annot-regs -s src.txt.gz -d dst.txt.gz -c chr,beg,end:chr,beg,end -m type,sample:type,smpl -t tp/fp:tp/fp
```

```
# Header is not present, match and transfer by column index (1-based)
annot-regs -s src.txt.gz -d dst.txt.gz -c 1,2,3:1,2,3 -m 4,5:4,5 -t 6:6
```

```
# If the dst part is not given, the program assumes that the src:dst columns are identical
annot-regs -s src.txt.gz -d dst.txt.gz -c chr,beg,end -m type,sample -t tp/fp
```