

Database Setup

sonar setup

<code>--db FILE</code>	specify the name of the new database
<code>--gbk FILE</code>	set a custom reference based on the specified Genbank file [opt.]
<code>-a</code>	add pre-defined sample properties to the new database [opt.]

Show Infos

sonar info

<code>--db FILE</code>	specify name of the database
------------------------	------------------------------

Sample Management

sonar import *to import data*

<code>--db FILE</code>	specify name of the database
<code>--fasta FILE [FILE, ...]</code>	specify fasta file to import sequences [opt]
<code>--tsv FILE [FILE, ...]</code>	specify tab-delimited text file to import meta information [opt]
<code>--cols STR [STR, ...]</code>	link properties with tsv columns in the form of <i>prop_name=col_header</i> [opt]
<code>--no-autodetect</code>	do not auto-link properties with tsv columns based on identical names [opt]
<code>--no-update</code>	skip data of existing samples [opt]
<code>--cache DIR</code>	specify a folder to cache import data [opt]
<code>-t INT</code> <code>--threads INT</code>	specify number of threads / cpus to use [opt]

sonar delete *to delete sample(s)*

Sample Management (cont)

<code>--db FILE</code>	specify name of the database
<code>--sample STR [STR, ...]</code>	specify names of samples to delete [opt]
<code>--sample-file FILE</code>	specify file containing names of samples to delete [opt]
<code>--force FILE</code>	force deletion and skip user confirmation [opt]
sonar optimize	<i>} to clean database</i>
<code>--db FILE</code>	specify name of the database
sonar db-upgrade	upgrade database to the latest version
<code>--db FILE</code>	specify name of the database

Property Management

sonar list-prop	<i>to list available properties</i>
<code>--db FILE</code>	specify name of the database
sonar add-prop	add new property
<code>--db FILE</code>	specify name of the database
<code>--name STR</code>	specify new property name matching to [A-Z] [A-Z0-9_]+
<code>--descr STR</code>	provide a short property description
<code>--dtype STR</code>	specify data type
<code>--qtype STR</code>	specify query type [opt]
<code>--default</code>	specify default value [opt]
sonar delete-prop	delete property
<code>--db FILE</code>	specify name of the database
<code>--name STR</code>	specify new property name
<code>--force</code>	force deletion without user confirmation [opt]

Query Genomes

sonar match

<code>--sample STR [STR, ...]</code>	consider given samples only [opt]
<code>--sample-file *FILE</code>	consider samples listed in the given file only [opt]
<code>--profile STR [STR, ...]</code>	match given mutation profile (use argument multiple times to define alternate profiles) [opt]
<code>--PROP VALUE [VALUE, ...]</code>	filter based on sample property (<i>PROP</i> has to be replaced by the actual property name) [opt]
<code>--with-sublineage PROP</code>	include pangolin sub-lineages for the given property [opt] i Use <i>sonar update-lineage-info</i> to update lineage info before
<code>--showNX</code>	show uninformative variant alleles for genome profiles [opt]

`--out-cols STR [STR, ...]` specify columns to show (for tsv and csv only) [opt]

`--count` show number of matching genomes only [opt]

`--format {csv, tsv, vcf}` specify the output format [opt]

`-o FILE` write output to the given file [opt]
`--out FILE`



By **Stephan Fuchs** (fuchs)
cheatography.com/fuchs/

Published 14th February, 2023.
Last updated 15th February, 2023.
Page 1 of 3.

Sponsored by **CrosswordCheats.com**
Learn to solve cryptic crosswords!
<http://crosswordcheats.com>

Mutation Notations			Operators for Data Types (cont)		
	Genome level	Protein level			
Substitution	<i>REFposALT</i> e.g. A3451T	<i>PROT:REFposALT</i> e.g. A3451T	<	smaller than (e.g. <1)	integer, float, date
Insertion	<i>REFposALT</i> e.g. A4057TGAT	<i>PROT:REFposALT</i> e.g. N:A34AK	>=	larger than or equal to (e.g. >=1)	integer, float, date
1-bp Deletion	del: <i>pos</i> e.g. del:11288	<i>PROT:del:pos</i> e.g. ORF1ab:del:300	<=	smaller than or equal to (e.g. <=1)	integer, float, date
multi-bp Deletion	del: <i>start-end</i> e.g. del:112-115	<i>PROT:del:start-end</i> e.g. S:del:68-69	!=	different than (e.g. !=1)	integer, float, date
Deletion with fixed coordinates	del: <i>=start-end</i> e.g. del:=8-=11	<i>PROT:del:=start-end</i> e.g. S:del:=68-=69	:	<i>from:to</i> range (e.g. 2021-01-01:2021-12-31)	integer, float, date
i Any notation can be negated by a preceding caret (^), e.g. ^A1345G only matches target genomes not carrying this SNP. i <i>REF</i>: reference allele; <i>ALT</i>: variant allele; <i>pos</i>: reference position (1-based); <i>start</i> and <i>end</i>: start and end reference coordinates (1-based); <i>PROT</i>: protein symbol			^	not the same as (e.g. ^B.1.1.7)	text
			%	wildcard standing for any character(s) (e.g. %human%)	text
			A Make sure that expressions with > or < are quoted to prevent misinterpretation by the shell		

Data Types for Properties	
integer	for storing integers
float	for storing decimal numbers
text	for storing strings
dates	for storing dates in the form YYYY-MM-DD
zip	for storing zip codes

Operators for Data Types		
Operator	Description	Valid data type
>	larger than (e.g. >1)	integer, float, date

