

Database Setup		Sample Management (cont)		Query Genomes	
sonar setup				sonar match	
--db <i>FILE</i>	specify the name of the new database	--db <i>FILE</i>	specify name of the database	--sample <i>STR [STR, ...]</i>	consider given samples only [opt]
--gbk <i>FILE</i>	set a custom reference based on the specified Genbank file [opt.]	--sample <i>STR [STR, ...]</i>	specify names of samples to delete [opt]	--sample-file * <i>FILE</i>	consider samples listed in the given file only [opt]
-a	add pre-defined sample properties to the new database [opt.]	--sample-file <i>FILE</i>	specify file containing names of samples to delete [opt]	--profile <i>STR [STR, ...]</i>	match given mutation profile (use argument multiple times to define alternate profiles) [opt]
--auto-create		--force <i>FILE</i>	force deletion and skip user confirmation [opt]	--PROP <i>VALUE [VALUE, ...]</i>	filter based on sample property (<i>PROP</i> has to be replaced by the actual property name) [opt]
Show Infos		sonar optimize			
sonar info					
--db <i>FILE</i>	specify name of the database				
Sample Management					
sonar import	<i>to import data</i>				
--db <i>FILE</i>	specify name of the database	--db <i>FILE</i>	specify name of the database		
--fasta <i>FILE [FILE, ...]</i>	specify fasta file to import sequences [opt]	sonar db-upgrade	upgrade database to the latest version		
--tsv <i>FILE [FILE, ...]</i>	specify tab-delimited text file to import meta information [opt]	--db <i>FILE</i>	specify name of the database		
--cols <i>STR [STR, ...]</i>	link properties with tsv columns in the form of <i>prop_name=col_header</i> [opt]	Property Management			
--no-autodetect	do not auto-link properties with tsv columns based on identical names [opt]	sonar list-prop	<i>to list available properties</i>		
--no-update	skip data of existing samples [opt]	--db <i>FILE</i>	specify name of the database		
--cache <i>DIR</i>	specify a folder to cache import data [opt]	sonar add-prop	add new property		
-t <i>INT</i>	specify number of threads / cpus to use [opt]	--db <i>FILE</i>	specify name of the database		
--threads <i>INT</i>		--name <i>STR</i>	specify new property name matching to [A-Z] [A-Z0-9_]+		
sonar delete	<i>to delete sample(s)</i>	--descr <i>STR</i>	provide a short property description		
		--dtype <i>STR</i>	specify data type		
		--qtype <i>STR</i>	specify query type [opt]		
		--default	specify default value [opt]		
		sonar delete-prop	delete property		
		--db <i>FILE</i>	specify name of the database		
		--name <i>STR</i>	specify new property name		
		--force	force deletion without user confirmation [opt]		
				--showNX	show uninformative variant alleles for genome profiles [opt]
				--with-sublineage <i>PROP</i>	include pangolin sub-lineages for the given property [opt] i Use <i>sonar update-lineage-info</i> to update lineage info before

`--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`



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Mutation Notations

	Genome level	Protein level
Substitution	<i>REFposALT</i> e.g. A3451T	<i>PROT:REFposALT</i> e.g. A3451T
Insertion	<i>REFposALT</i> e.g. A4057TGAT	<i>PROT:REFposALT</i> e.g. N:A34AK
1-bp Deletion	<i>del:pos</i> e.g. del:11288	<i>PROT:del:pos</i> e.g. ORF1ab:del:300
multi-bp Deletion	<i>del:start-end</i> e.g. del:112-115	<i>PROT:del:start-end</i> e.g. S:del:68-69
Deletion with fixed coordinates	<i>del:=start=end</i> e.g. del:=8-=11	<i>PROT:del:=start=end</i> e.g. S:del:=68-=69

i Any notation can be negated by a preceding caret (^), e.g. ^A1345G only matches target genomes not carrying this SNP.

i *REF*: reference allele; *ALT*: variant allele; *pos*: reference position (1-based); *start* and *end*: start and end reference coordinates (1-based); *PROT*: protein symbol

Operators for Data Types (cont)

<	smaller than (e.g. <1)	integer, float, date
>=	larger than or equal to (e.g. >=1)	integer, float, date
<=	smaller than or equal to (e.g. <=1)	integer, float, date
!=	different than (e.g. !=1)	integer, float, date
:	<i>from:to</i> range (e.g. 2021-01-01:2021-12-31)	integer, float, date
^	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

