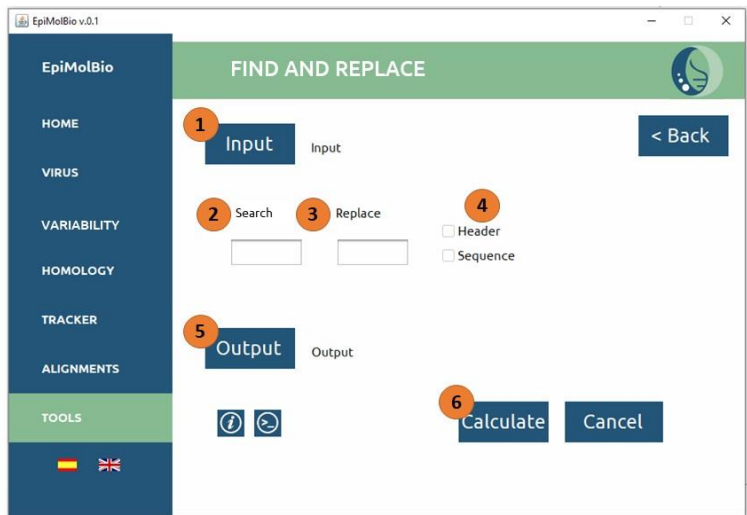


Tools Find and Replace

It allows you to replace a series of characters with others in both the header and the genetic sequence of one or multiple .fasta files.



- ① Select the input folder. It should only contain the .fasta files you want to modify.
- ② Enter the characters to be replaced.
- ③ Enter the new characters that will replace the previous ones.
- ④ Choose where the characters will be modified: header or sequence.
- ⑤ Select the output folder without entering the file name. It will be automatically named as 'Replace_InputFileName.fasta'.
- ⑥ Click Calculate.

A .fasta file with modified headers or sequences will be generated.

Input file:

```
>HCOV/19/SPAIN/AS/232252631/2022.EPI|ISL|8818639.2022/01/05  
MYSFVSEETGTLIVNSVLLFLAFVVFLVTLAILTALRLCAYCCNIVNVSLVKPS  
FYVYSRVKNLNSSRVPDLLV  
>HCOV/19/SPAIN/AS/232253923/2022.EPI|ISL|8818658.2022/01/05  
MYSFVSEEIGTLIVNSVLLFLAFVVFLVTLAILTALRLCAYCCNIVNVSLVKPSF  
YVYSRVKNLNSSRVPDLLV
```

Modified file:

```
>HCOV/19/SPAIN/AS/232252631/2022.EPI|ISL|8818639.2022/01/05  
MYSFVSEETGTLIVNSVLLFLAFVVFLVTLAILTALRLCAYCCNIVNVSLVKPS  
FYVYSRVKNLNSSRVPDLLV  
>HCOV/19/SPAIN/AS/232253923/2022.EPI|ISL|8818658.2022/01/05  
MYSFVSEEIGTLIVNSVLLFLAFVVFLVTLAILTALRLCAYCCNIVNVSLVKPSF  
YVYSRVKNLNSSRVPDLLV
```

More information about this function can be found in the User Manual, section:

VI. TOOLS VI.1 FILE EDITING VI.1.D) FIND AND REPLACE