

Notes on how to use the code inference_primer.py :

Input example :

PRIMERNAME	PRIMID	READS	COPIES
Culex_pipiens	1	25807	43
Culex_pipiens	2	19195	43
Culex_pipiens	3	18844	43
Aedes_albop	1	8233	2
Aedes_albop	2	44200	2
Aedes_albop	3	18833	2
Aedes_caspi	1	20985	49
Aedes_caspi	2	18833	49
Aedes_caspi	3	117030	49
Anopheles_m	1	1114	1
Anopheles_m	2	9872	1
Anopheles_m	3	6327	1
Culex_thai	1	2095	5
Culex_thai	2	487	5
Culex_thai	3	8891	5

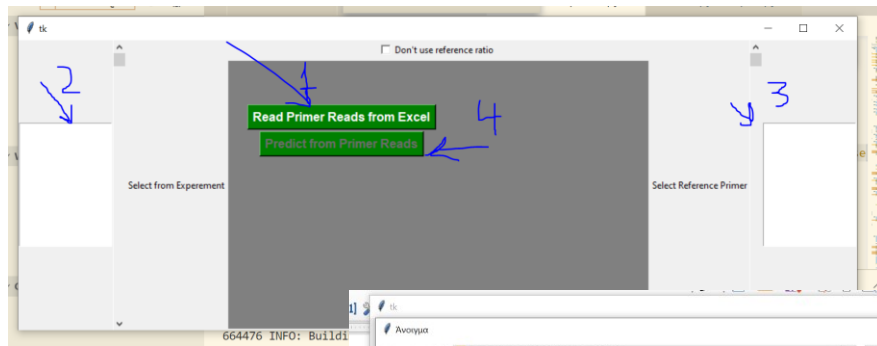
Provide input in a form of an excel file (.xlsx) using the following 4 headers, in a set of excel sheets

PRIMNAME	PRIMID	READS	COPIES1
Culex_pipiens	1	18422	30
Culex_pipiens	2	117267	30
Culex_pipiens	3	72937	30
Aedes_detritu	1	9011	3
Aedes_detritu	2	60343	3
Aedes_detritu	3	31881	3
Aedes_caspi	1	35276	60
Aedes_caspi	2	177433	60
Aedes_caspi	3	153307	60
Culiseta_annu	1	488	1
Culiseta_annu	2	3243	1
Culiseta_annu	3	2124	1
Aedes_albopi	1	626	1
Aedes_albopi	2	67	1
Aedes_albopi	3	2013	1
Culex_thai	1	1437	1
Culex_thai	2	367	1
Culex_thai	3	4067	1
Aedes_vexan	1	1532	3
Aedes_vexan	2	5636	3
Aedes_vexan	3	5729	3
Anopheles_m	1	869	1
Anopheles_m	2	6466	1
Anopheles_m	3	13866	1

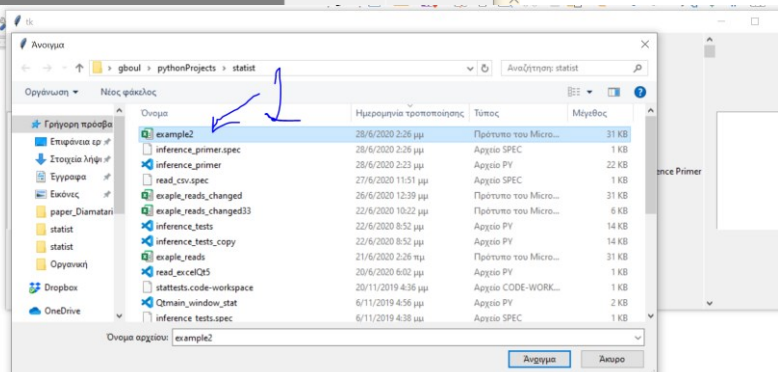
Use a different header (anything different that COPIES) to set that a data set is only used for predistortion and the data are not to be used during retraction.

Run program:

Step 1 select input :



Select experiment or experiments and on Primer common to all experiments to act as reference Culex_pipiens_Primer1 as the reference Primer. Note that One can select multiple experiments but only one reference primer.



Depending on the heads use in the input excel file the one gets a comparison between the measured copies (used:) and the predicted copies (pred:) or only the predicted copies in the case that the header has been set not to match COPIES in some of the experiments.

The screenshot displays a software interface with a Tkinter window. The window has two buttons: "Read Primer Reads from Excel" and "Predict from Primer Reads". Below the window, there are two terminal windows showing the output of the prediction process.

Experiment 48 Output:

```
Culex pipiens_PRIMERS1, pred :28.290770018011192
Aedes detritus_PRIMERS1, pred :42.68071240214435
Aedes caspius_PRIMERS1, pred :61.9595141451165
Culiseta annulata_PRIMERS1, pred :0.4900617095611327
Aedes albopictus_PRIMERS1, pred :1.3882786476830906
Culex theileri_PRIMERS1, pred :1.0623924874926665
Aedes vexans_PRIMERS1, pred :2.6505447415944166
Anopheles melanoon_PRIMERS1, pred :0.6777258483817385
```

Experiment 47 Output:

```
Culex pipiens_PRIMERS1, pred :43.12078047446103, used :43
Aedes detritus_PRIMERS1, pred :1.6938874632603552, used :2
Aedes caspius_PRIMERS1, pred :49.664118242720924, used :49
Anopheles melanoon_PRIMERS1, pred :0.9961931975324773, used :1
Culex theileri_PRIMERS1, pred :4.525070622125204, used :5
Used in the Fit : p value :0.9907588923507189 x2 value :0.10133727832317319
```