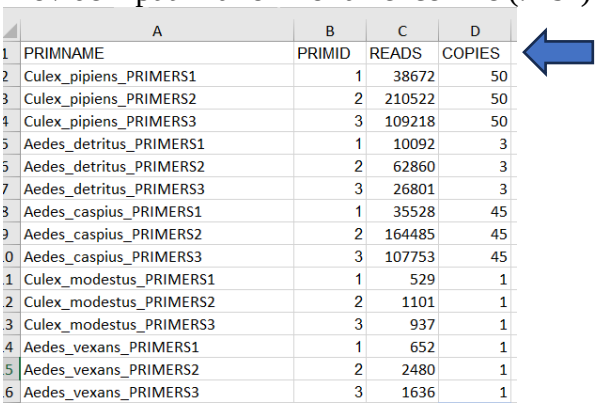
Notes on how to use the code inference_primer.py :

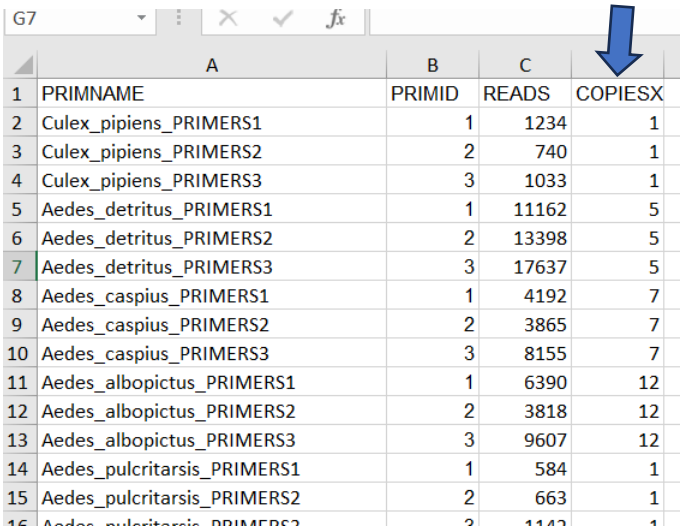
Input example :

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



	A	B	C	D
1	PRIMNAME	PRIMID	READS	COPIES
2	Culex_pipiens_PRIMERS1	1	38672	50
3	Culex_pipiens_PRIMERS2	2	210522	50
4	Culex_pipiens_PRIMERS3	3	109218	50
5	Aedes_detritus_PRIMERS1	1	10092	3
6	Aedes_detritus_PRIMERS2	2	62860	3
7	Aedes_detritus_PRIMERS3	3	26801	3
8	Aedes_caspius_PRIMERS1	1	35528	45
9	Aedes_caspius_PRIMERS2	2	164485	45
10	Aedes_caspius_PRIMERS3	3	107753	45
11	Culex_modestus_PRIMERS1	1	529	1
12	Culex_modestus_PRIMERS2	2	1101	1
13	Culex_modestus_PRIMERS3	3	937	1
14	Aedes_vexans_PRIMERS1	1	652	1
15	Aedes_vexans_PRIMERS2	2	2480	1
16	Aedes_vexans_PRIMERS3	3	1636	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



G7

	A	B	C	COPIESX
1	PRIMNAME	PRIMID	READS	
2	Culex_pipiens_PRIMERS1	1	1234	1
3	Culex_pipiens_PRIMERS2	2	740	1
4	Culex_pipiens_PRIMERS3	3	1033	1
5	Aedes_detritus_PRIMERS1	1	11162	5
6	Aedes_detritus_PRIMERS2	2	13398	5
7	Aedes_detritus_PRIMERS3	3	17637	5
8	Aedes_caspius_PRIMERS1	1	4192	7
9	Aedes_caspius_PRIMERS2	2	3865	7
10	Aedes_caspius_PRIMERS3	3	8155	7
11	Aedes_albopictus_PRIMERS1	1	6390	12
12	Aedes_albopictus_PRIMERS2	2	3818	12
13	Aedes_albopictus_PRIMERS3	3	9607	12
14	Aedes_pulcritarsis_PRIMERS1	1	584	1
15	Aedes_pulcritarsis_PRIMERS2	2	663	1

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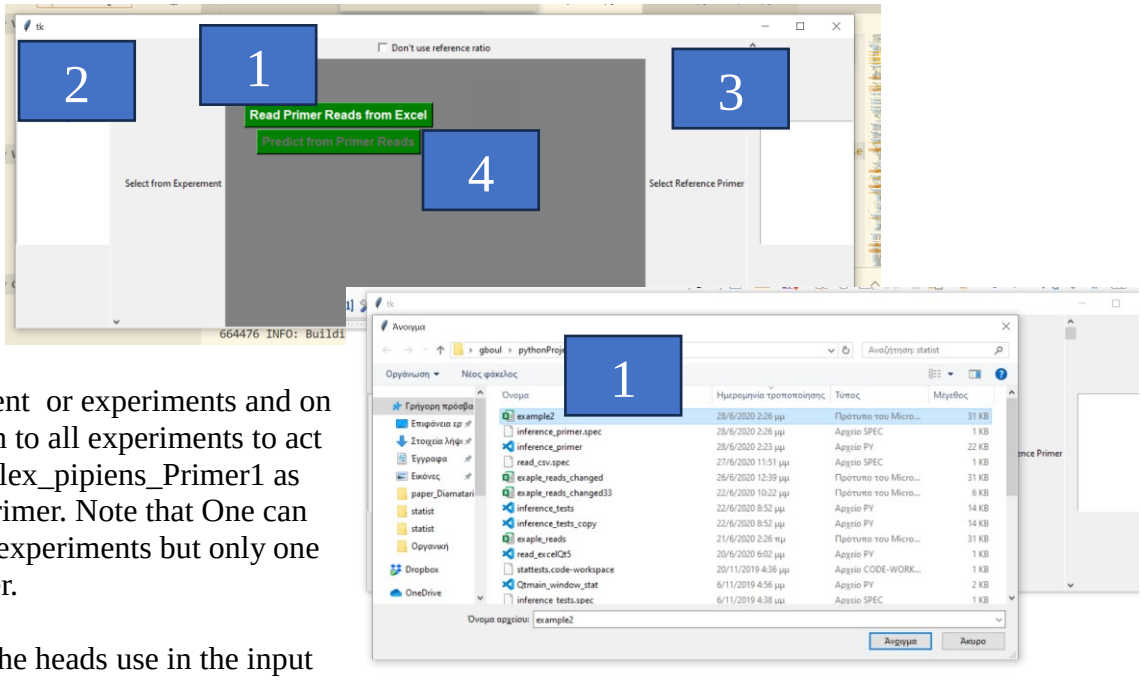
Run program:
Step 1 select input :



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.