



1 title

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3 1 filler1 2 filler2

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Software

- [Review](#) 
- [Repository](#)
- [Archive](#)

4 **Summary**

5 This is a summary

6 **Statement of need**

7 This is my statement of need

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8 **Comparing primerForge to swga2**

9 Referencing the firsta table [Table 1](#). Referencing the second table [Table 2](#).

Table 1: Datasets used to compare primerForge to swga2.

Dataset	Name	NCBI Accession	Group
plasmid ¹	pcDNA	not provided	ingroup
plasmid ²	pLTR	not provided	outgroup
<i>M. mycooides</i> ³	<i>My-coplasma mycooides</i> subsp. mycooides str. KH3J	GCF_003034305.1	ingroup
<i>M. mycooides</i> ⁴	<i>My-coplasma mycooides</i> subsp. mycooides str. B345/93	GCF_003034275.1	ingroup
<i>M. mycooides</i> ⁵	<i>My-coplasma mycooides</i> subsp. mycooides str. Gemu Goffa	GCF_003034345.1	ingroup

¹The plasmid dataset is provided as an example in the swga2 repository.

²The plasmid dataset is provided as an example in the swga2 repository.

³The *M. mycooides* is provided as an example in the primerForge repository.

⁴The *M. mycooides* is provided as an example in the primerForge repository.

⁵The *M. mycooides* is provided as an example in the primerForge repository.

Dataset	Name	NCBI Accession	Group
<i>M. mycoides</i> ⁶	<i>My-coplasma mycoides</i> subsp. capri str. GM12	GCF_900489555.1	outgroup
<i>M. mycoides</i> ⁷	<i>My-coplasma mycoides</i> subsp. capri str. 80/93	GCF_018389745.1	outgroup
<i>E. coli</i>	<i>Escherichia coli</i> O157 str. 644-PT8	GCF_001650295.1	ingroup
<i>E. coli</i>	<i>Escherichia coli</i> O157 str. AR-0428	GCF_008727175.1	ingroup
<i>E. coli</i>	<i>Escherichia coli</i> O157 str. FDAAR-GOS_293	GCF_002208865.2	ingroup
<i>E. coli</i>	<i>Escherichia coli</i> K12 str. MG1655	GCF_000005845	outgroup
<i>E. coli</i>	<i>Salmonella enterica</i> subsp. enterica serovar Typhimurium str. LT2	GCF_000006945	outgroup
SARS-CoV-2	SARS-CoV-2 isolate hu-man/USA/MA_MGH_00230/2020	MT520374	ingroup
SARS-CoV-2	SARS-CoV-2 isolate hu-man/USA/MA_MGH_00229/2020	MT520263	ingroup
SARS-CoV-2	SARS-CoV-2 isolate hu-man/USA/MA_MGH_00257/2020	MT520479	ingroup

⁶The *M. mycoides* is provided as an example in the primerForge repository.

⁷The *M. mycoides* is provided as an example in the primerForge repository.

Dataset	Name	NCBI Accession	Group
SARS-CoV-2	SARS-CoV-2 isolate Wuhan-Hu-1	NC_045512	outgroup

Table 2: Comparing swga2 to primerForge

program	dataset	runtime (mm:ss)	RAM (Gb)	primer pairs ^a <small>^aThe number of primer pairs identified by the program</small>	isPcr-compatible pairs ^a <small>^aThe number of primer pairs that generated PCR products with isPcr</small>	validated pairs ^a <small>^aThe number of primer pairs that produced a PCR product in every ingroup genome and no products in any of the outgroup genomes</small>	optimized pairs ^a <small>^aThe number of valid primer pairs that produced exactly one PCR product in each ingroup genome</small>
swga2	plasmid	23:21	0.136	94	22	22	11
primerForge	plasmid	00:10	0.051	3,210	3,210	3,168	2,934
swga2	<i>M. mycoides</i>	05:13	0.221	run failed	NA	NA	NA
primerForge	<i>M. mycoides</i>	02:52	1.478	1446	1,446	989	884
swga2	<i>E. coli</i>	21:10	4.452	run failed	NA	NA	NA
primerForge	<i>E. coli</i>	83:33	10.329	1,451,164	1,451,164	318,927	125,932
swga2	SARS-CoV-2	10:38	0.141	63	7	0	0
primerForge	SARS-CoV-2	00:19	0.122	39	39	15	15

10 A potential workaround

11 Lets reference the hacked tables here [Table 3](#) [Table 4](#)

Table 3: Datasets used to compare primerForge to swga2.

Dataset	Name	NCBI Accession	Group
plasmid ¹	pcDNA	not provided	ingroup
plasmid ¹	pLTR	not provided	outgroup

Dataset	Name	NCBI Accession	Group
<i>M. mycoides</i> ²	<i>My-coplasma mycoides</i> subsp. <i>mycoides</i> str. KH3J	GCF_003034305.1	ingroup
<i>M. mycoides</i> ²	<i>My-coplasma mycoides</i> subsp. <i>mycoides</i> str. B345/93	GCF_003034275.1	ingroup
<i>M. mycoides</i> ²	<i>My-coplasma mycoides</i> subsp. <i>mycoides</i> str. Gemu Goffa	GCF_003034345.1	ingroup
<i>M. mycoides</i> ²	<i>My-coplasma mycoides</i> subsp. <i>capri</i> str. GM12	GCF_900489555.1	outgroup
<i>M. mycoides</i> ²	<i>My-coplasma mycoides</i> subsp. <i>capri</i> str. 80/93	GCF_018389745.1	outgroup
<i>E. coli</i>	<i>Escherichia coli</i> O157 str. 644-PT8	GCF_001650295.1	ingroup
<i>E. coli</i>	<i>Escherichia coli</i> O157 str. AR-0428	GCF_008727175.1	ingroup
<i>E. coli</i>	<i>Escherichia coli</i> O157 str. FDAAR-GOS_293	GCF_002208865.2	ingroup
<i>E. coli</i>	<i>Escherichia coli</i> K12 str. MG1655	GCF_000005845	outgroup

Dataset	Name	NCBI Accession	Group
<i>E. coli</i>	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhimurium str. LT2	GCF_000006945	outgroup
SARS-CoV-2	SARS-CoV-2 isolate hu-man/USA/MA_MGH_00230/2020	MT520374	ingroup
SARS-CoV-2	SARS-CoV-2 isolate hu-man/USA/MA_MGH_00229/2020	MT520263	ingroup
SARS-CoV-2	SARS-CoV-2 isolate hu-man/USA/MA_MGH_00257/2020	MT520479	ingroup
SARS-CoV-2	SARS-CoV-2 isolate Wuhan-Hu-1	NC_045512	outgroup

¹² ¹: The plasmid dataset is provided as an example in the swga2 repository.

¹³ ²: The *M. mycoides* is provided as an example in the primerForge repository.

Table 4: Comparing swga2 to primerForge

program	dataset	runtime (mm:ss)	RAM (Gb)	primer pairs ¹	isPcr-compatible pairs ²	validated pairs ³	optimized pairs ⁴
swga2	plasmid	23:21	0.136	94	22	22	11
primerForge	plasmid	00:10	0.051	3,210	3,210	3,168	2,934
swga2	<i>M. mycoides</i>	05:13	0.221	run failed	NA	NA	NA
primerForge	<i>M. mycoides</i>	02:52	1.478	1446	1,446	989	884
swga2	<i>E. coli</i>	21:10	4.452	run failed	NA	NA	NA
primerForge	<i>E. coli</i>	83:33	10.329	1,451,164	1,451,164	318,927	125,932
swga2	SARS-CoV-2	10:38	0.141	63	7	0	0
primerForge	SARS-CoV-2	00:19	0.122	39	39	15	15

- 14 1: The number of primer pairs identified by the program
15 2: The number of primer pairs that generated PCR products with `isPcr`
16 3: The number of primer pairs that produced a PCR product in every ingroup genome and no
17 products in any of the outgroup genomes
18 4: The number of valid primer pairs that produced exactly one PCR product in each ingroup
19 genome

20 Acknowledgements

21 I'm doing my part! o7

22 References

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