

Web Material

Epidemiologic Utility of a Framework for Partition Number Selection When Dissecting Hierarchically

Clustered Genetic Data Evaluated on the Intestinal Parasite *Cyclospora Cayetanensis*

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Web Table 1

Cyclospora cayetanensis genotypes displayed in haplotype data sheet (HDS) format which is the format required as input for Barratt's heuristic.

Web Table 2

Pairwise genetic distance matrix computed from the *C. cayetanensis* genotypes using Barratt's heuristic.

Web Table 3

Partition memberships for each *C. cayetanensis* genotyped for a partition number of 46 as predicted using the present framework.

Web Table 4

Partition memberships for each *C. cayetanensis* genotyped for a partition number of 9 as predicted using the elbow method.

Web Table 5

Partition memberships for each *C. cayetanensis* genotyped for a partition number of 11 as predicted using the silhouette method.

Web Table 6

Partition memberships for each *C. cayetanensis* genotyped for a partition number of 100 as predicted using the gap statistic.