Additional information

A new long-read mitochondrial-genome protocol (PacBio HiFi) for haemosporidian parasites: A tool for population and biodiversity studies.

M. Andreína Pacheco^{1,*,&}, Axl S. Cepeda^{1,&}, Erica A. Miller², Scott Beckerman³, Mitchell Oswald³, Evan London⁴, Nohra E. Mateus-Pinilla^{4,5,6,7}, and Ananias A. Escalante^{1,*}.

¹Biology Department/Institute of Genomics and Evolutionary Medicine (iGEM), Temple University, Philadelphia, Pennsylvania 19122-1801, USA.

²Wildlife Futures Program, University of Pennsylvania, Kennett Square, PA 19348.

³USDA Wildlife Services, Springfield, IL. 62711, USA

⁴Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA.

⁵Illinois Natural History Survey-Prairie Research Institute, University of Illinois at Urbana-Champaign, Champaign, IL 61820, USA.

⁶Department of Natural Resources and Environmental Sciences, University of Illinois at Urbana-Champaign, Champaign, IL 61820, USA.

⁷Department of Pathobiology, College of Veterinary Medicine, University of Illinois at Urbana-Champaign, Urbana, IL 61802, USA.

*Corresponding authors:

M. Andreína Pacheco: Maria.Pacheco@temple.edu

Biology Department/Institute of Genomics and Evolutionary Medicine (iGEM), Temple University (SERC - 645), 1925 N. 12th St. Philadelphia, PA 19122-1801, USA.

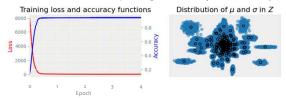
Ananias A. Escalante: Ananias. Escalante@temple.edu

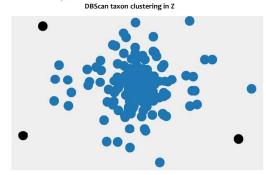
Biology Department/Institute of Genomics and Evolutionary Medicine (iGEM), Temple University (SERC - 653), 1925 N. 12th St. Philadelphia, PA 19122-1801, USA.

&Equal contribution

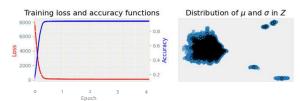
Additional file 1: Figure S1. HmtG-PacBio Pipeline graph output for each sample used in this study. (A) Visualization of the training process, (B) mean (μ : black unfilled dots) and standard deviation (σ : blue filled dots) in Z, and (C) DBScan OTUs clustering in Z. Species/lineages names are indicated for each sample. Black solid dots are noise. Different clusters in a sample are shown in different colors. See Table 3 for details.

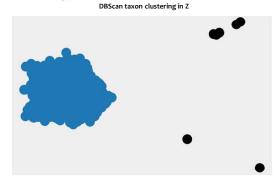
1. Plasmodium falciparum (Ghana 3)



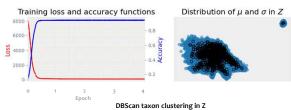


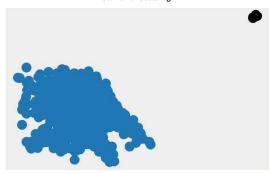
3. Plasmodium vivax (Mauritania)



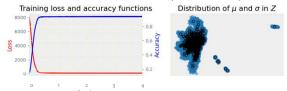


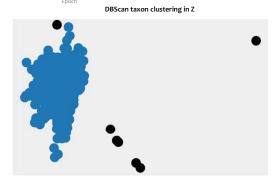
5. Plasmodium malariae



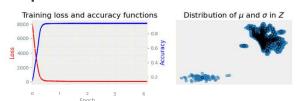


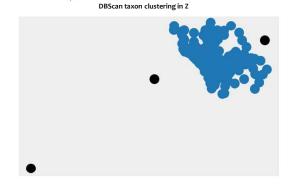
2. Plasmodium vivax (Sumatra)



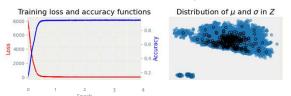


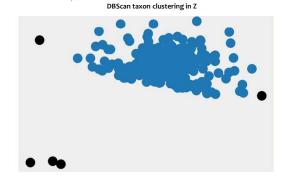
4. Plasmodium ovale



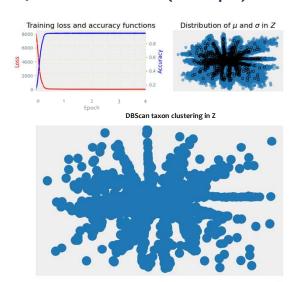


6. Plasmodium cynomolgi (macaque)

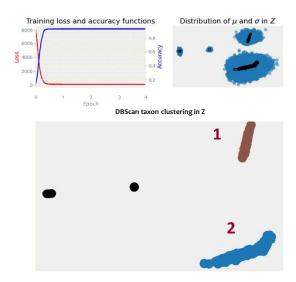




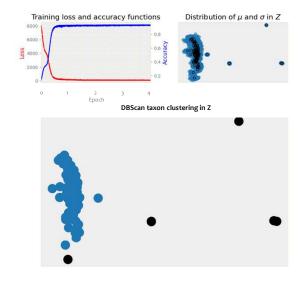
7. Plasmodium inui (macaque)



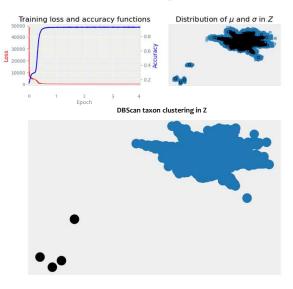
9. Plasmodium sp. (Osprey)



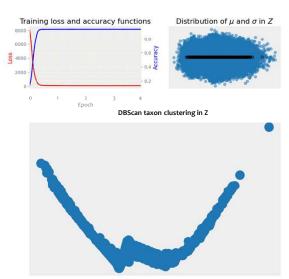
11. Hemoproteus catharti (Turkey Vulture)



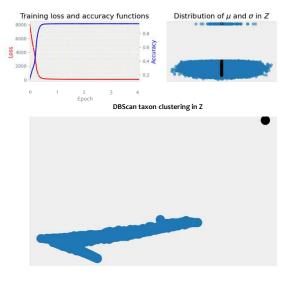
8. Plasmodium sp. (Agama aculeata)



10. Plasmodium sp. (Eastern Screech Owl)



12. Hemoproteus sp. (Great horned Owl)



13. Plasmodium elongatum (Red-tailed Hawk)

Training loss and accuracy functions Distribution of μ and σ in Z 0.8 0.6 0.9 0.4 0.2 DBScan taxon clustering in Z

14. Leucocytozoon sp. (Red-tailed Hawk)

