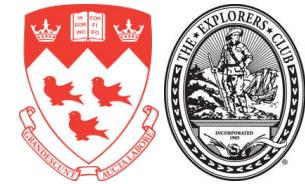
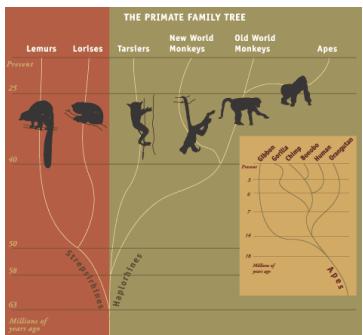
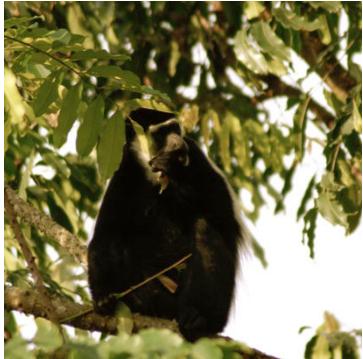


Factors impacting bacterial gut microbiome community composition in wild non-human primates in Taï National Park, Côte d'Ivoire



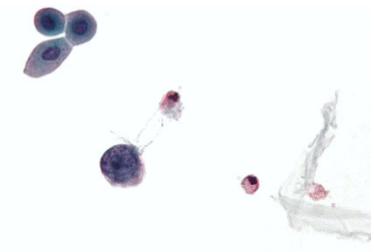
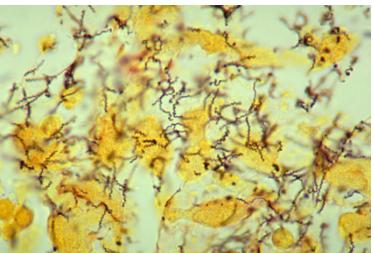
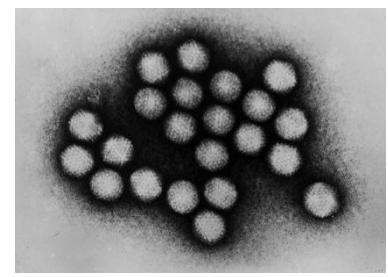
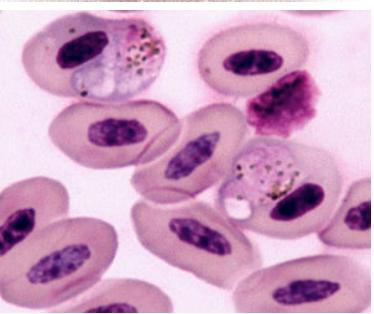
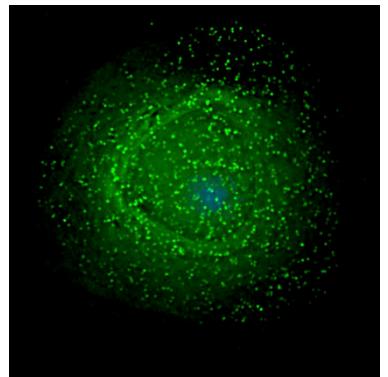
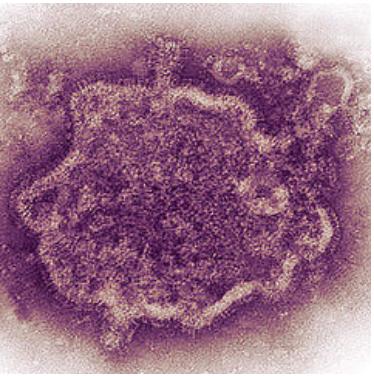
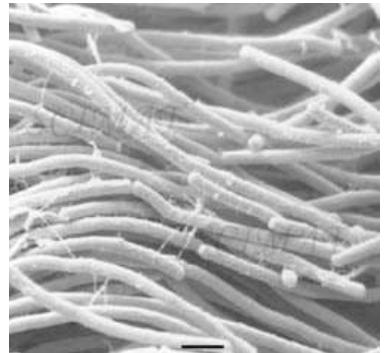
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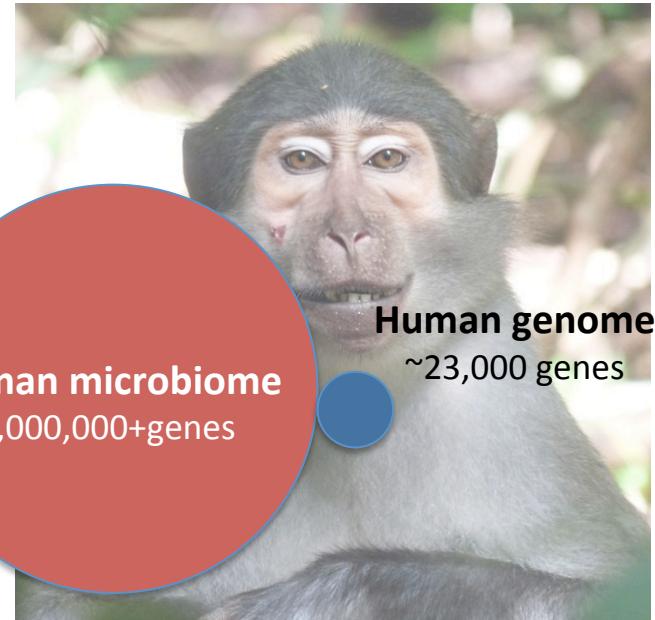
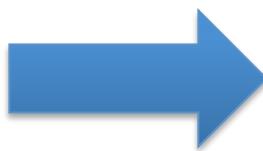
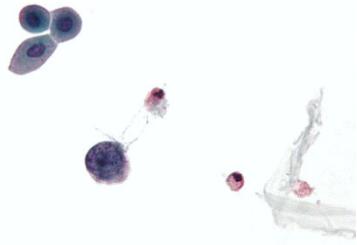
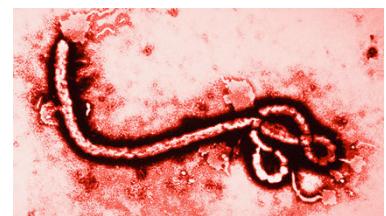
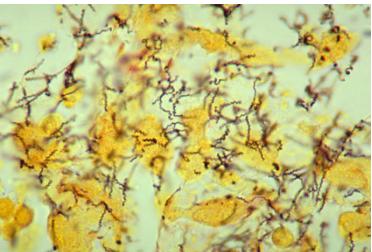
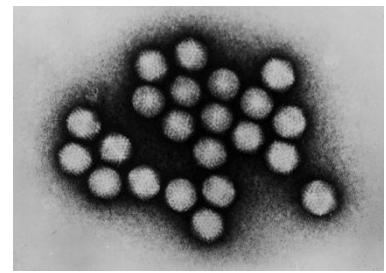
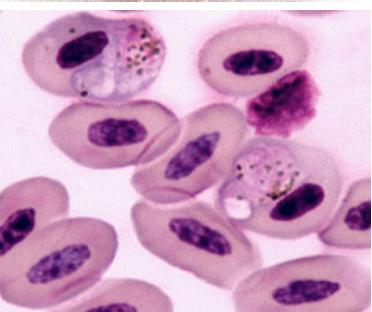
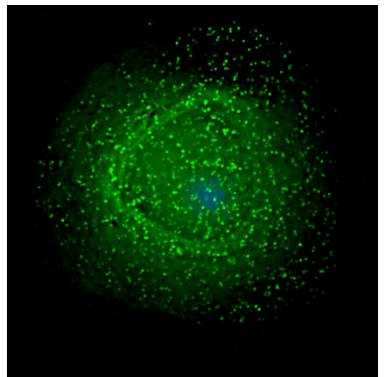
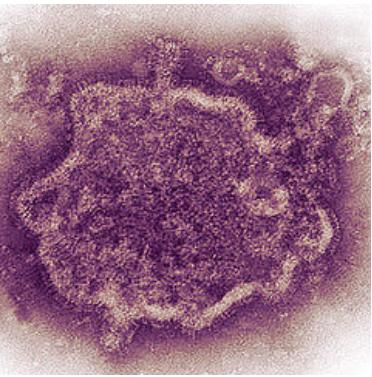
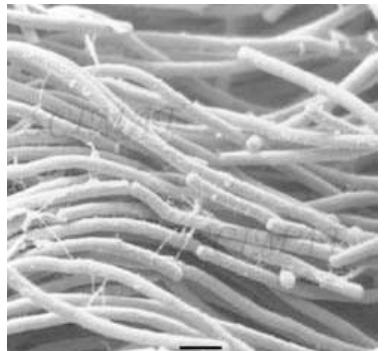


Jan F. Gogarten

M.C. Nelson, J. Graf, J.P. Gogarten, R. Wittig, S. Calvignac-Spencer, F.H. Leendertz

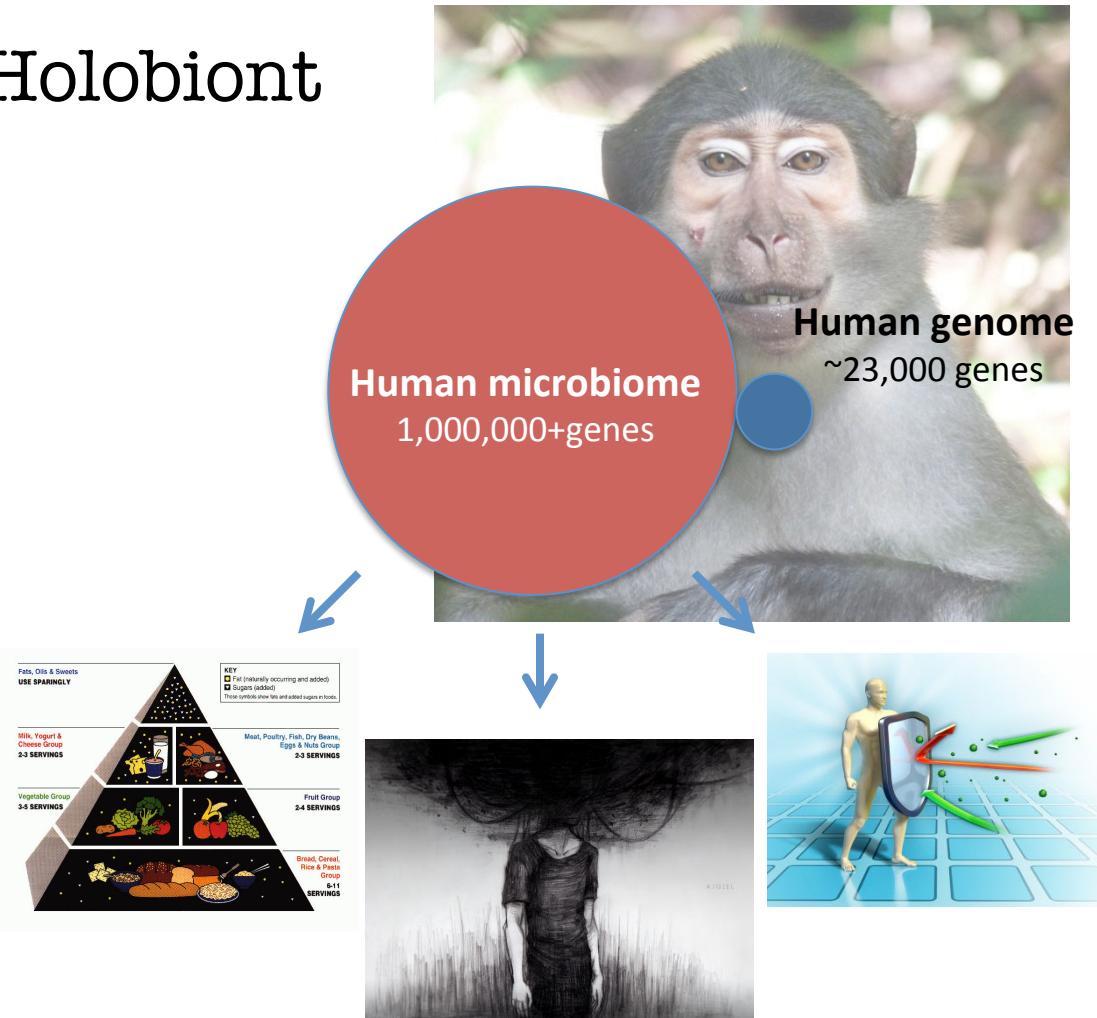
Department of Biology, McGill University, Canada; Robert Koch Institut, Berlin, Germany
and the Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany





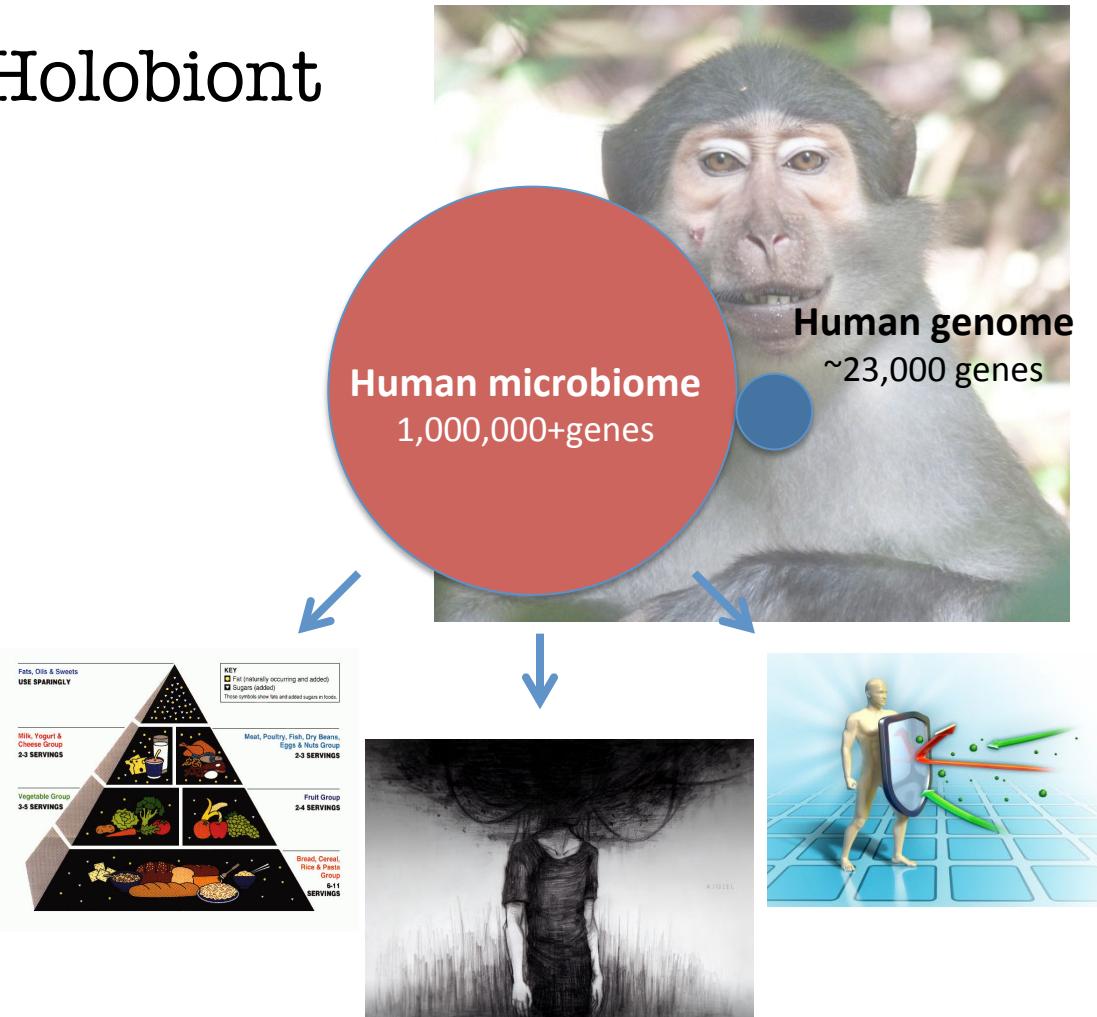
Microbiomes + Host = Holobiont

- Human microbiome outnumbers human cells 10 to 1



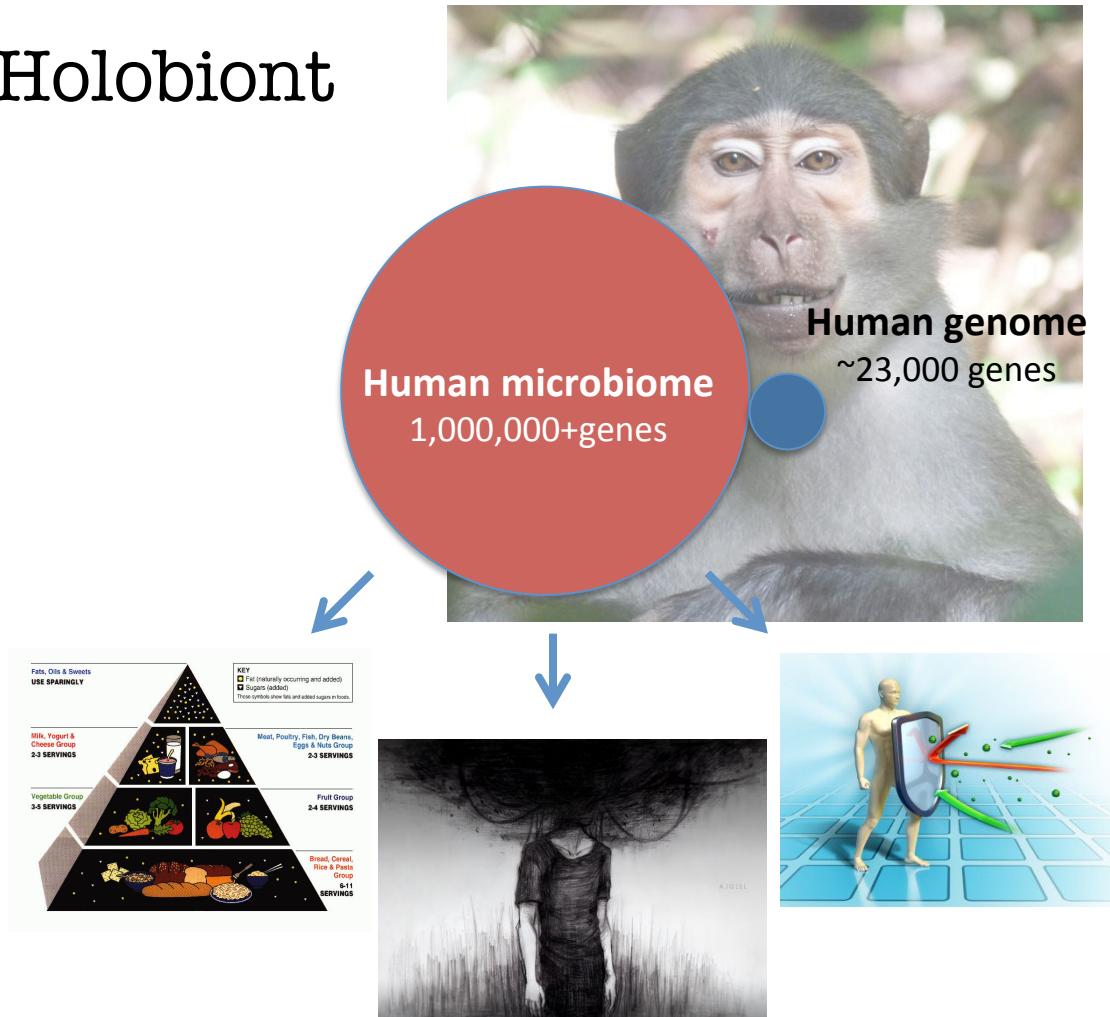
Microbiomes + Host = Holobiont

- Human microbiome outnumbers human cells 10 to 1
- Process of community assembly poorly understood



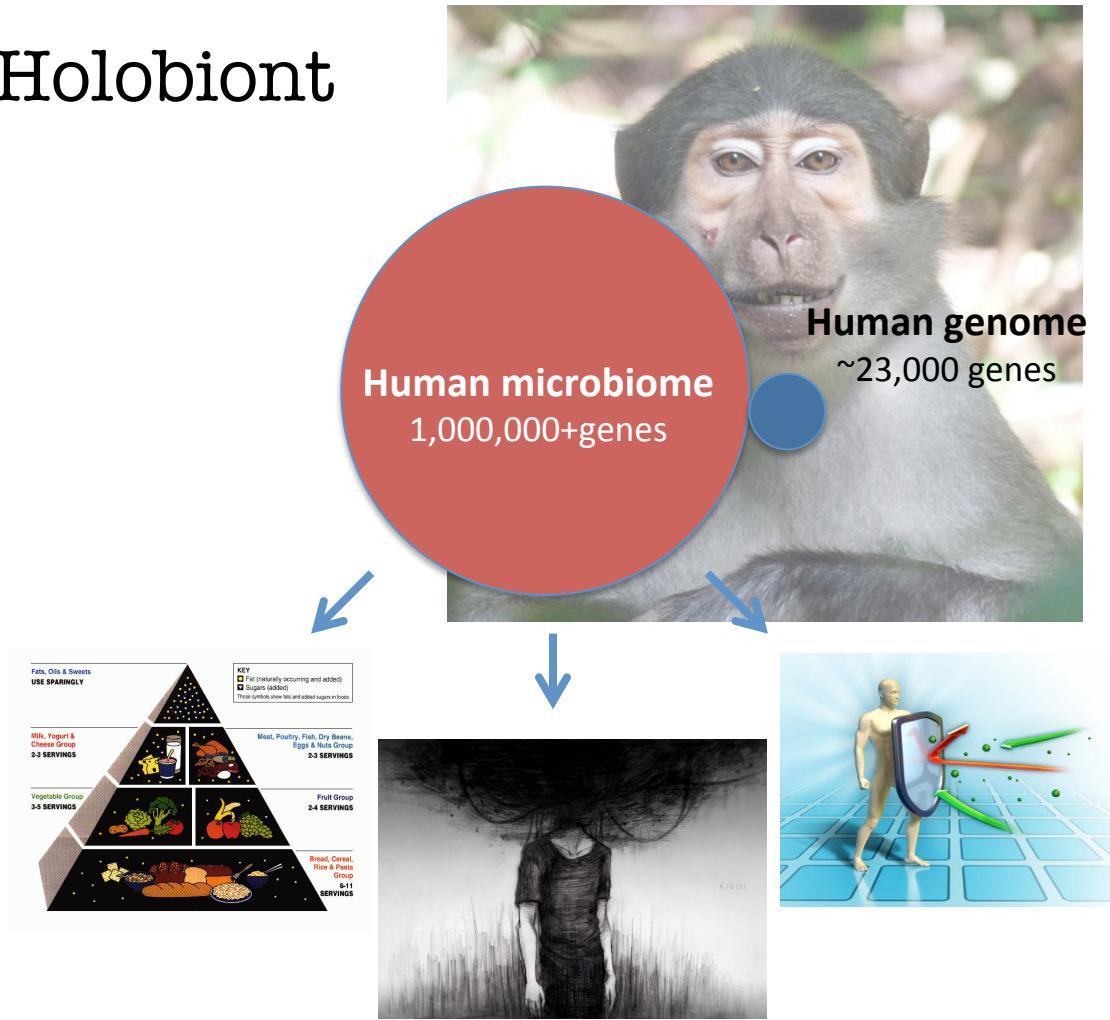
Microbiomes + Host = Holobiont

- Human microbiome outnumbers human cells 10 to 1
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- Human microbiome species depauperate



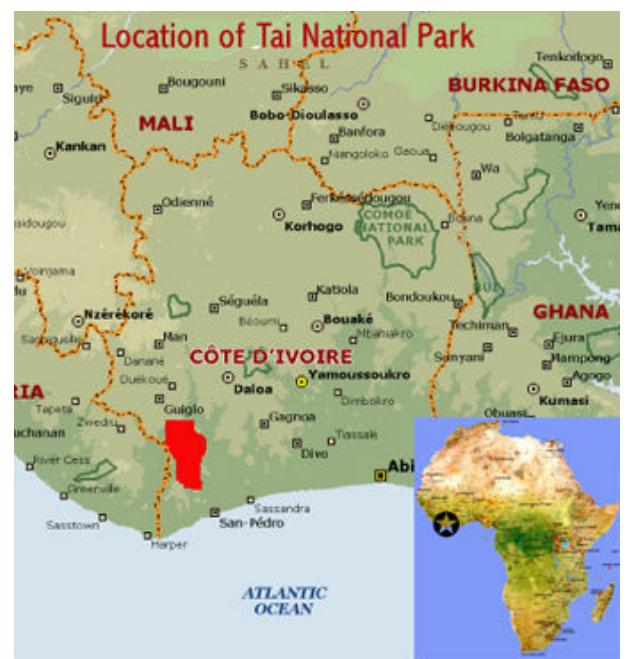
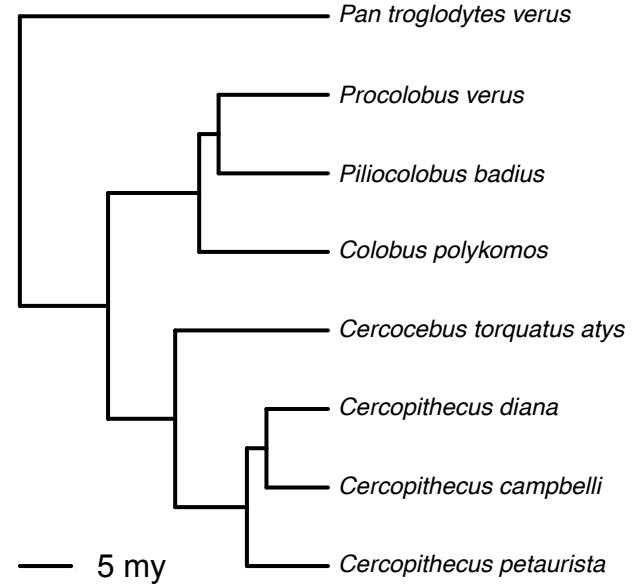
Microbiomes + Host = Holobiont

- Human microbiome outnumbers human cells 10 to 1
- Process of community assembly poorly understood
- Human microbiome species depauperate
- How holobionts evolve largely unknown



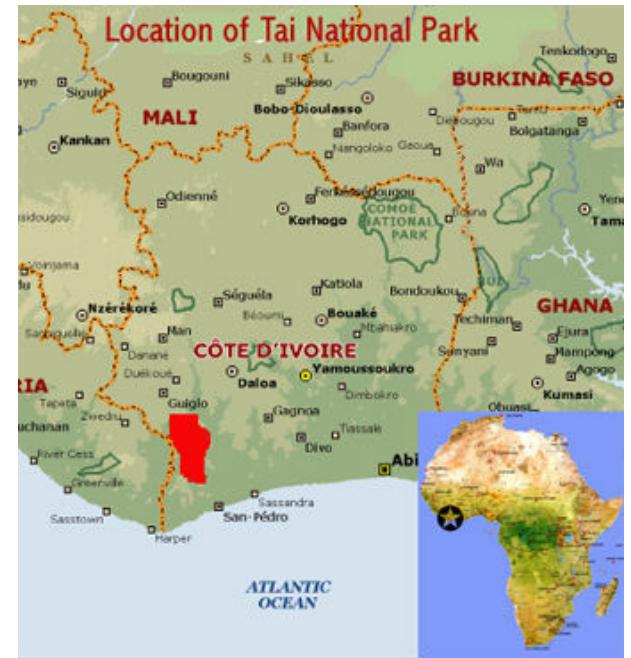
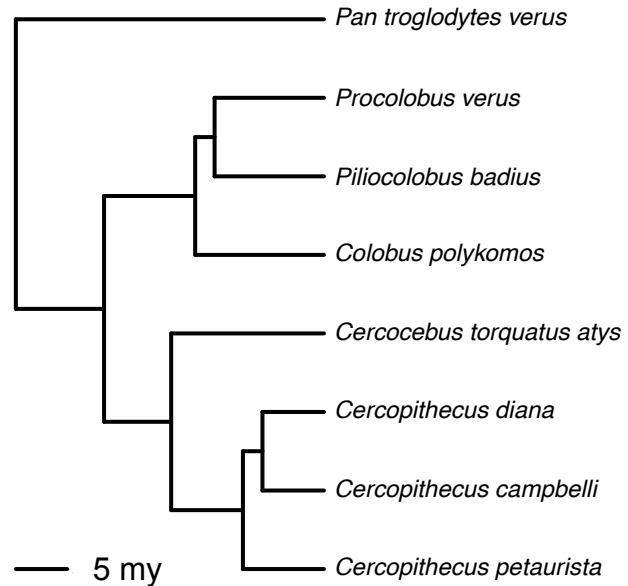
Methods

- Fecal samples from 8 wild diurnal primate species in Tai National Park, Côte d'Ivoire



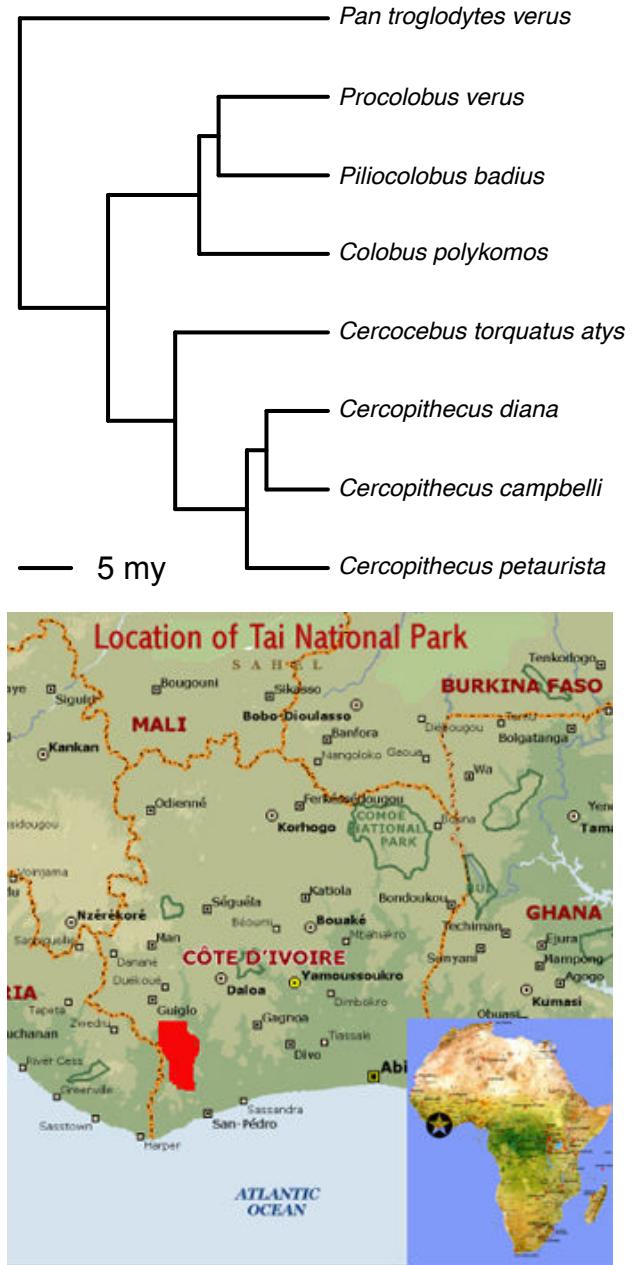
Methods

- Fecal samples from 8 wild diurnal primate species in Tai National Park, Côte d'Ivoire
- Extracted DNA -> generated amplicons covering 16S V4 hypervariable region -> sequenced using Illumina MiSeq

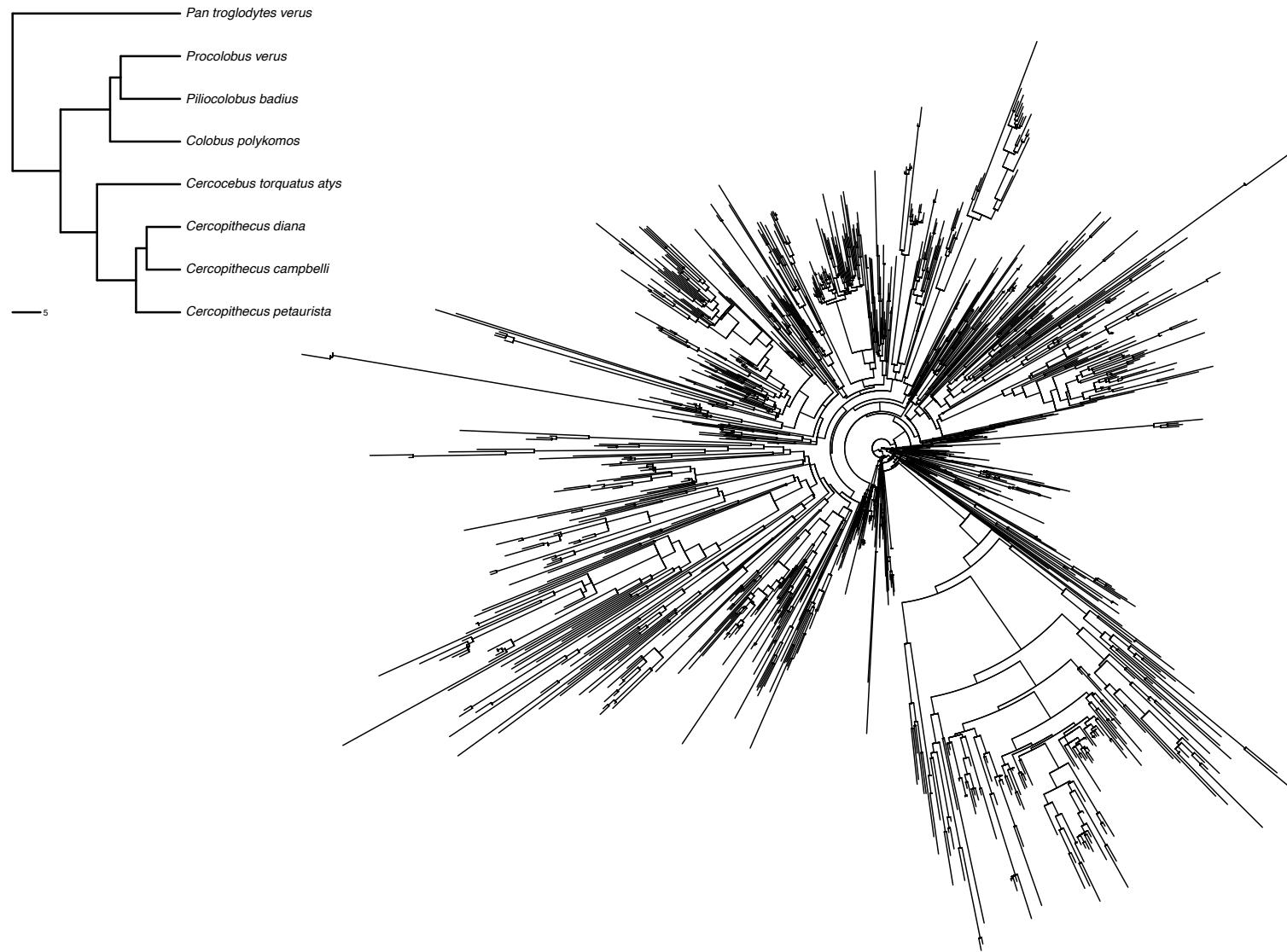


Methods

- Fecal samples from 8 wild diurnal primate species in Tai National Park, Côte d'Ivoire
- Extracted DNA -> generated amplicons covering 16S V4 hypervariable region -> sequenced using Illumina MiSeq
- nMDS approach with ENVFIT to examine impact of species, social group, familial relationships + disease

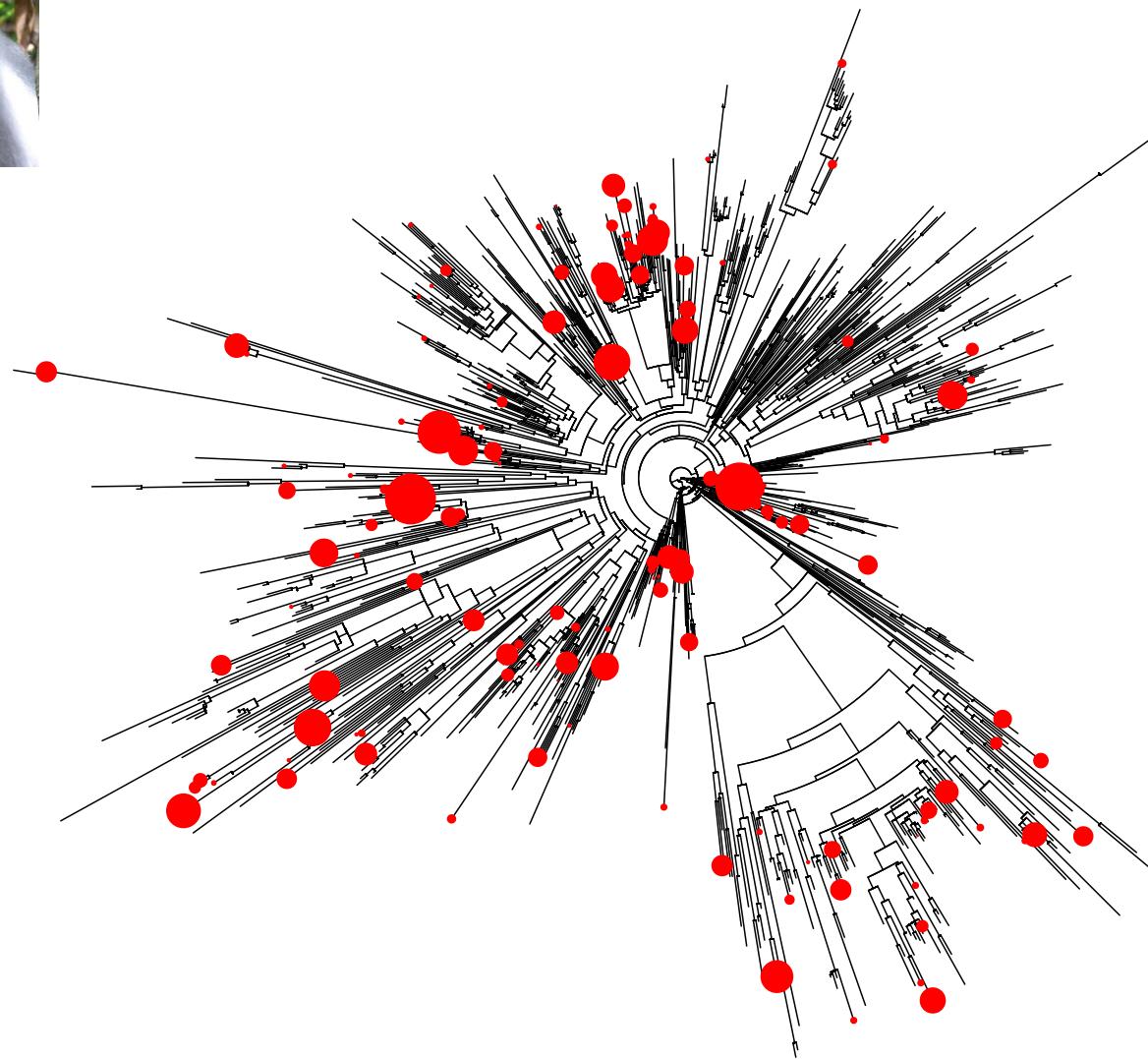


Phylogeny of primate gut bacteria



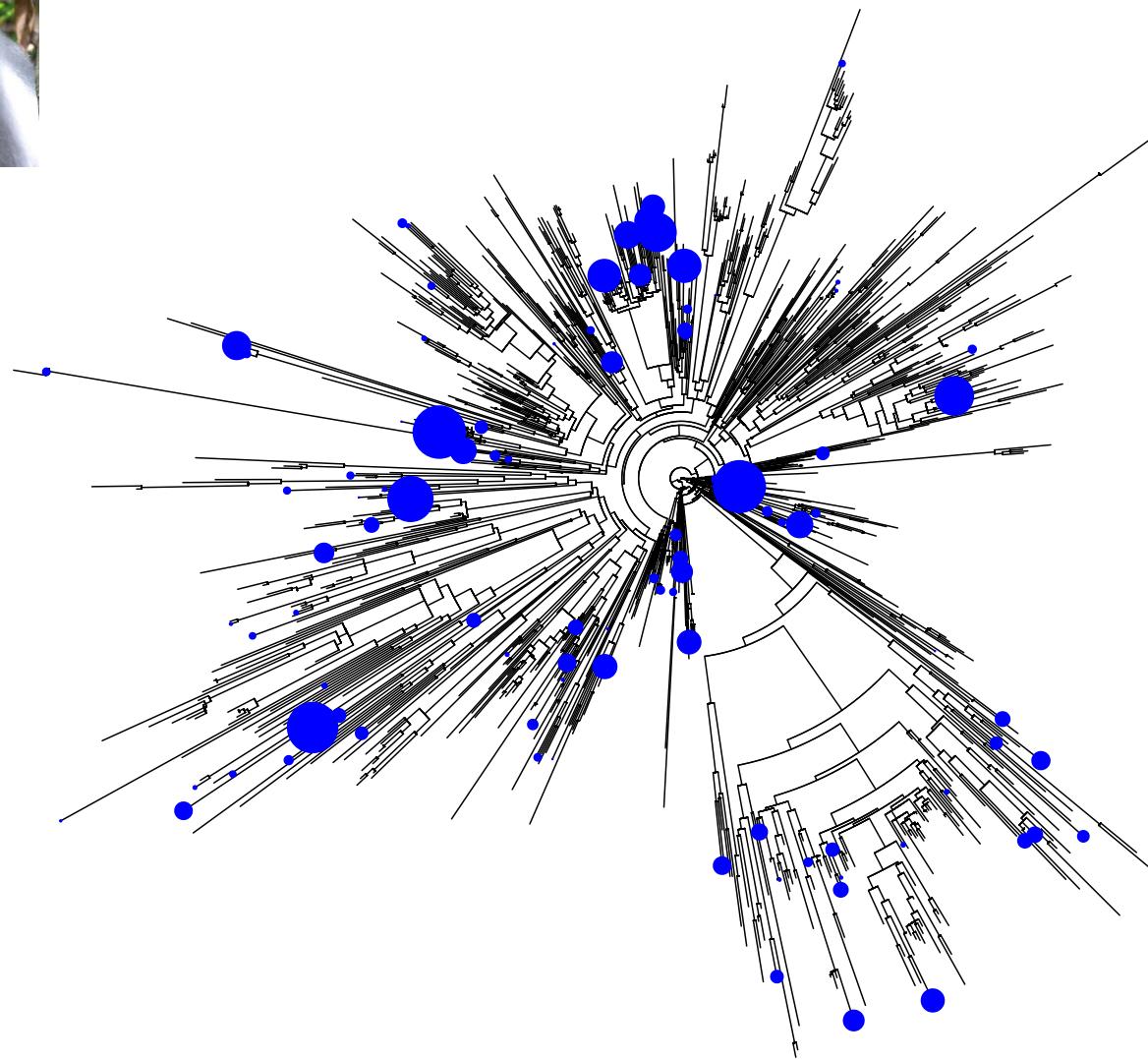


April 28th 2014



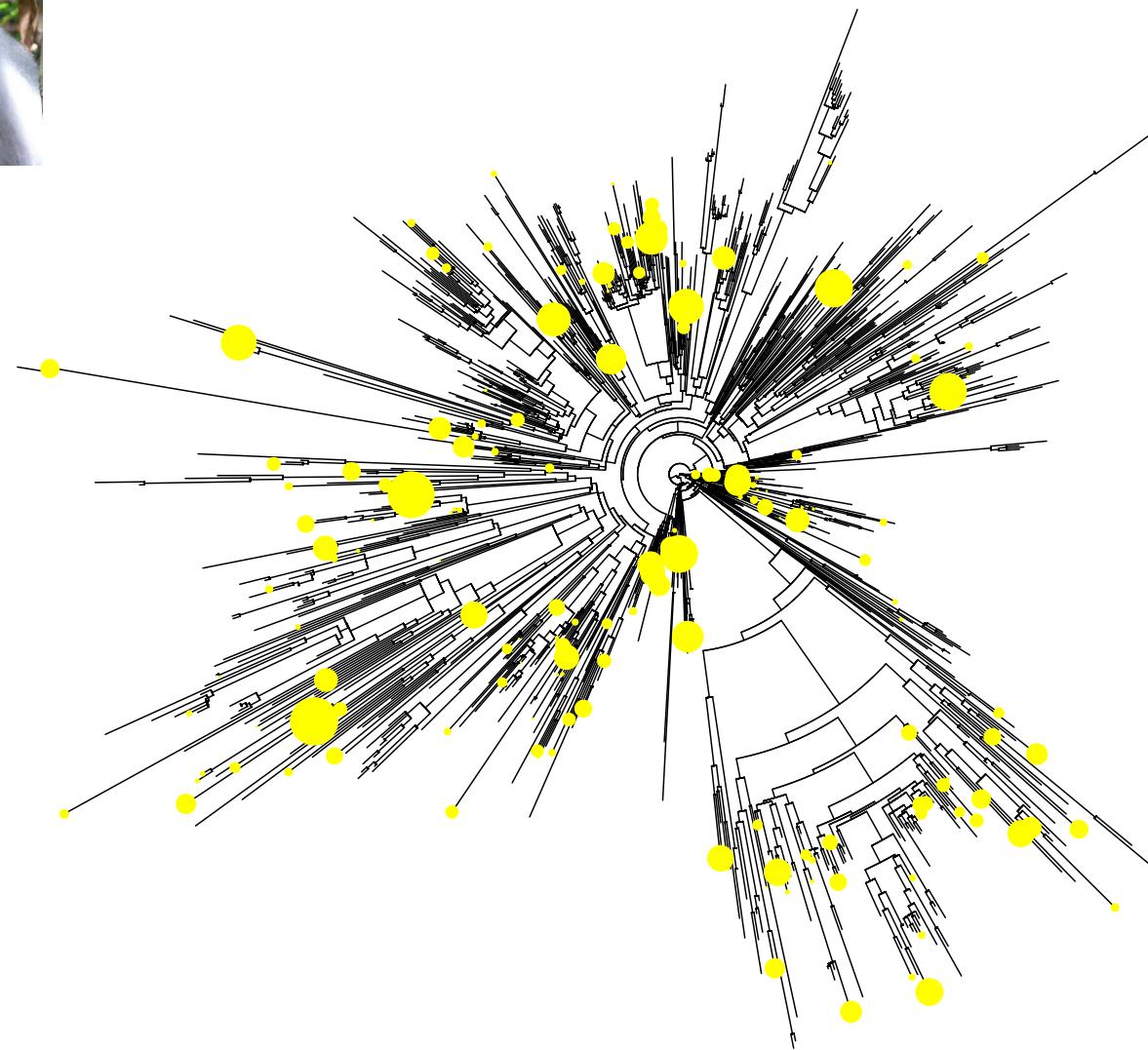


May 5th 2014



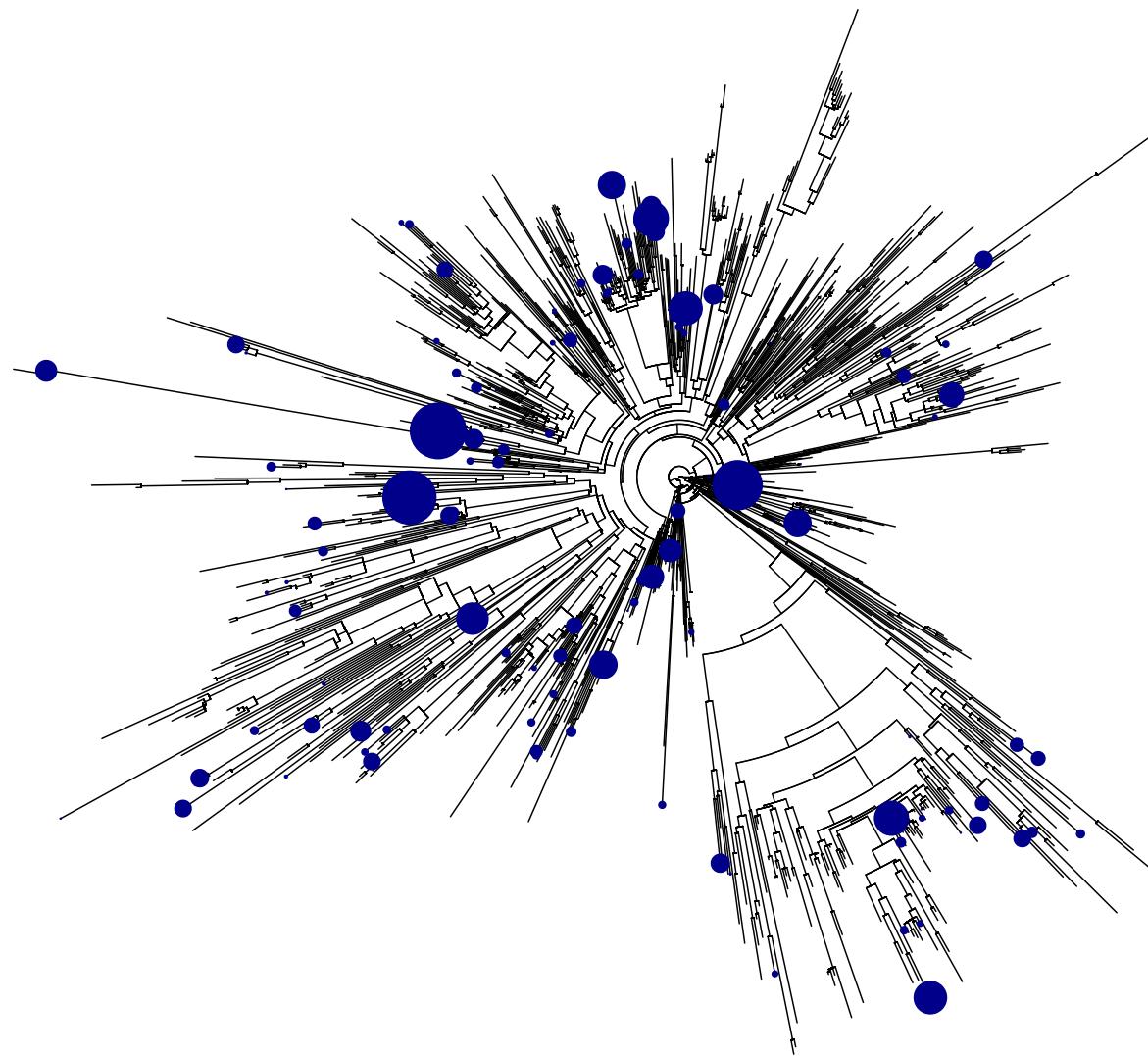


May 19th 2014



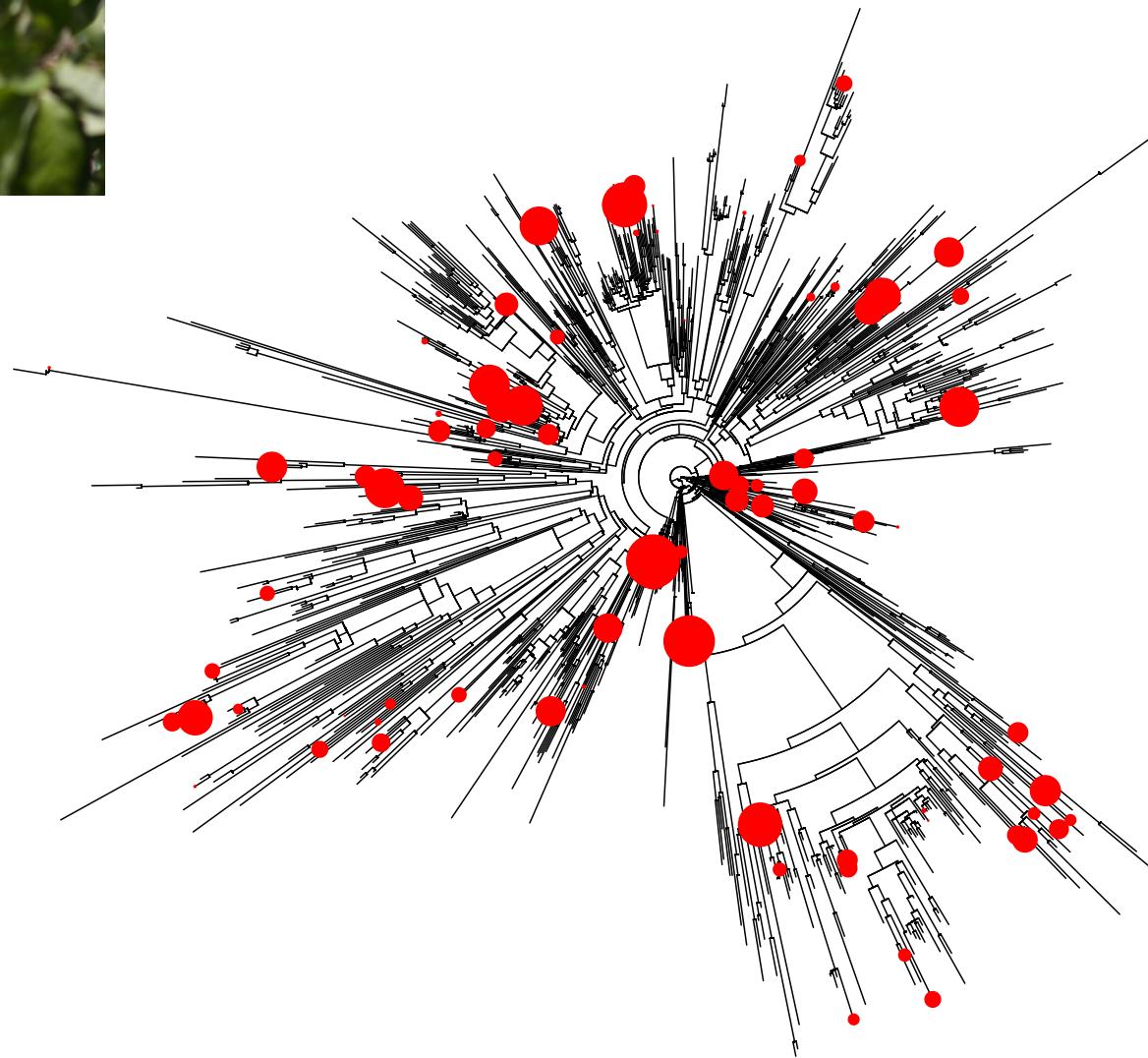


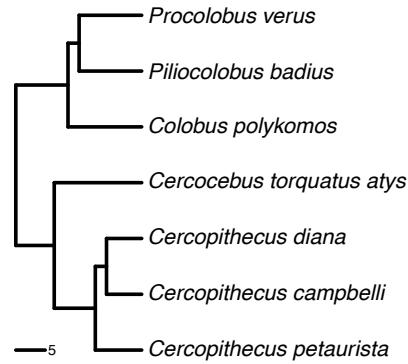
May 26th 2014



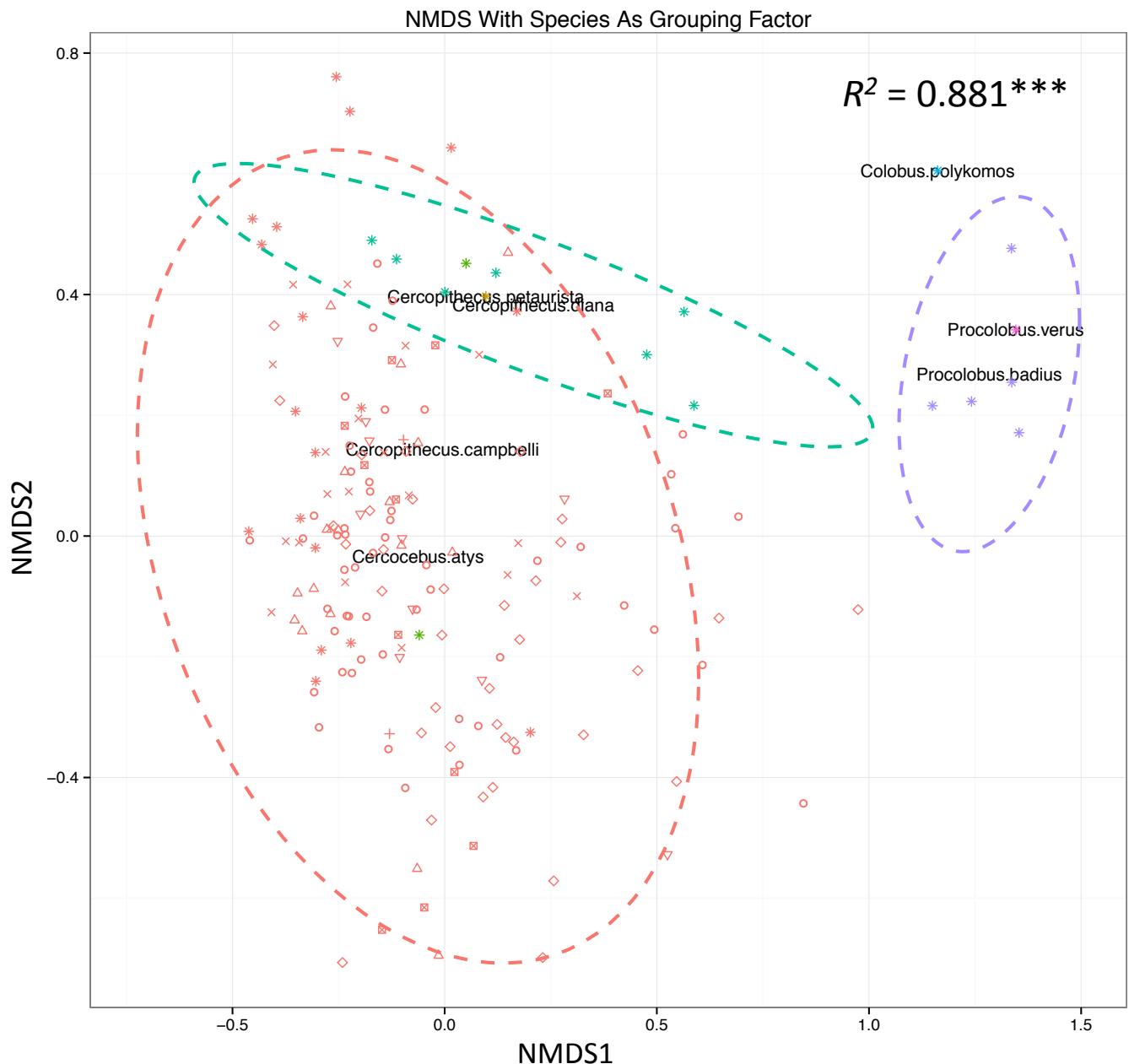
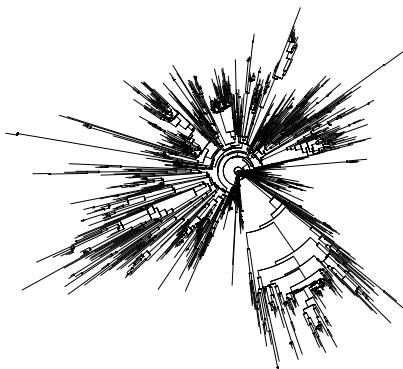


May 13th 2014





Primate bacterial community

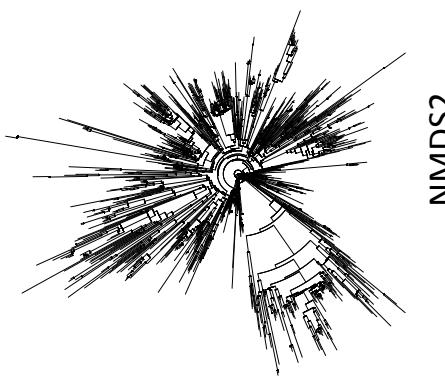




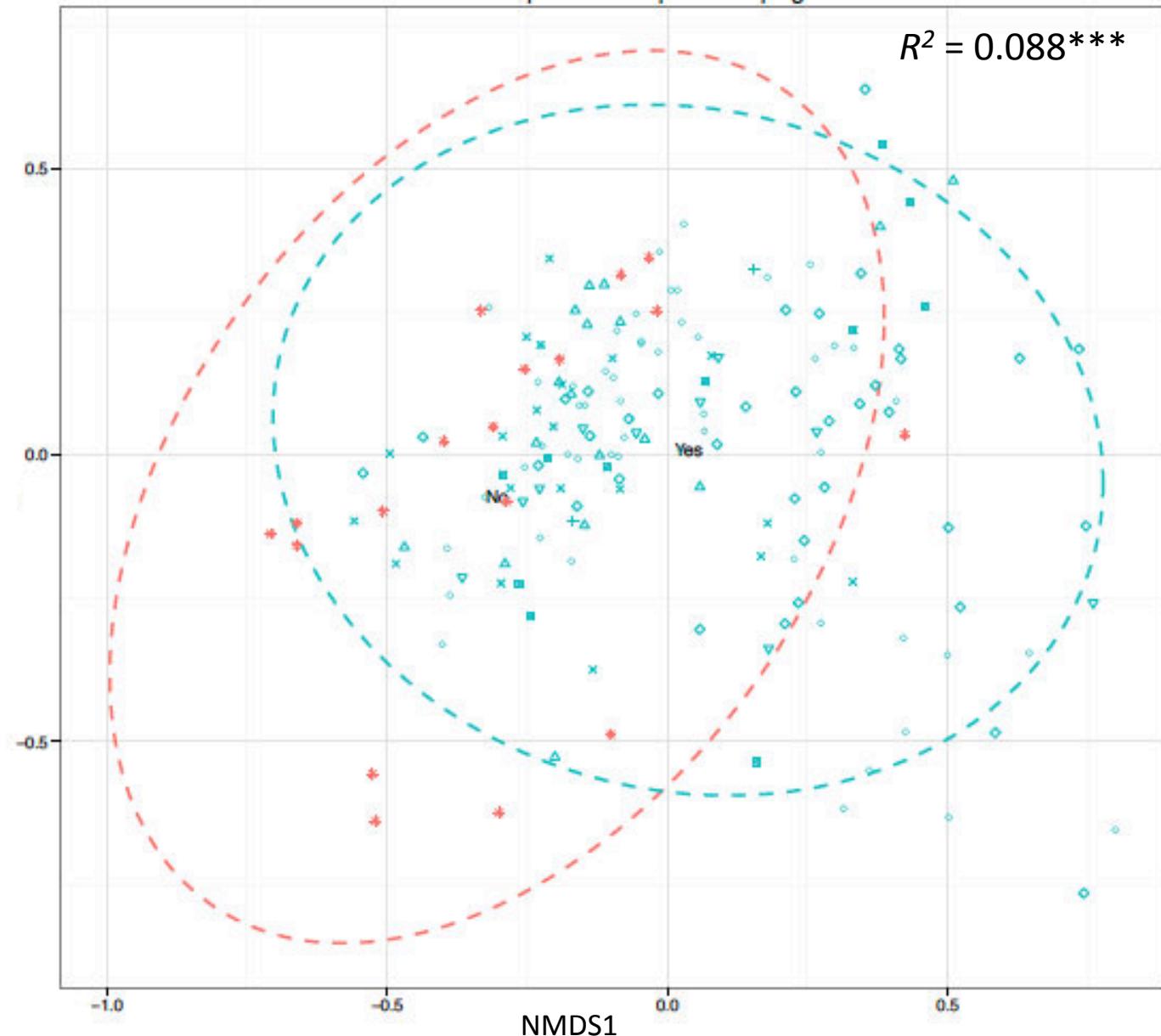
NMDS With Group Membership As Grouping Factor

$R^2 = 0.088^{***}$

Primate bacterial community

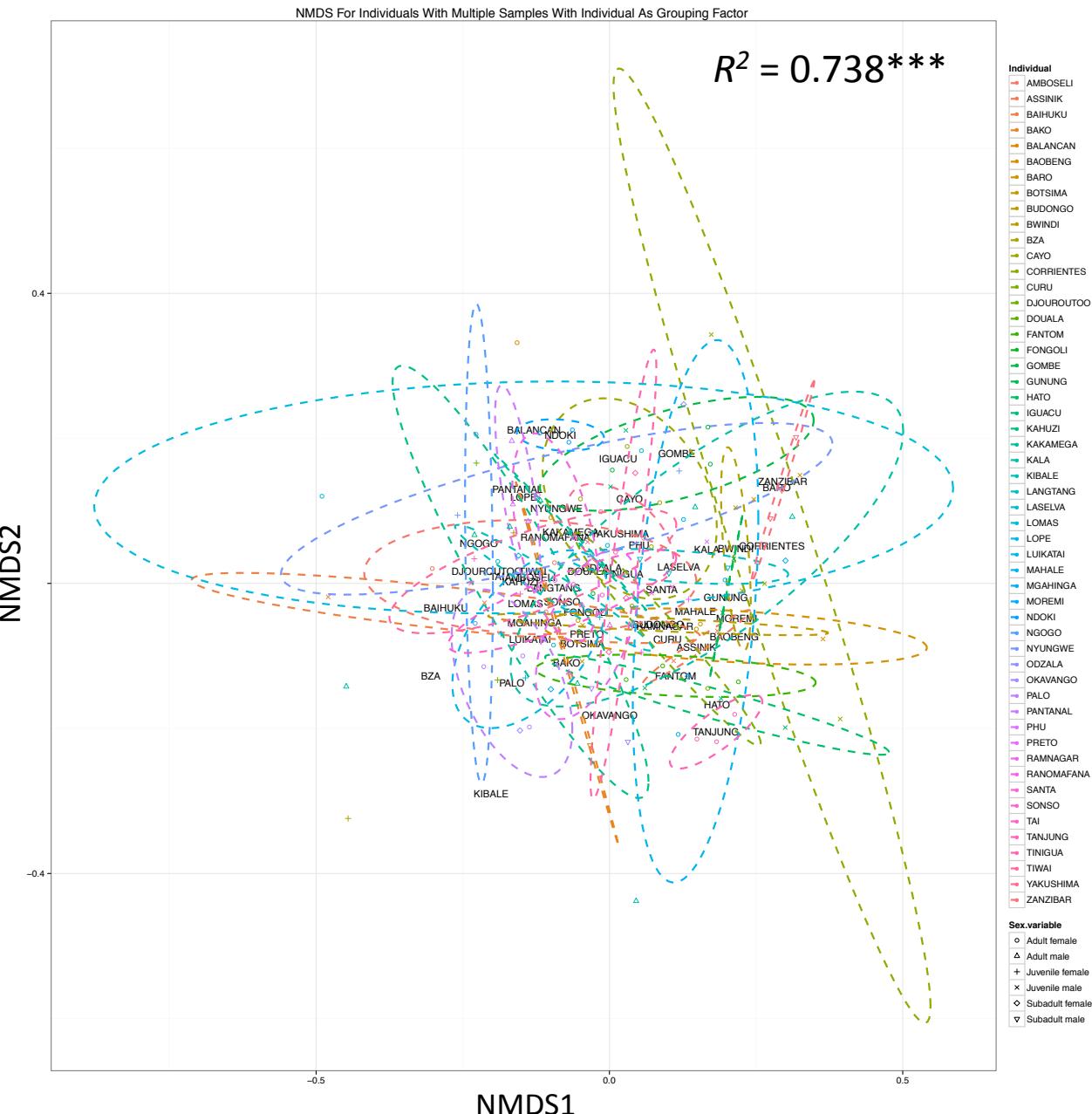
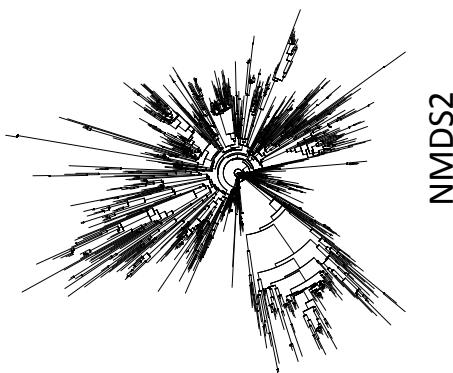


NMDS2





Primate bacterial community

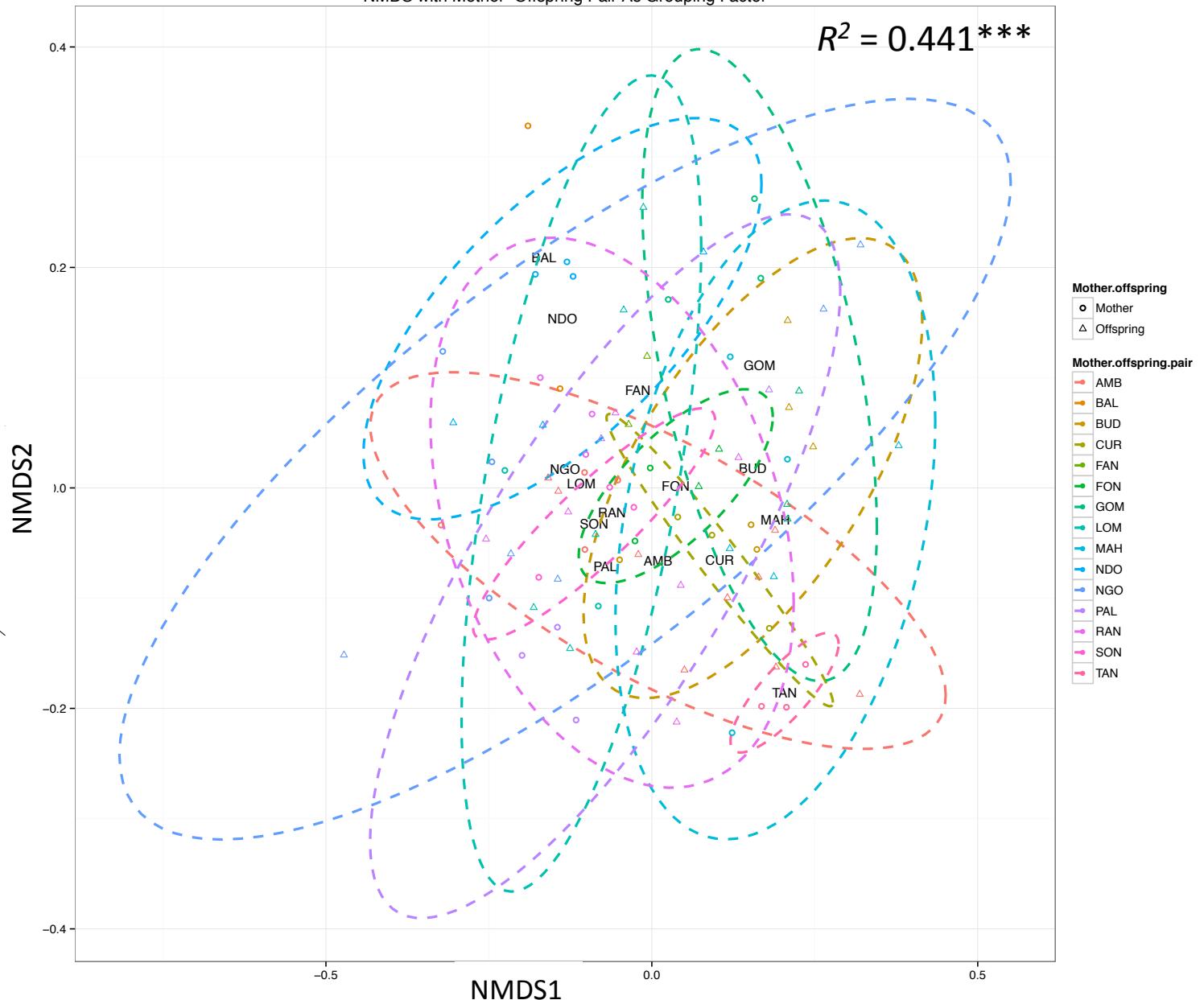
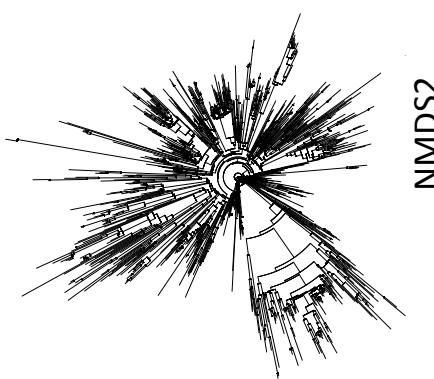




NMDS with Mother–Offspring Pair As Grouping Factor

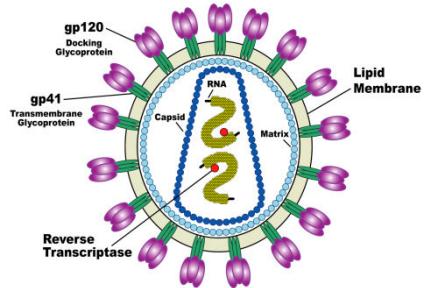
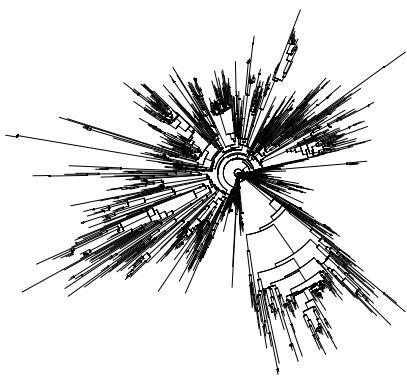
$R^2 = 0.441^{***}$

Primate bacterial community



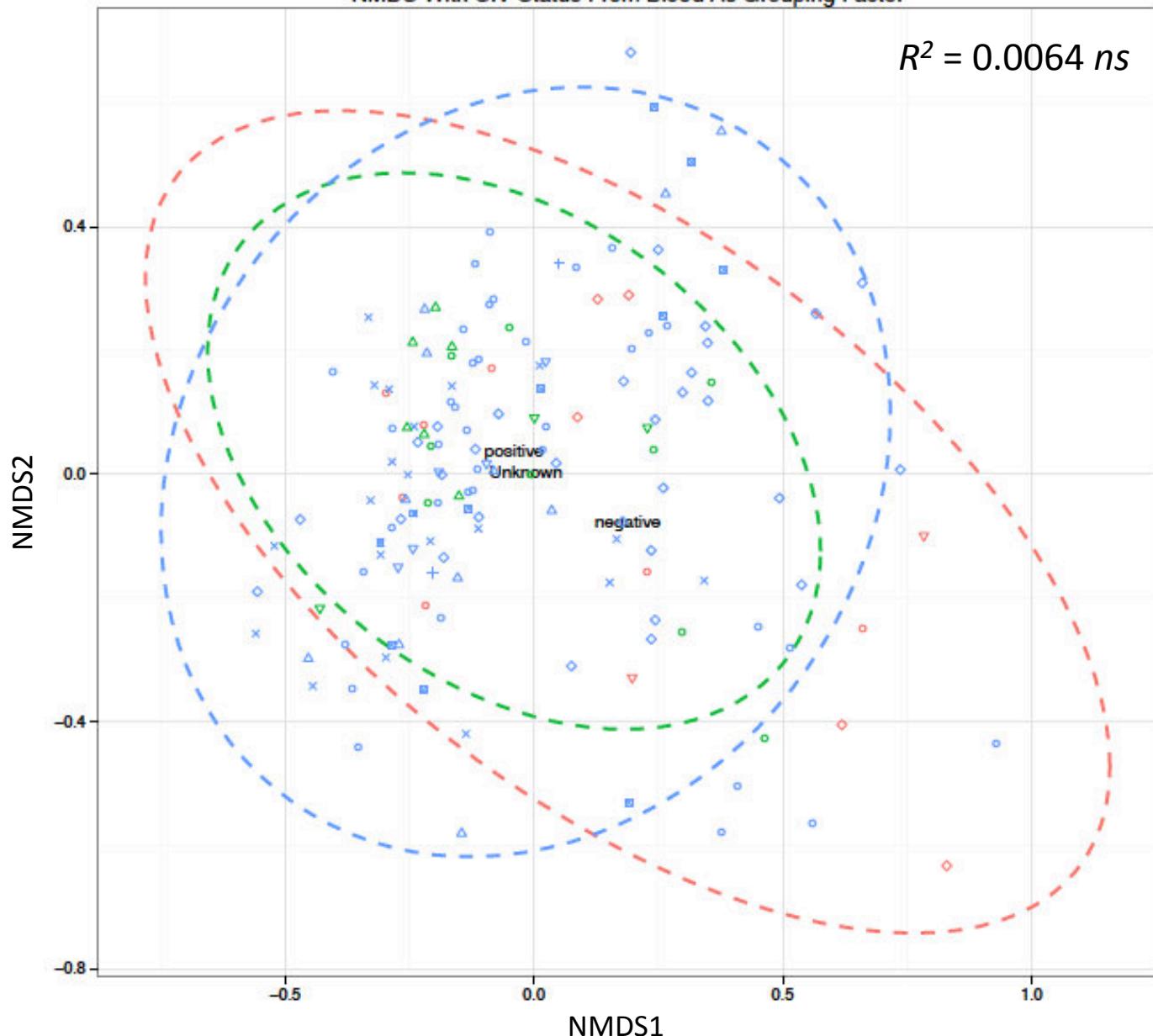


Primate bacterial community

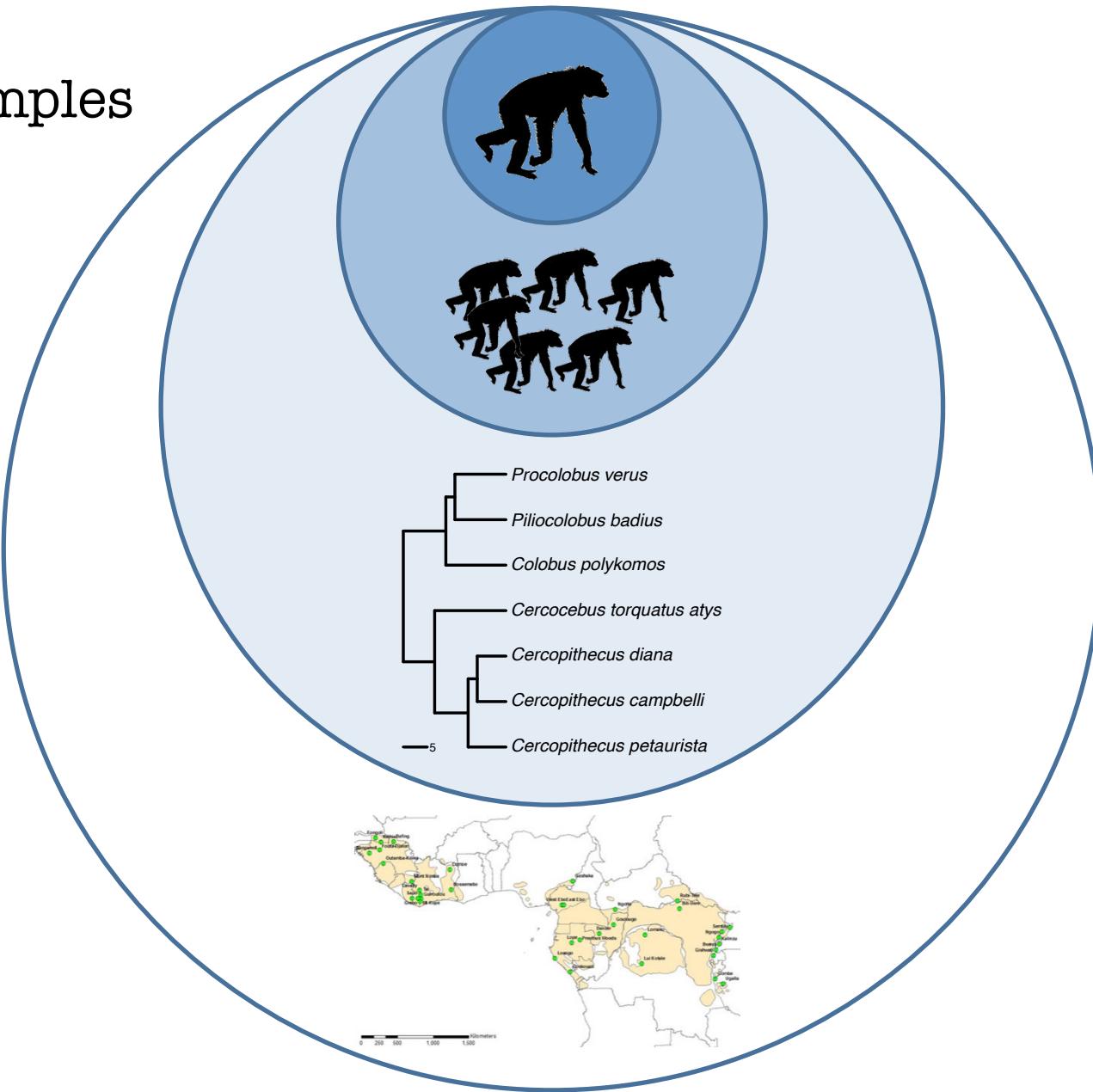


NMDS With SIV Status From Blood As Grouping Factor

$$R^2 = 0.0064 \text{ ns}$$

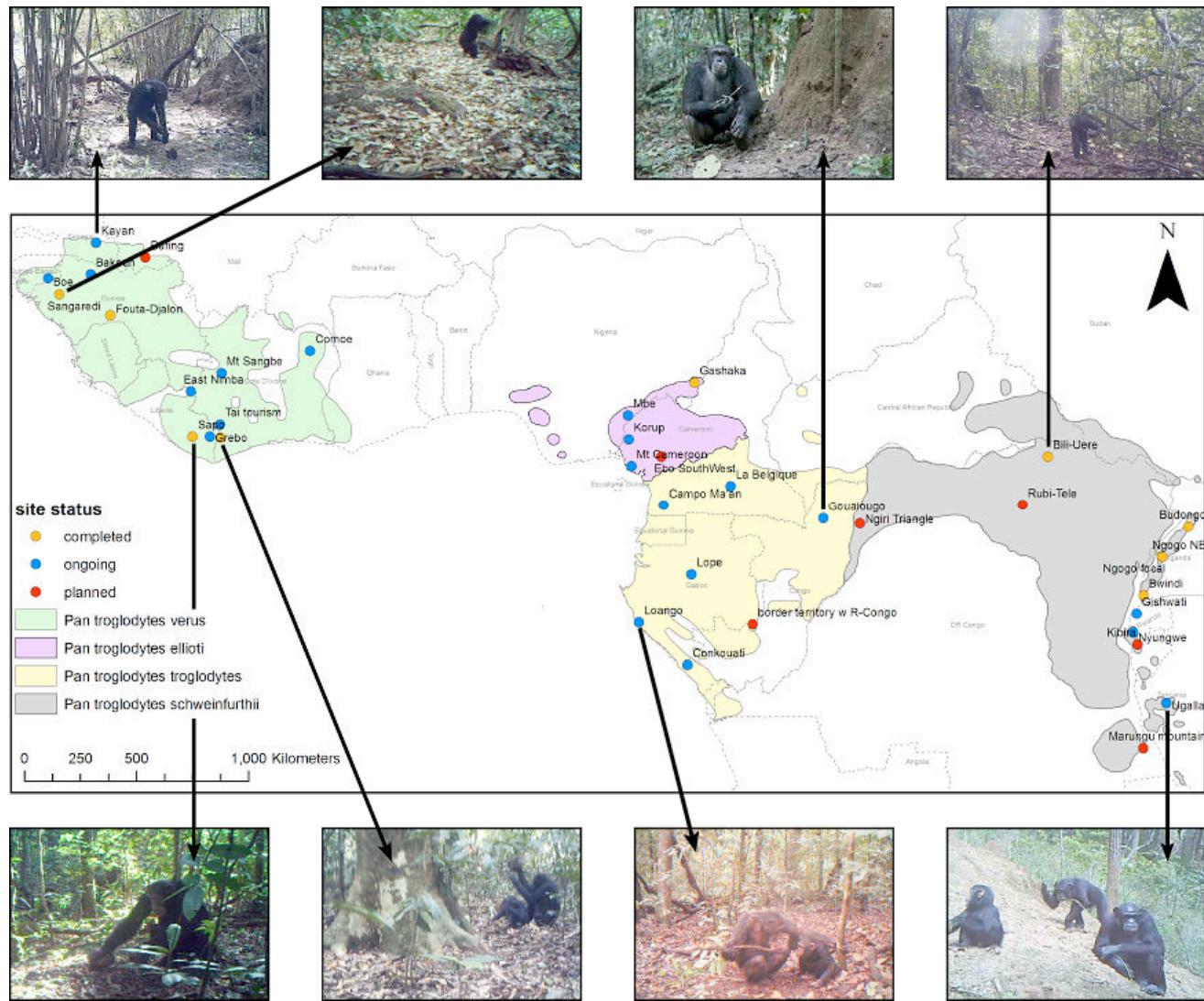


- Non-invasive samples
- Different scales
 - host
 - social groups
 - ecosystems
 - evolutionary
- Eco-Evo
 - Facilitation
 - Exclusion
 - Competition



Future directions

- Examining the virome (particularly phages)
- More flexible modeling approaches like PGLMMs

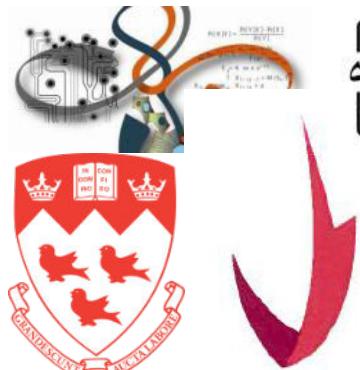


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Jonathan Davies

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and the Robert Koch Institute.

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