Vignettes for the publication

treehouse: a user-friendly application to obtain subtrees from large phylogenies

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Overview of treehouse vignettes.

To provide an example of how this workflow could be implemented in a real research scenario, we implement the *treehouse* workflow in two vignettes that use phylogenies available through the *treehouse* database. These two vignettes show-case the utility of *treehouse* to obtain evolutionary relationships with meaningful branch lengths for the development of evolutionary-based hypotheses.
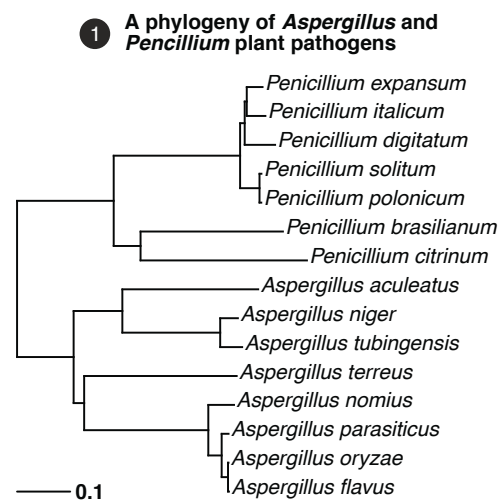
• First, we will consider a research scenario focused on studying plant pathogens among *Aspergillus* and *Penicillium* species. For this scenario, researchers desire a phylogeny of all plant pathogenic *Aspergillus* and *Penicillium* species from the (Steenwyk, et al. 2019) phylogeny.

• Second, we will examine a lineage of historically hypermutating yeast, *Hanseniaspora* (Steenwyk, Opulente, et al. 2019), and qualitatively examine branch lengths between two lineages of budding yeast.

Vignette 1: *The evolutionary relationships among plant pathogens in the genera* Aspergillus *and* Penicillium.

Research scenario: Due to the increasing food security threat posed by plant pathogens, researchers may be interested in obtaining the evolutionary relationships among plant pathogens in the genera *Aspergillus* and *Penicillium*. A subtree of plant pathogenic species of *Aspergillus* and *Penicillium* can easily be obtained from the genome-scale phylogeny of 81 *Aspergillus* and *Penicillium* species (Steenwyk, et al. 2019).

Instructions to obtain the desired subtree

• First, select the *Aspergillaceae* phylogeny from the database of fungi.
• Second, upload a list of plant pathogenic species of *Aspergillus* and *Penicillium* (File S1).
• Third, examine the resulting phylogeny. The resulting phylogeny can serve as the backdrop in developing and testing evolutionary-based hypotheses about pathogenicity of these species.
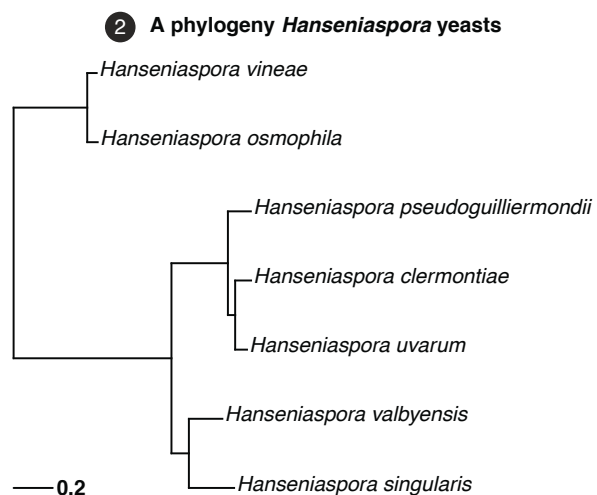

① A phylogeny of *Aspergillus* and *Penicillium* plant pathogens

Penicillium expansum
Penicillium italicum
Penicillium digitatum
Penicillium solitum
Penicillium polonicum
Penicillium brasilianum
Penicillium citrinum
Aspergillus aculeatus
Aspergillus niger
Aspergillus tubingensis
Aspergillus terreus
Aspergillus nomius
Aspergillus parasiticus
Aspergillus oryzae
Aspergillus flavus

0.1

Vignette 2: *The long stem branch in the faster-evolving lineage of* Hanseniaspora.

Research scenario: Branch lengths represent substitutions per site and are included in subtrees obtained from *treehouse*. A subtree of the budding yeast genus, *Hanseniaspora* (phylum: *Saccharomycotina*, kingdom: Fungi), will be used to demonstrate the utility of maintaining this information for informing downstream hypotheses.

Instructions to obtain the desired subtree
• First, select the *Saccharomycotina* phylogeny from the database of fungi (Shen et al. 2018).
• Second, upload a list of *Hanseniaspora* species (File S2).
• Third, examine the resulting phylogeny. The resulting phylogeny reveals a faster-evolving lineage and slower-evolving lineage as delineated by the stem branch length leading up to the two major clades. This observation lead researchers to further investigate these two lineages and discovery the massive loss of DNA repair genes in the faster-evolving lineage which, is likely responsible for the long stem branch (Steenwyk, et al. 2019).

2 A phylogeny *Hanseniaspora* yeasts
Hanseniaspora vineae
Hanseniaspora osmophila
Hanseniaspora pseudoguilliermondii
Hanseniaspora clermontiae
Hanseniaspora uvarum
Hanseniaspora valbyensis
Hanseniaspora singularis
0.2

Notes

• Example taxa lists for subtree acquisition can be found in the 'example_taxa_lists' directory in the *treehouse* github.

• There, you will find File S1 and S2 (Vign1-Aspergillaceae_plant_pathogens.txt and Vign2-Hanseniaspora_branch_lengths.txt, respectively) which, have also been placed in this document for your convenience.

File S1 contents:

Aspergillus_terreus
Penicillium_citrinum
Penicillium_brasilianum
Penicillium_polonicum
Penicillium_solitum
Penicillium_digitatum
Penicillium_italicum
Penicillium_expansum
Aspergillus_tubingensis
Aspergillus_niger
Aspergillus_aculeatus
Aspergillus_flavus
Aspergillus_oryzae
Aspergillus_parasiticus
Aspergillus_nomius

File S2 contents:

Hanseniaspora_singularis
Hanseniaspora_valbyensis
Hanseniaspora_uvarum
Hanseniaspora_clermontiae
Hanseniaspora_pseudoguilliermondii
Hanseniaspora_osmophila
Hanseniaspora_vinae

References

Shen X-X, Opulente DA, Kominek J, Zhou X, Steenwyk JL, Buh K V., Haase MAB, Wisecaver JH, Wang M, Doering DT, et al. 2018. Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. Cell 175:1533–1545.e20.

Steenwyk JL, Opulente DA, Kominek J, Shen X-X, Zhou X, Labella AL, Bradley NP, Eichman BF, Čadež N, Libkind D, et al. 2019. Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts.Kamoun S, editor. PLOS Biol. 17:e3000255.

Steenwyk JL, Rokas A. 2019. Treehouse: a user-friendly application to obtain subtrees from large phylogenies. BMC Res. Notes 12:541.

Steenwyk JL, Shen X-X, Lind AL, Goldman GH, Rokas A. 2019. A Robust Phylogenomic Time Tree for Biotechnologically and Medically Important Fungi in the Genera Aspergillus and Penicillium.Boyle JP, editor. MBio 10.