

Date of study: May 2019

*Date of public archiving (should be published at similar time to Tree Traits 2015): **Spring 2025***

Last modified:

Dec 17, 2024

Goal

To collect functional trait data (SLA, height, branch wood density, & C:N) for 21 dominant woody species in Smithers, Alex Fraser research forest, Kamloops, and E. C. Manning Park, British Columbia, Canada.

Contributors:

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Github

[Github Treetraits](#)

General Files

Files	Where	What
traitPheno.Rnw	docs	Outline for manuscript
README	Github	Outline of repo and experimental aims

Data and Code

Files	Where	What
traits_ht_dbh.csv	data/western/uncleaned	Raw trait data for height, dbh, stem volume collected in 2019
area_mass.csv	data/western/uncleaned	Raw leaf mass and leaf area data for samples collected in 2019
traits_stem_vol.csv	data/western/uncleaned	Raw stem volume for stem specific density for samples collected in 2019
stem.wt.total.csv	data/western/uncleaned	Raw stem weights for stem specific density for samples collected in 2019

Traits_cn_2019.csv	data/western/uncleaned	CN data recieved from S. Guichon
Loughnan_Deirdre_sample_submission_form.xlsx	data/western/uncleaned	Submission form for C:N with sample weights
westTrait.csv	data/western/cleaned	Combined data file for all trait data
data/eastern	data/eastern	Folder copied directly from DF repo containing data from eastern transect
Cleaning_compiling_data.R	analysis/rcode	Code to compile a single dataset for all traits measured
bc_trait_only_testdata.R	analysis/rcode	Developing test data for trait portion of joint model
pheno_traits_na_testdata.R	analysis/rcode	R code making test data
testDataTransectTraitPhenoNoGr and.R	analysis/rcode	Test data for full model
checkPriorPosterior.R	analysis/rcode	Code to do visualizations and prior/posterior predictive checks
ppc_XX.R	analysis/rcode	Code to run prior predictive checks for each trait individually (XX—specific file for each trait)
jointMdlContLat100.R	analysis/rcode	Main model code, joint model with continuous cues and some traits rescaled by 100.
manuscriptVales.R	analysis/rcode	Code extracting values to be referenced in sweave files.
traitMuPlots.R	analysis/rcode	Code to make mu plots
traitGradientBBPlot.R	analysis/rcode	Code to plot of species estimates organized by bb date
traitEyePlots.R	analysis/rcode	Code to make eye plots using model posteriors.

slopes_vs_cues_100.R	analysis/rcode	Code to make figure comparing slopes and cues.
figModelFit.R	analysis/rcode	Code to make eyeplot figure comparing model estimates to raw data

Notes:

