*Date of study: May 2019*

*Date of public archiving (should be published at similar time to Tree Traits 2015)*: **September 2024**

*Last modified*:

May 19, 2024

*Goal*

To collect functional trait data (SLA, height, stem density, & C:N) for 21 dominant woody species in British Columbia, Canada.

*Contributors:*

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**Github**

[Github Treetraits](https://github.com/DeirdreLoughnan/Treetraits)

*General Files*

| **Files** | **Where** | **What** |
| --- | --- | --- |
| traits\_pheno.tex | [Github](https://github.com/DeirdreLoughnan/Treetraits/blob/master/docs/traitPheno.Rnw) | Outline for manuscript |
| README | [Github](https://github.com/DeirdreLoughnan/Treetraits/blob/master/README.md) | Outline of repo and experimental aims |

*Data and Code*

| **Files** | **Where** | **What** |
| --- | --- | --- |
| traits\_ht\_dbh\_final.csv | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/data/western/cleaned) | Trait data for height, dbh, stem volume collected in 2019 |
| mergedareamass\_final.csv | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/data/western/cleaned) | Leaf mass and leaf area data for samples collected in 2019 |
| traits\_stemvol.csv | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/data/western/cleaned) | Stem volume for stem specific density for samples collected in 2019 |
| stem.wt.total.csv | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/data/western/cleaned) | Stem weights for stem specific density for samples collected in 2019 |
| mergedareamass\_final.csv | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/data/western/cleaned) | Leaf areas and mass for leaves collected in 2019 |
| Loughnan\_Deirdre\_sample\_submission\_form.xlsx | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/data/western) | Submission form for C:N with sample weights |
| rcode/Cleaning\_compiling\_data.R | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/rcode) | Code to compile a single dataset for all traits measured |
| pheno\_trait\_na\_spsitepooled.R | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/analyses/testdata) | Developing test data with partial pooling with site and species |
| pheno\_traits\_na\_testdata.R | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/analyses/testdata) | R code making test data |
| FRST507 | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/analyses) | Code created as part of 507 course |
| data/eastern | [Github](https://github.com/DeirdreLoughnan/Treetraits/tree/master/data/eastern) | Folder copied directly from DF repo containing data from eastern transect |

Notes:

