

*Date of study: November 2019*

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*Last modified:*

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### *Goal*

To collect phenology budburst data for 21 dominant woody species in British Columbia, Canada.

### *Contributors:*

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### *General files*

Files	Where	What
dailylog_dl_2019_fall.txt	<a href="#">Github</a>	Daily notes on both the sample collection and experiment
Detailed_methods_phenology.tex	<a href="#">Github</a>	Methods used for experiment and sample collection
bc_phenology.csv	<a href="#">Github</a>	Cleaned phenology data
pheno_data	<a href="#">Github</a>	Folder with raw datafiles
README	<a href="#">Github</a>	Outline of repo and experimental aims

### *Data and Code*

#### **Github**

[Github pheno\\_bc](#)

Files	Where	What
indiv.no.cleaned.csv	<a href="#">Github</a>	List of tagged sample number branch taken from
test_phenobcdata.csv	<a href="#">Github</a>	Test data for model
raw/	<a href="#">Github</a>	Includes all files from each day of observations in their

		unaltered state
typos_cleaned/	<a href="#">Github</a>	Includes all files from each day of observations that have been cleaned of typos
day.of.bb.csv	<a href="#">Github</a>	Dataset of calculated day of budburst for terminal and lateral buds
SBphylo_phenobc.tre	<a href="#">Github</a>	Phylogeny of species pruned from Smith et al. (2018)
rcode/cleaning/cleaningcode.R	<a href="#">Github</a>	Code used to clean the observation data and produce bc_phenology.csv
rcode/cleaning/pheno_bb_calc.R	<a href="#">Github</a>	Code used to calculate the day of bb and produce day.of.bb.csv
pheno_bb_fixingrepno.R	<a href="#">Github</a>	Adding the correct rep number for each sample
cleaning.indivno.R	<a href="#">Github</a>	Cleaning and combining list of individuals sampled from those tagged
randomizing_Oct25.R	<a href="#">Github</a>	Rcode for randomly assigning samples to treatments
bc_bb.analysis_dldf_continuous.R	<a href="#">Github</a>	R code for running main model
bc.bb.stan	<a href="#">Github</a>	Stan model based on DF model
phenologyMsValues.R	<a href="#">Github/rcode</a>	Source file for calling all values in manuscript
phenologyMsFigures.R	<a href="#">Github/rcode</a>	File to make general figures in manuscript
phenologyEyePlots.R	<a href="#">Github/rcode</a>	Rcode for eyeplots in manuscript
gradientBBPlot.R	<a href="#">Github/rcode</a>	Rcode for figures of bb gradients in manuscript

phenoBcMapping.R	<a href="#">Github/rcode</a>	Rcode for mapping sampled sites
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