

# Draft Manuscript

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**Title:** Can gradients in annual rainfall & forest type predict the distribution & abundance of 4 Ericaceous shrubs? -  
BIOL 548T LDP

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**Author Contributions:** EM conceived of the study, conducted the analyses, and wrote the original, and revised drafts of the manuscript.

**Data Availability:** The data and code that support the findings of this study are openly available on GitHub at <https://github.com/emench/Menchions-BIOL548T>.

**Conflict of Interest statement**

No conflicts of interest

## Abstract

Patterns in plant distributions are driven by a multitude of factors, one of which is soil properties. For many ericaceous shrubs, high acidity soils are often an important determinant of distribution. Here I used data collected from Thiffault *et al.* (2015a) across plots in the understory of boreal forests of Quebec from 1985 to 2000 to determine if the abundance of four species of ericaceous shrubs (*Chamaedaphne caliculata*, *Rhododendron groenlandicum*, *Kalmia angustifolia* and *Vaccinium sp.*) can be predicted by patterns in soil acidity with habitat. Specifically, since conifer forests with

high rainfall are typically associated with more highly acidic soils, I predicted this habitat type would contain the highest abundance of these shrubs, and in particular *C. caliculata* and *R. groenlandicum* since they also prefer wetter habitats. For *K. angustifolia* and *Vaccinium sp.* I predicted that low rainfall coniferous forests would contain the greatest abundance due to high acidity from the conifers and lower moisture which these species supposedly prefer. I used box plots and pairwise Wilcoxon tests to compare medians between percent cover of different types of habitats defined by high or low rainfall and forest type. I found that for *C. caliculata* and *R. groenlandicum*, my predictions were quite close to the observed patterns, suggesting that perhaps soil acidity and moisture are primary drivers of distribution. However, for *K. angustifolia* and *Vaccinium sp.* my predictions did not match the results. However, conifer forests and non-forested (presumably boggy areas) plots did tend to contain the highest median abundance which may also suggest soil acidity as a strong driver of distribution. Future studies and analyses should use more direct observations of soil pH measurements to study these patterns rather than relying on the proxy variable of rainfall and forest type used here to avoid the many confounding factors that this index introduces.

**Key-words:** Ecology, Ericaceae, LDP, Plant Ecology, Vegetation Mapping, Vegetation Patterns

## Introduction

Four species of Ericaceae dominate the understory in the northern boreal forests of Quebec, Canada. Two of these species *Rhododendron groenlandicum* and *Chamaedaphne calyculata* are said to prefer acidic soils and wetter habitats whereas the other dominant species *Kalmia angustifolia*, *Vaccinium angustifolium*, and *Vaccinium myrtillodes* are known to prefer drier, but also acidic soils. Many factors contribute to soil acidity, but a few variables in particular, rainfall and forest type have been observed to drive broad patterns in soil pH in the United States “Soil acidity - an overview | ScienceDirect topics” (n.d.a). Therefore, I ask, can annual rainfall and forest type (conifer, deciduous, or mixed) predict patterns of abundance for these species in the boreal zone of Northern Quebec between 1985 and 2000?

Acidic soils are often associated with conifer forests and higher rainfall (Hornung 1985; “Soil acidity - an overview | ScienceDirect topics” n.d.b). Therefore, species with a preference for more acidic soils should be more often found in conifer forest types with higher precipitation. Therefore, I predict that *R. groenlandicum* and *C. calyculata*, will have the highest mean percent cover in areas with conifer forest types and higher annual precipitation. In contrast, I predict that *K. angustifolia* and *Vaccinium sp.*, will have the highest mean percent cover in conifer forests with lower annual precipitation.

Specifically, I predict the following pattern of mean percent cover for *R. groenlandicum* and *C. calyculata*: (H = high precipitation, L = low precipitation, c= conifer forests, d=deciduous forests, m=mixed forest)

From highest to lowest predicted mean percent cover with high rainfall and conifer forests being indicative of higher abundance: H-c, L-c, H-m, H-d, L-m, L-d

For *K. angustifolia* and *Vaccinium sp.* I predict the following pattern, with less rainfall being of greater importance to abundance: L-c, L-m, L-d, H-c, H-m, H-d

## Methods

### Data collection

Data was retrieved from Thiffault *et al.* (2015b): <https://datadryad.org/stash/dataset/doi:10.5061%2Fdryad.4767v>. According to Thiffault *et al.* (2015c), the data on abundance of the 4 species were collected from 15,339 circular plots across central and northern Quebec along 1.5 – 2 km long transects of which supported 5-7 plots. Forest type: was determined by visual estimations at the time that the plots were visited by assigning a type corresponding to the two most dominant tree species within the plot. This led to a total of 15 total forest types. Climate data was collected by identifying the closest meteorological station (51 in the study region) and correcting for differences in latitude,

63 longitude and elevation between the plot and the station using distance weighting and multiple linear regression.

#### 64 **Data download (script: “part-1\_data\_download”)**

65 All data download, preparation and statistical analyses were carried out in R 4.2.1 (R Core Team 2022). All scripts  
66 used are available on GitHub <https://github.com/emench/Menchions-BIOL548T>. I first retrieved this data from Dryad  
67 using a script that automates the download from Dryad.

#### 68 **Data preparation (script: “part-2\_data\_preparation”)**

69 I then prepared the data for analysis by altering the forest type classification and creating a variable indicating whether  
70 the plot was in a high or low rainfall area. For the forest type classifications, I used the metadata on forest type codes  
71 provided to create 4 categories of forest type: “c” (coniferous, if the two dominant tree species in the plot were both  
72 coniferous, n=1282), “d” (deciduous, if the two dominant species were both deciduous, n=45), “m” (mixed, if the two  
73 most dominant species contained a conifer and a deciduous species, n=69), and “n” (non-forested, n=26).

74 `## [1] 1282 49`

75 `## [1] 45 49`

76 `## [1] 69 49`

77 `## [1] 26 49`

78 I then created a rainfall index. I calculated the median annual usable precipitation (cm) which was 5cm/ year. I used  
79 this as a threshold and defined any plot with annual usable precipitation > 5cm to a high precipitation category (H) and  
80 below this threshold to low annual rainfall (L).

```
# Classifying as high or low precipitation ----  
# PRECU is the annual rainfall variable  
  
med <- median(X_mat$PRECU)  
  
# will use the median as the threshold  
  
X_mat <- X_mat %>%  
  mutate(., RainFall = case_when(PRECU < med ~ "L",  
    PRECU >= med ~ "H"))
```

81 Finally, I combined the forest type and rainfall variables into an index (rf index) that described the rainfall category  
82 followed by the forest type (e.g. H\_c = high rainfall, conifer forest).

```
# Combining and classifying as forest type - rainfall index
X_mat <-
  X_mat %>%
  unite(., rf_index, c("RainFall","Forest_Type"), sep = "_", remove =F, na.rm = FALSE)

# writing altered data as .csv ----
write.csv(X_mat, here::here("data","X_mat_processed.csv"))
```

### 83 **Plotting (script: “part-3\_data\_analysis”)**

84 I constructed box plots displaying percent cover of each species as the response variable and rf (rainfall forest cover  
85 index) as the grouping variable using using ggplot2::ggplot. I decided to log-transform the response variable since the  
86 data was skewed with outliers making the display and comparison between groups difficult in all of the plots.

```
# loading in prepared data ----
X_mat <- read.csv(here::here("data","X_mat_processed.csv"))
X_mat <- X_mat %>%
  select(CLE, Forest_Type, PRECU, RainFall,rf_index)

Y_mat <- read.csv(here::here("data","Matrice_Y.csv"),
  sep = ";") # response variables (mean ericaceous cover, in %)
clim <- read.csv(here::here("data","Climate_value.csv"),
  sep = ";") # numerical codes used for clim vars in X_mat

# PLOTTING WITH BOX PLOTS----

# For Chamaedaphne calyculata
# creating dataframe with only this species
CAL <- data.frame(Y_mat$V_CAL,X_mat$PRECU, X_mat$rf_index)
colnames(CAL) <- c("V_CAL","PRECU","rf_index") # renaming columns
CAL_plot <- ggplot(data=CAL, aes(x=rf_index, y=V_CAL)) +
  geom_boxplot() # plotting only this species with the rainfall-forest
```

```

# type index in box plots

CAL_plot <- ggplot(data=CAL, aes(x=rf_index, y=log(V_CAL))) + # log transforming the y axis
  geom_boxplot() # automatically removes observations with 0 % cover - which is ok

# Repeating for Rhododendron groenlandicum
RHG <- data.frame(Y_mat$V_RHG,X_mat$PRECU,X_mat$rf_index)
colnames(RHG) <- c("V_RHG","PRECU","rf_index")
RHG_plot <- ggplot(data=RHG, aes(x=rf_index, y=V_RHG)) +
  geom_boxplot()

RHG_plot <- ggplot(data=RHG, aes(x=rf_index, y=log(V_RHG))) + # log transforming the y axis
  geom_boxplot()

## Repeating for Kalmia angustifolia
# Plotting:
KAA <- data.frame(Y_mat$V_KAA,X_mat$PRECU,X_mat$rf_index)
colnames(KAA) <- c("V_KAA","PRECU","rf_index")
KAA_plot <- ggplot(data=KAA, aes(x=rf_index, y=V_KAA)) +
  geom_boxplot()

KAA_plot <- ggplot(data=KAA, aes(x=rf_index, y=log(V_KAA))) + # log transforming the y axis
  geom_boxplot()

## Repeating for Vaccinium sp.
VAAM <- data.frame(Y_mat$V_VAAM,X_mat$PRECU,X_mat$rf_index)
colnames(VAAM) <- c("V_VAAM","PRECU","rf_index")

VAAM_plot <-ggplot(data=VAAM, aes(x=rf_index, y=V_VAAM)) +
  geom_boxplot()

VAAM_plot <- ggplot(data=VAAM, aes(x=rf_index, y=log(V_VAAM))) + # log transforming the y axis

```

```
geom_boxplot()
```

I then combined all of the above plots into one single chart for easier comparison.

## Statistical analysis

I used a Kruksal-Wallis test to determine if any any groups were significantly different from the rest, or in other words, if at least one rainfall forest cateogry contains a significantly different percent cover of a given species than the other groups. For all species,  $p < 0.05$  indicating we can reject the null hypothesis that percent cover is the same across rainfall forest type categories for all species. To further assess the relationships, I performed a pairwise wilcox test to determine whether percent cover differed significantly from each other in pairs. This was not in the initial pre-registration but is an extended step to further test the hypothesis.

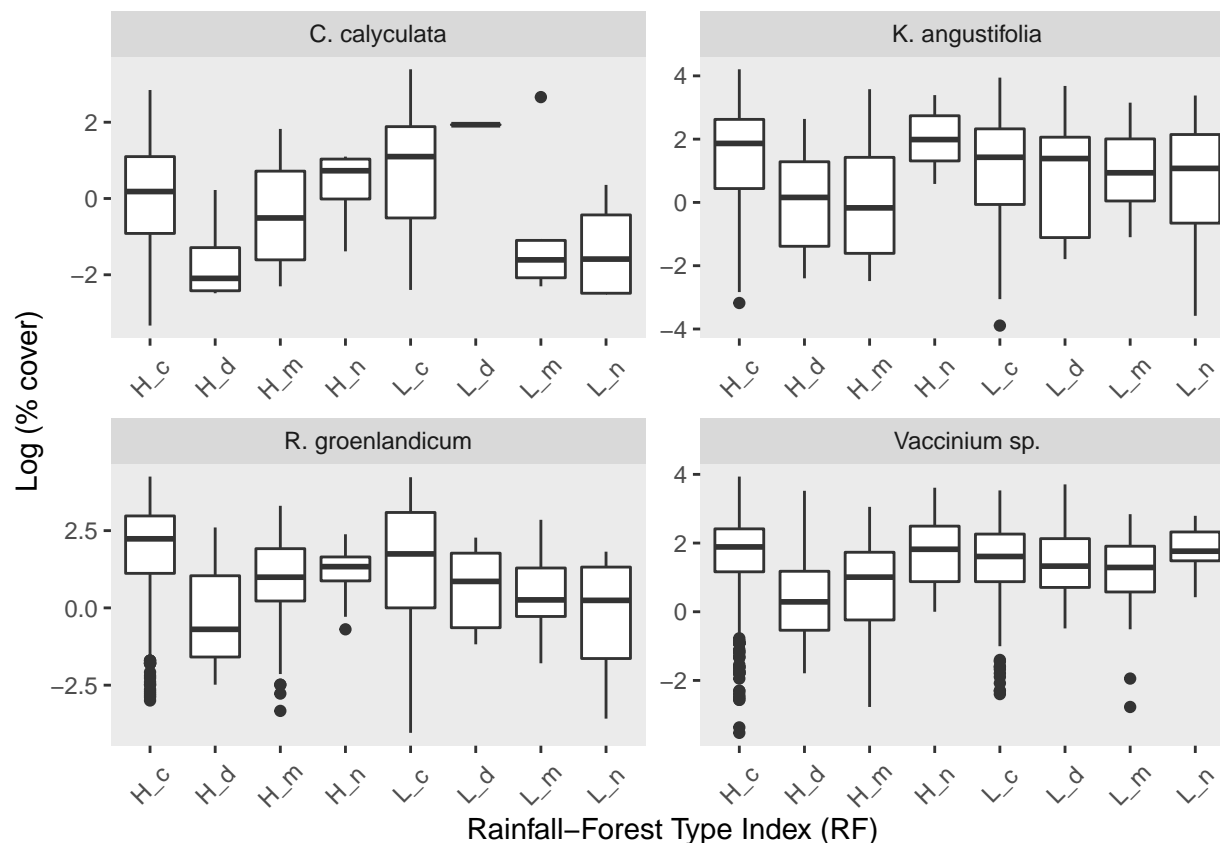
## Results & Discussion

```
p + facet_wrap( ~ species, scales="free",  
               labeller=species_labeller)
```

```
## Warning: The labeller API has been updated. Labellers taking `variable` and
```

```
## `value` arguments are now deprecated. See labellers documentation.
```

```
## Warning: Removed 1084 rows containing non-finite values (stat_boxplot).
```



**Figure 1.** Box plots of *C. calyculata*, *K. angustifolia*, *R. groenlandicum*, and *Vaccinium sp.* percent cover in plots that fall in each of the rainfall-forest type categories. The thick horizontal lines represent the median for each category. The y axis was log-transformed for display purposes.

**Table 1.** Mean % cover for *C. calyculata* in different rainfall forest type categories.

```
CAL_cover %>% group_by(rf_index) %>% summarise(median = median(cover, na.rm=T))%>%
  arrange(desc(median))
```

```
## # A tibble: 8 x 2
##   rf_index median
##   <chr>      <dbl>
## 1 H_c      0.0357
## 2 H_d      0
## 3 H_m      0
## 4 H_n      0
## 5 L_c      0
```



```

112 ## 6 L_d      0
113 ## 7 L_m      0
114 ## 8 L_n      0

```

115 For *C. calyculata*, the only rainfall forest type category that had median percent cover above 0 was high rainfall  
 116 coniferous forests. This supports the prediction that this species would have a greater preference for this category  
 117 possibly due to the higher acidity and moisture provided.

118 **Table 2.** Mean % cover for *R. groenlandicum* in different rainfall forest type categories.

```

RHG_cover %>% group_by(rf_index) %>% summarise(median = median(cover, na.rm=T)) %>%
  arrange(desc(median))

```

```

119 ## # A tibble: 8 x 2
120 ##   rf_index median
121 ##   <chr>      <dbl>
122 ## 1 H_c      8.5
123 ## 2 L_c      3.67
124 ## 3 H_n      3.48
125 ## 4 H_m      2.17
126 ## 5 L_n      1.66
127 ## 6 L_m      1
128 ## 7 H_d      0.4
129 ## 8 L_d      0.321

```

130 For *R. groenlandicum*, the order of my predictions also matched those observed. H\_c had significantly higher per-  
 131 cent cover than any other rf type ( $p < 0.05$ ), followed by L-c, H\_m, L\_m H\_d and L\_d. This may indicate that *R.*  
 132 *groenlandicum* indeed prefers more acidic soils created by higher rainfall, but more importantly coniferous forests.  
 133 However, this is confounded with other factors that may drive its preference for coniferous habitat such as other soil  
 134 properties associated with conifer needles and light availability.

135 **Table 3.** Mean % cover for *K. angustifolium* in different rainfall forest type categories.

```

KAA_cover %>% group_by(rf_index) %>% summarise(median = median(cover, na.rm=T)) %>%
  arrange(desc(median))

```

```

136 ## # A tibble: 8 x 2
137 ##   rf_index median
138 ##   <chr>      <dbl>
139 ## 1 H_n        7.58
140 ## 2 H_c        4.5
141 ## 3 L_n        3.74
142 ## 4 L_d        2.6
143 ## 5 L_m        1.96
144 ## 6 L_c        1.33
145 ## 7 H_d        0.667
146 ## 8 H_m        0.5

```

147 For *K. angustifolium* the patterns in abundance that I predicted (L-c, L-m, L-d, H-c, H-m, H-d) were not supported  
 148 by those observed. The category with the highest median percent cover was non-forested area however this was  
 149 not significantly different from abundance in high rainfall coniferous forests ( $p>0.05$ ). This may indicate that light-  
 150 availability is a more important determinant of its distribution. Additionally, non-forested plots may often be boggy  
 151 areas with acidic soils from sphagnum growth, so perhaps this species' distribution is highly driven by soil acidity,  
 152 so much so that the acidity produced by conifer needles and high rainfall is not sufficient. The fact that low rainfall  
 153 coniferous forests had one of the lowest percent covers is curious. It suggests that other factors not included here should  
 154 be included in further assessments of distribution.

```

VAAM_cover %>% group_by(rf_index) %>% summarise(median = median(cover, na.rm=T)) %>%
  arrange(desc(median))

```

```

155 ## # A tibble: 8 x 2
156 ##   rf_index median
157 ##   <chr>      <dbl>
158 ## 1 H_c        6.6
159 ## 2 H_n        5.99
160 ## 3 L_n        5.83
161 ## 4 L_c        5
162 ## 5 L_d        3.83
163 ## 6 L_m        3.22
164 ## 7 H_m        2.75

```

## 8 H\_d 1.33

Finally, for *Vaccinium sp.* median percent cover again did not follow the pattern I predicted, except for H\_d and H\_m having the lowest values, however, they were not significantly different from each other ( $p < 0.05$ ). the categories with higher abundance were H\_c, H\_n and L\_n although they were not significantly different from each other ( $p > 0.05$ ). H\_c was significantly higher than L\_c ( $p < 0.05$ ) which I originally thought would contain the greatest abundance. This pattern might be similar in nature to the one observed for *K. angustifolium*, where coniferous and non-forested (presumably boggy) areas with high rainfall contain the most abundance, possibly due to the importance of acidity in these environments compared to those associated with deciduous or mixed forests.

Analysis to test if these species distributions are driven partly by soil acidity could ideally be performed using direct measures of soil acidity at the plots rather than the proxy variables used here. Upon future visits to the sites, these measurements could be taken to construct models and compare preferences between species to better predict what drives their distribution patterns and regenerative ability in logging and fire disturbed habitats.

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```
grateful::cite_packages(output = "paragraph")
```

We used R version 4.2.1 (R Core Team 2022) and the following R packages: grateful v. 0.1.11 (Rodríguez-Sánchez *et al.* 2022), groundhog v. 2.0.1 (Simonsohn & Gruson 2022), here v. 1.0.1 (Müller 2020), knitr v. 1.40 (Xie 2014, 2015, 2022), prereg v. 0.6.0 (Aust & Spitzer 2022), Rfast v. 2.0.6 (Papadakis *et al.* 2022), rmarkdown v. 2.16 (Xie *et al.* 2018, 2020; Allaire *et al.* 2022), tidyverse v. 1.3.2 (Wickham *et al.* 2019).

## Appendix

**Table A1.** P-Values for Pairwise Wilcox test for *C. calyculata*

CAL\_wt\_pframe

| ##     | H_c          | H_d        | H_m       | H_n       | L_c        | L_d       | L_m       |
|--------|--------------|------------|-----------|-----------|------------|-----------|-----------|
| ## H_d | 0.0003184252 | NA         | NA        | NA        | NA         | NA        | NA        |
| ## H_m | 0.1858401983 | 0.04590974 | NA        | NA        | NA         | NA        | NA        |
| ## H_n | 0.5004745729 | 0.17309149 | 1.0000000 | NA        | NA         | NA        | NA        |
| ## L_c | 0.4543463732 | 0.00536943 | 0.4543464 | 0.5923667 | NA         | NA        | NA        |
| ## L_d | 0.0707266386 | 0.84421956 | 0.2318784 | 0.3633565 | 0.15627824 | NA        | NA        |
| ## L_m | 0.0051409599 | 0.59236673 | 0.1562782 | 0.3633565 | 0.04590974 | 0.5923667 | NA        |
| ## L_n | 0.1562782421 | 0.36335646 | 0.5309553 | 0.5923667 | 0.34415728 | 0.4543464 | 0.5790773 |

**Table A2.** P-Values for Pairwise Wilcox test for *R. groenlandicum*

RHG\_wt\_pframe

| ##     | H_c          | H_d        | H_m        | H_n       | L_c        | L_d       | L_m       |
|--------|--------------|------------|------------|-----------|------------|-----------|-----------|
| ## H_d | 3.378207e-10 | NA         | NA         | NA        | NA         | NA        | NA        |
| ## H_m | 4.416647e-04 | 0.01272471 | NA         | NA        | NA         | NA        | NA        |
| ## H_n | 2.573869e-02 | 0.01272471 | 0.88769677 | NA        | NA         | NA        | NA        |
| ## L_c | 3.929857e-03 | 0.00012994 | 0.16511102 | 0.4562412 | NA         | NA        | NA        |
| ## L_d | 4.451922e-04 | 0.75177373 | 0.09693363 | 0.1508120 | 0.01272471 | NA        | NA        |
| ## L_m | 7.730911e-07 | 0.33233183 | 0.09693363 | 0.1051708 | 0.00574138 | 0.4148958 | NA        |
| ## L_n | 9.136257e-04 | 0.16672719 | 0.41489583 | 0.3561606 | 0.09693363 | 0.3561606 | 0.7530249 |

**Table A3.** P-Values for Pairwise Wilcox test for *K. angustifolium*

KAA\_wt\_pframe

| ##     | H_c          | H_d         | H_m | H_n | L_c | L_d |
|--------|--------------|-------------|-----|-----|-----|-----|
| ## H_d | 1.936238e-03 | NA          | NA  | NA  | NA  | NA  |
| ## H_m | 5.685952e-04 | 0.664338226 | NA  | NA  | NA  | NA  |

|     |    |     |              |             |             |            |           |           |
|-----|----|-----|--------------|-------------|-------------|------------|-----------|-----------|
| 233 | ## | H_n | 2.376205e-01 | 0.001833148 | 0.001833148 | NA         | NA        | NA        |
| 234 | ## | L_c | 9.968487e-07 | 0.575015629 | 0.339490167 | 0.01756374 | NA        | NA        |
| 235 | ## | L_d | 4.283907e-01 | 0.408532106 | 0.339490167 | 0.18243733 | 0.6290323 | NA        |
| 236 | ## | L_m | 3.394902e-01 | 0.104272082 | 0.035632366 | 0.04610518 | 0.3394902 | 0.7356280 |
| 237 | ## | L_n | 7.356280e-01 | 0.135600896 | 0.113185867 | 0.20464047 | 0.3394902 | 0.6130469 |
| 238 | ## |     | L_m          |             |             |            |           |           |
| 239 | ## | H_d |              | NA          |             |            |           |           |
| 240 | ## | H_m |              | NA          |             |            |           |           |
| 241 | ## | H_n |              | NA          |             |            |           |           |
| 242 | ## | L_c |              | NA          |             |            |           |           |
| 243 | ## | L_d |              | NA          |             |            |           |           |
| 244 | ## | L_m |              | NA          |             |            |           |           |
| 245 | ## | L_n | 0.9793181    |             |             |            |           |           |

246 **Table A4.** P-Values for Pairwise Wilcox test for *Vaccinium sp.*

VAAM\_wt\_pframe

|     |    |     |              |              |            |           |           |           |     |    |     |    |     |
|-----|----|-----|--------------|--------------|------------|-----------|-----------|-----------|-----|----|-----|----|-----|
| 247 | ## |     | H_c          |              | H_d        |           | H_m       |           | H_n |    | L_c |    | L_d |
| 248 | ## | H_d | 6.927476e-07 |              | NA         |           | NA        |           | NA  |    | NA  |    | NA  |
| 249 | ## | H_m | 1.873071e-05 | 0.3507908097 |            | NA        |           | NA        |     | NA |     | NA | NA  |
| 250 | ## | H_n | 7.349944e-01 | 0.0763626626 | 0.20662594 |           | NA        |           | NA  |    | NA  |    | NA  |
| 251 | ## | L_c | 9.360567e-03 | 0.0001889474 | 0.00652134 | 0.9333849 |           | NA        |     | NA |     | NA | NA  |
| 252 | ## | L_d | 4.632609e-01 | 0.0528171906 | 0.24486419 | 0.9654529 | 0.8776301 |           |     |    |     | NA | NA  |
| 253 | ## | L_m | 9.360567e-03 | 0.1187779551 | 0.46326089 | 0.4632609 | 0.1814597 | 0.5917751 |     |    |     |    |     |
| 254 | ## | L_n | 9.802611e-01 | 0.0040257523 | 0.01772142 | 0.8162312 | 0.4632609 | 0.4632609 |     |    |     |    |     |
| 255 | ## |     | L_m          |              |            |           |           |           |     |    |     |    |     |
| 256 | ## | H_d |              | NA           |            |           |           |           |     |    |     |    |     |
| 257 | ## | H_m |              | NA           |            |           |           |           |     |    |     |    |     |
| 258 | ## | H_n |              | NA           |            |           |           |           |     |    |     |    |     |
| 259 | ## | L_c |              | NA           |            |           |           |           |     |    |     |    |     |
| 260 | ## | L_d |              | NA           |            |           |           |           |     |    |     |    |     |
| 261 | ## | L_m |              | NA           |            |           |           |           |     |    |     |    |     |
| 262 | ## | L_n | 0.1248045    |              |            |           |           |           |     |    |     |    |     |