Analyse des grilles d'évaluation RDA SHARC

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This is an R Markdown Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Cmd+Shift+Enter*.

Import et nettoyage des données

```
data <- read.csv2("clean_data.csv", header = TRUE, sep = ",", row.names = "Code") %>%
  mutate(Cluster=factor(Cluster, levels = c("Findable", "Accessible", "Interoperable", "Reusable")))

data_wide <- data %>%
  filter (Cluster != "NA")
```

Classons les réponses possibles à chaque critère

```
cols <- c("GenTree", "Phénotypage.DROPS", "Carbone.talveg", "Données.Lidar", "Herbier.de.Guyane", "Rhiz

data_wide[,cols] <- lapply(data_wide[,cols], factor, levels = c("Never", "Mandatory", "Sometimes", "Alw

data_wide[,cols] <- lapply(data_wide[,cols], fct_explicit_na, na_level = "NA")

data_wide[,cols] <- lapply(data_wide[,cols], factor, levels = c("NA", "Never", "Mandatory", "Sometimes"
```

Passons de données wide à des données narrow

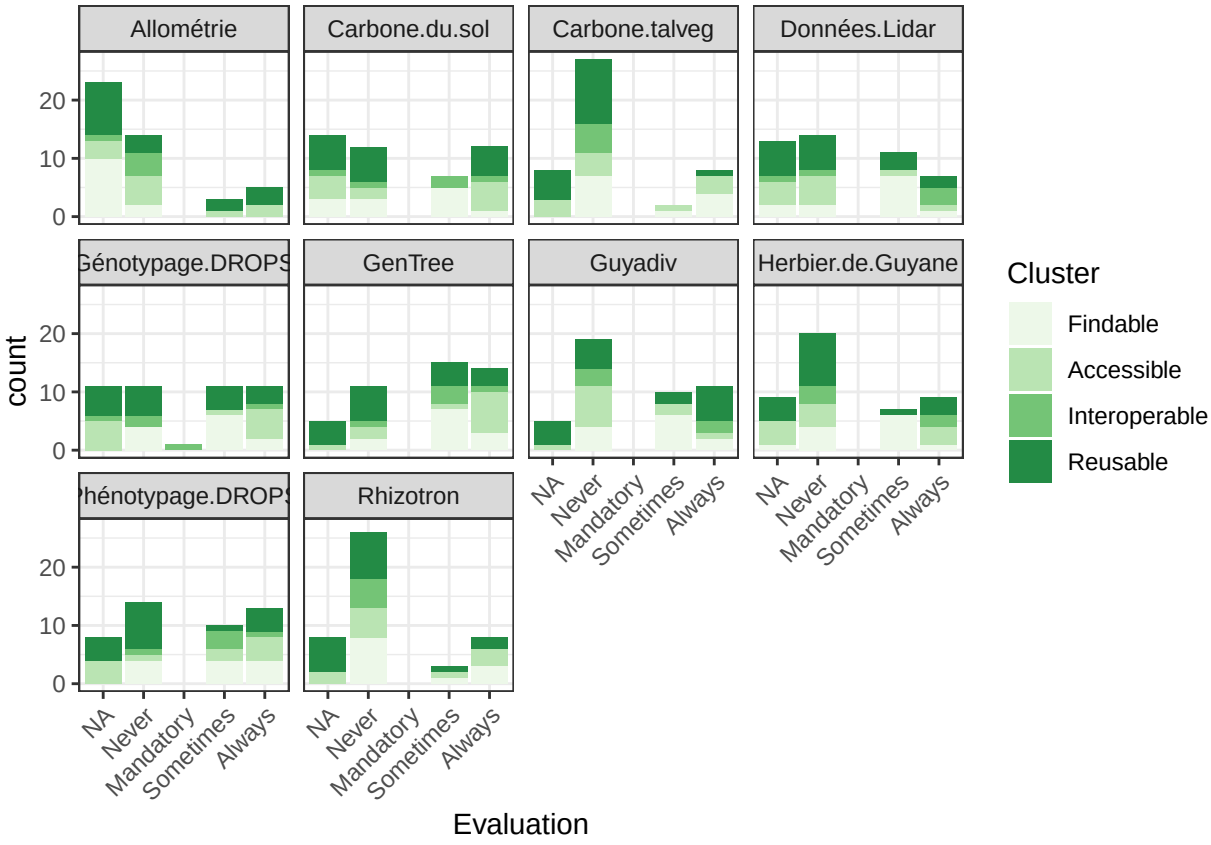
```
data_narrow <- data_wide %>%
  pivot_longer (cols = cols, names_to = "Dataset", values_to = "Evaluation") %>%
  mutate(Dataset=factor(Dataset))
```

```
## Note: Using an external vector in selections is ambiguous.
## i Use `all_of(cols)` instead of `cols` to silence this message.
## i See <https://tidyselect.r-lib.org/reference/faq-external-vector.html>.
## This message is displayed once per session.
```

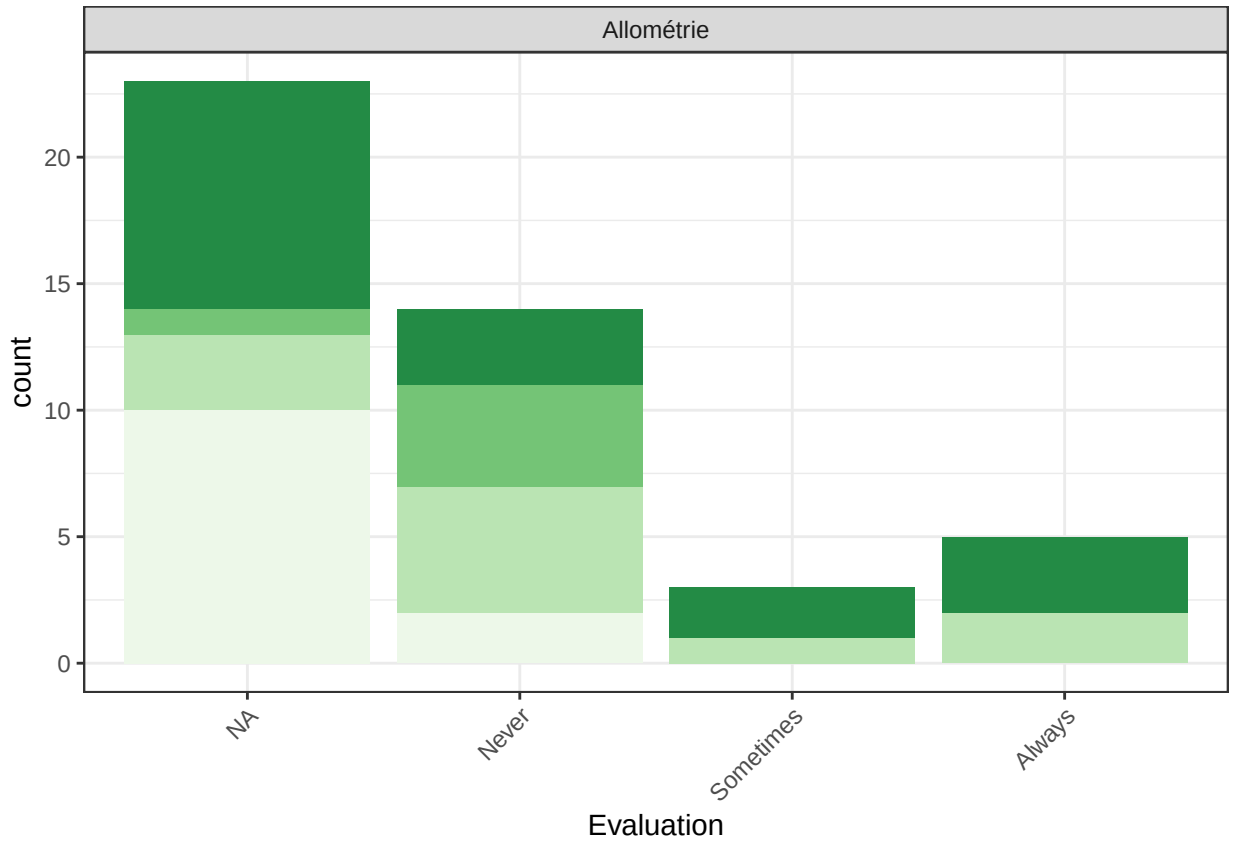
Représentons graphiquement les réponses à chaque critère

```
data_narrow %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
```

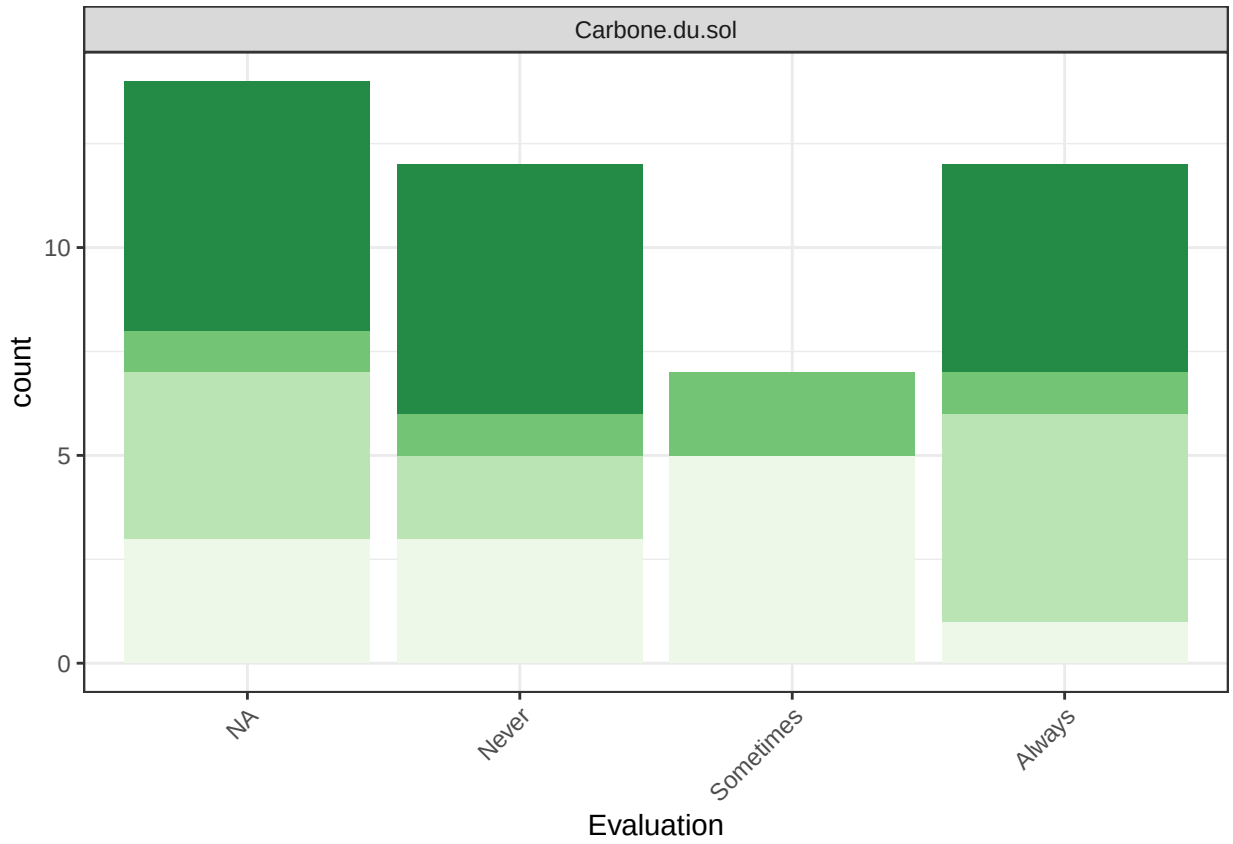
```
    scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))
```



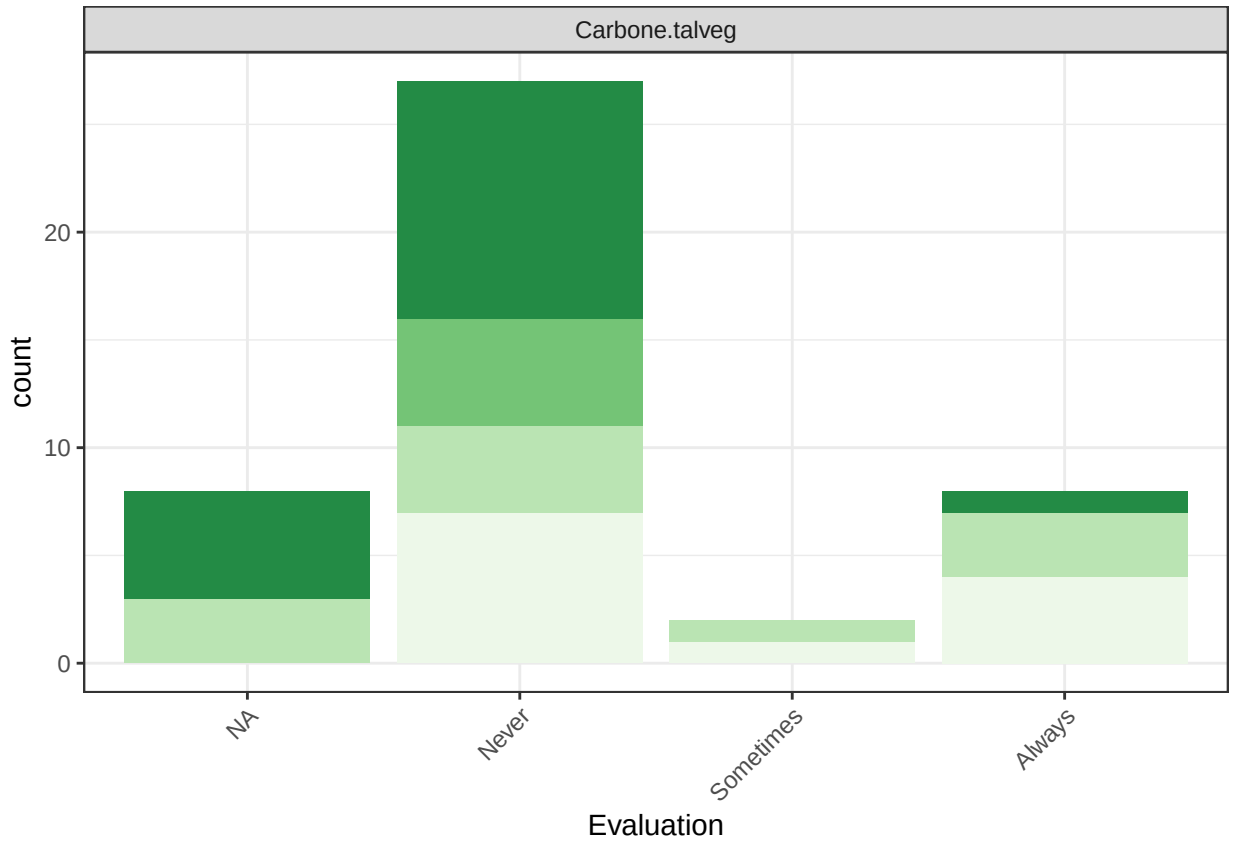

```
data_narrow %>%
  filter(Dataset == "Allométrie") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```



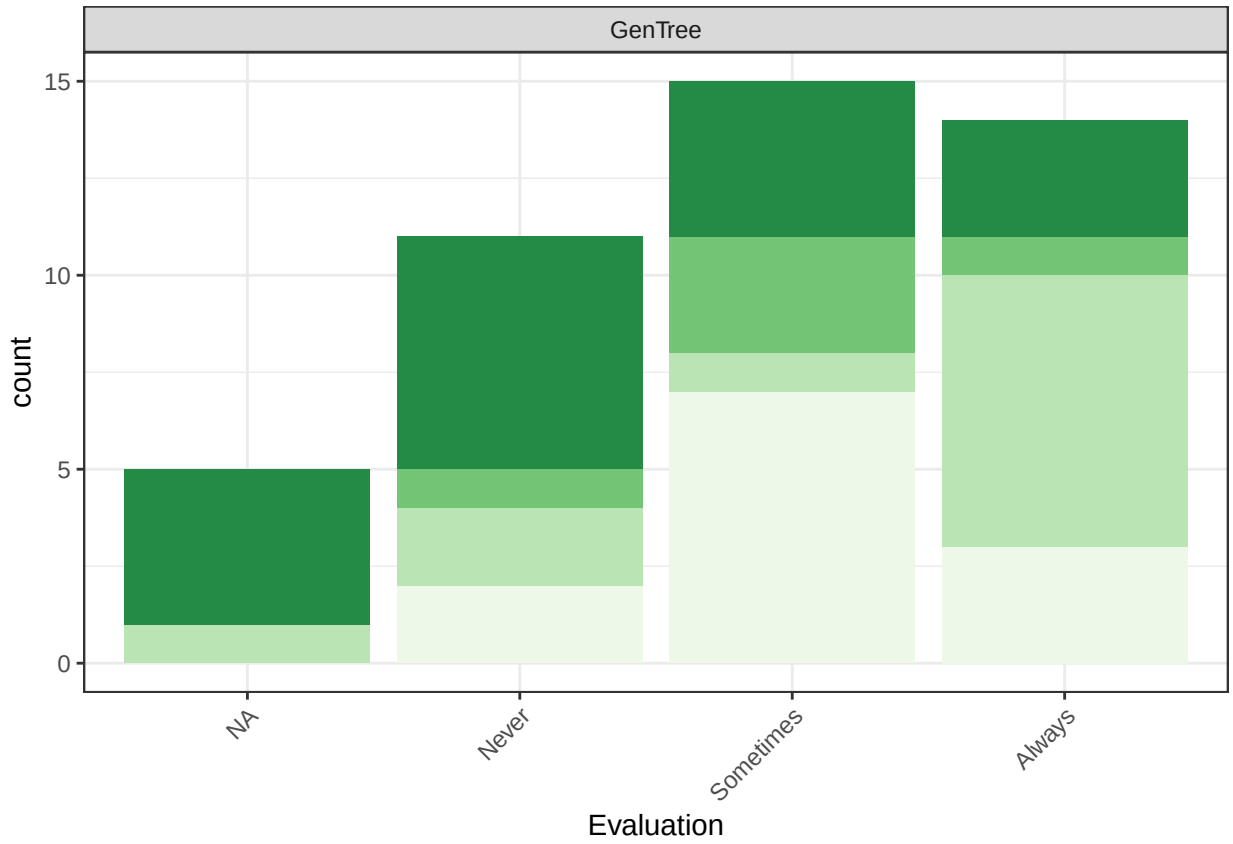

```
data_narrow %>%
  filter(Dataset == "Carbone.du.sol") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```



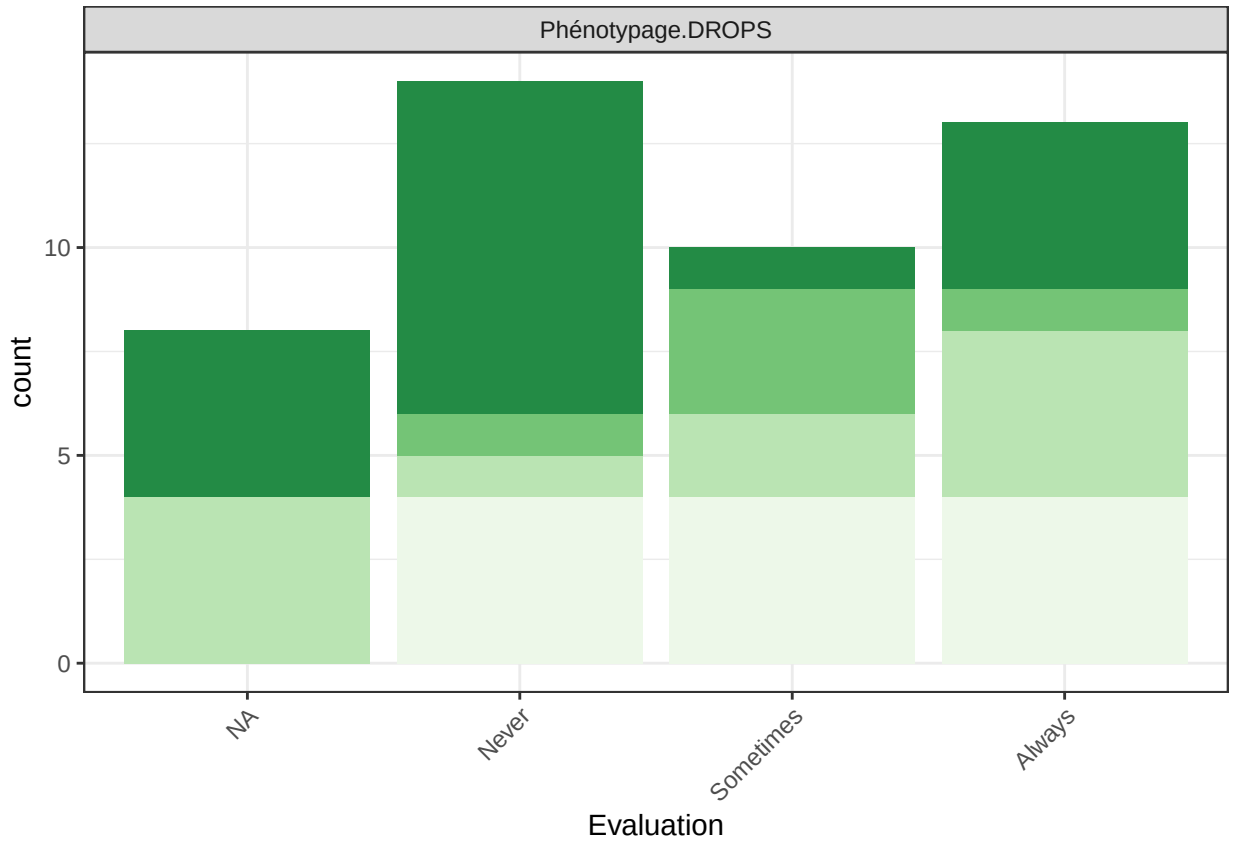

```
data_narrow %>%
  filter(Dataset == "Carbone.talveg") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```



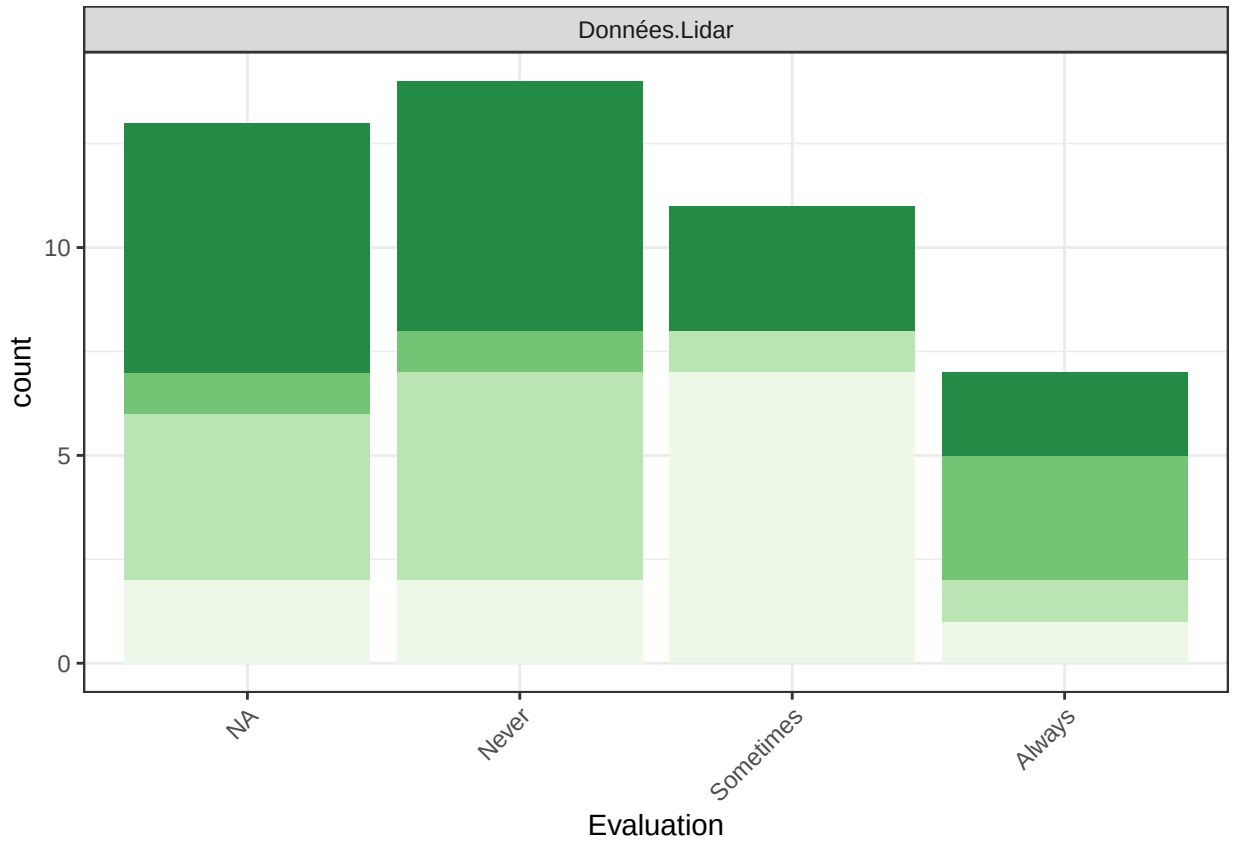

```
data_narrow %>%
  filter(Dataset == "GenTree") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```



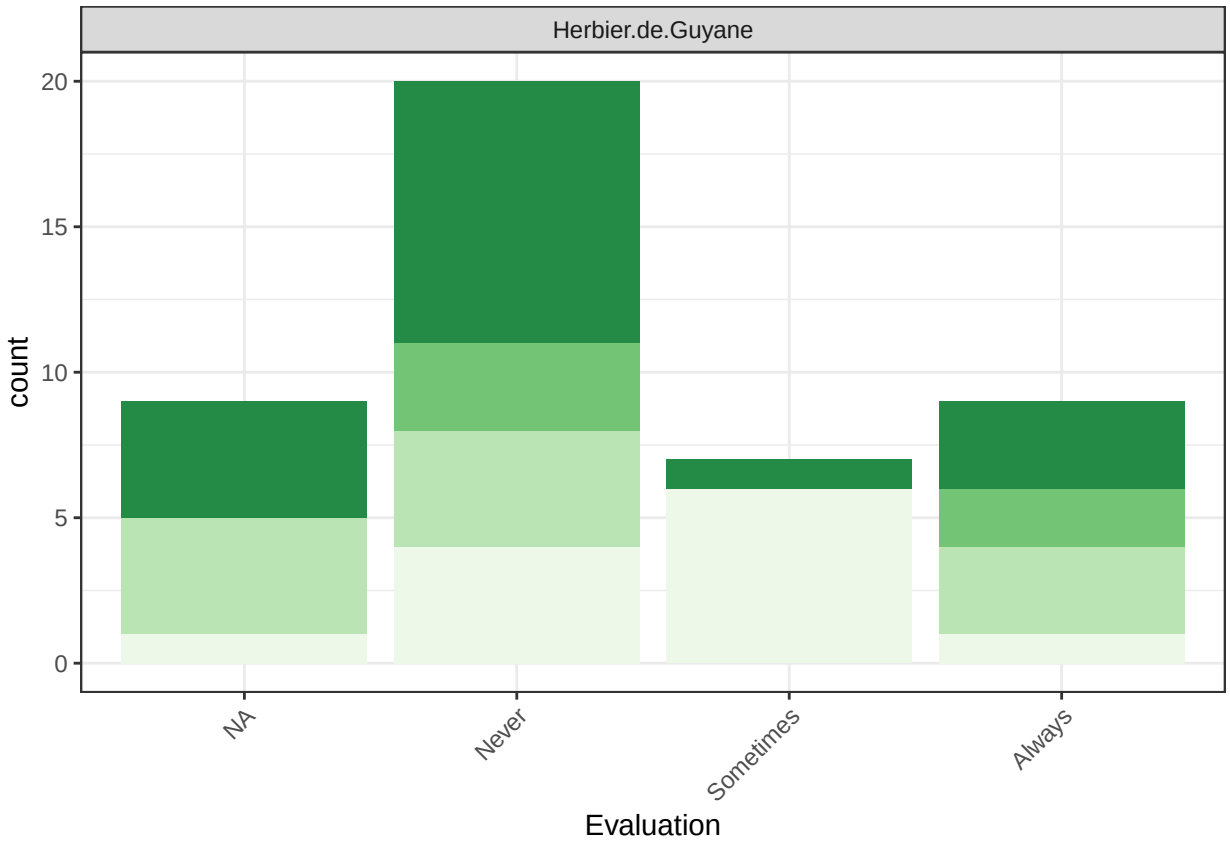

```
data_narrow %>%
  filter(Dataset == "Phénotypage.DROPS") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```



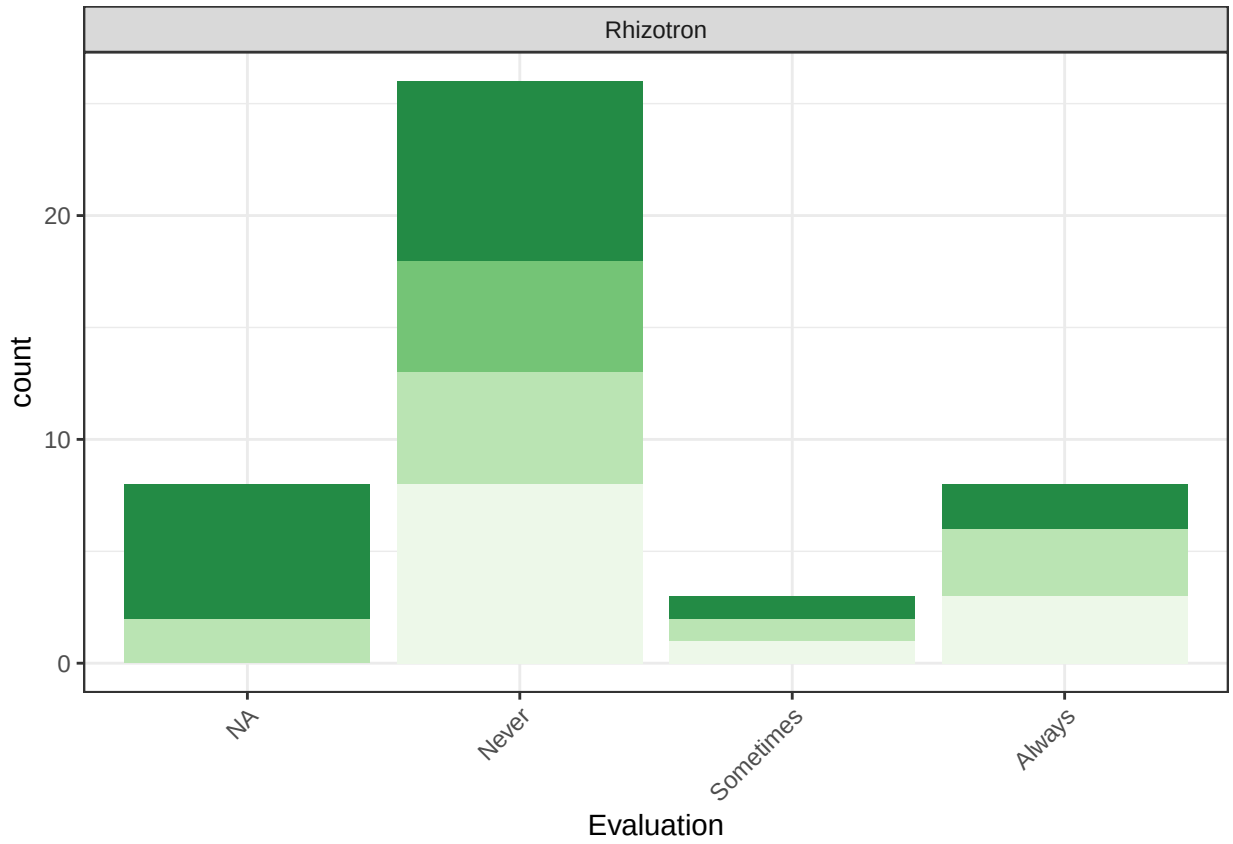

```
data_narrow %>%
  filter(Dataset == "Données.Lidar") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```



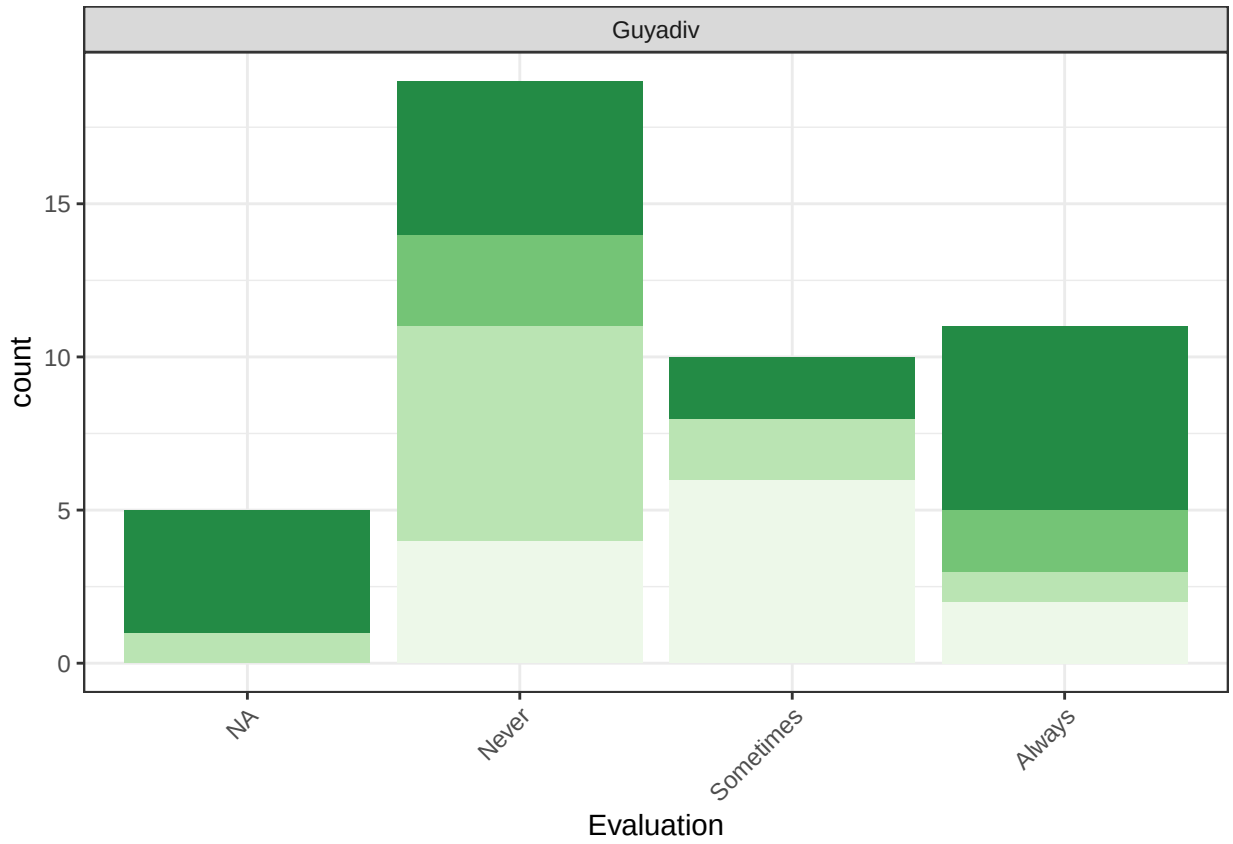

```
data_narrow %>%
  filter(Dataset == "Herbier.de.Guyane") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```



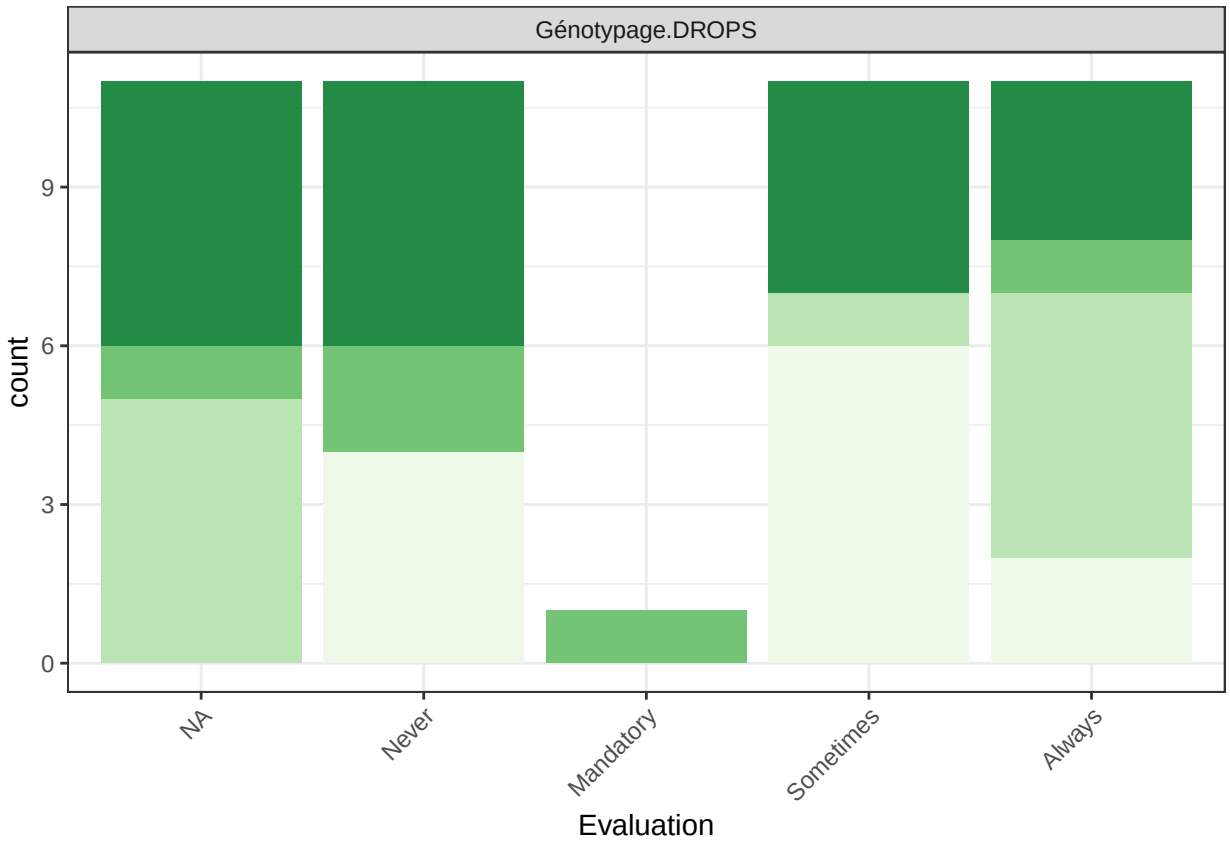

```
data_narrow %>%
  filter(Dataset == "Rhizotron") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```




```
data_narrow %>%
  filter(Dataset == "Guyadiv") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```




```
data_narrow %>%
  filter(Dataset == "Génotypage.DROPS") %>%
  ggplot(aes(x = Evaluation, fill = Cluster)) +
  geom_bar(position = position_stack(reverse = TRUE)) +
  facet_wrap(~ Dataset, ncol = 4) +
  scale_fill_manual(values = brewer.pal(4, "Greens")) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  theme(legend.position = "none")
```


Génotypage.DROPS
count
9
6
3
0
NA
Never
Mandatory
Sometimes
Always
Evaluation