

# Plant analysis data

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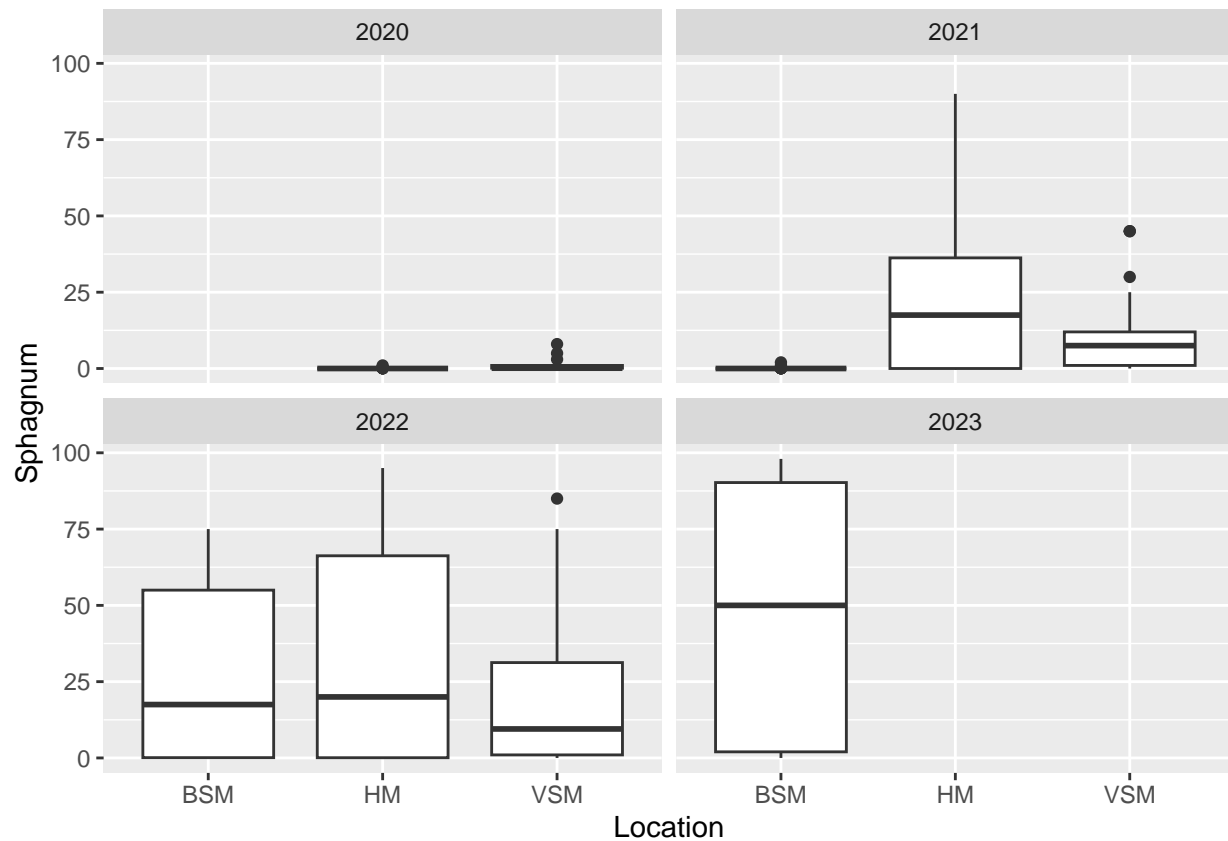
Upload and clean dataset

## Investigating data

### Sphagnum

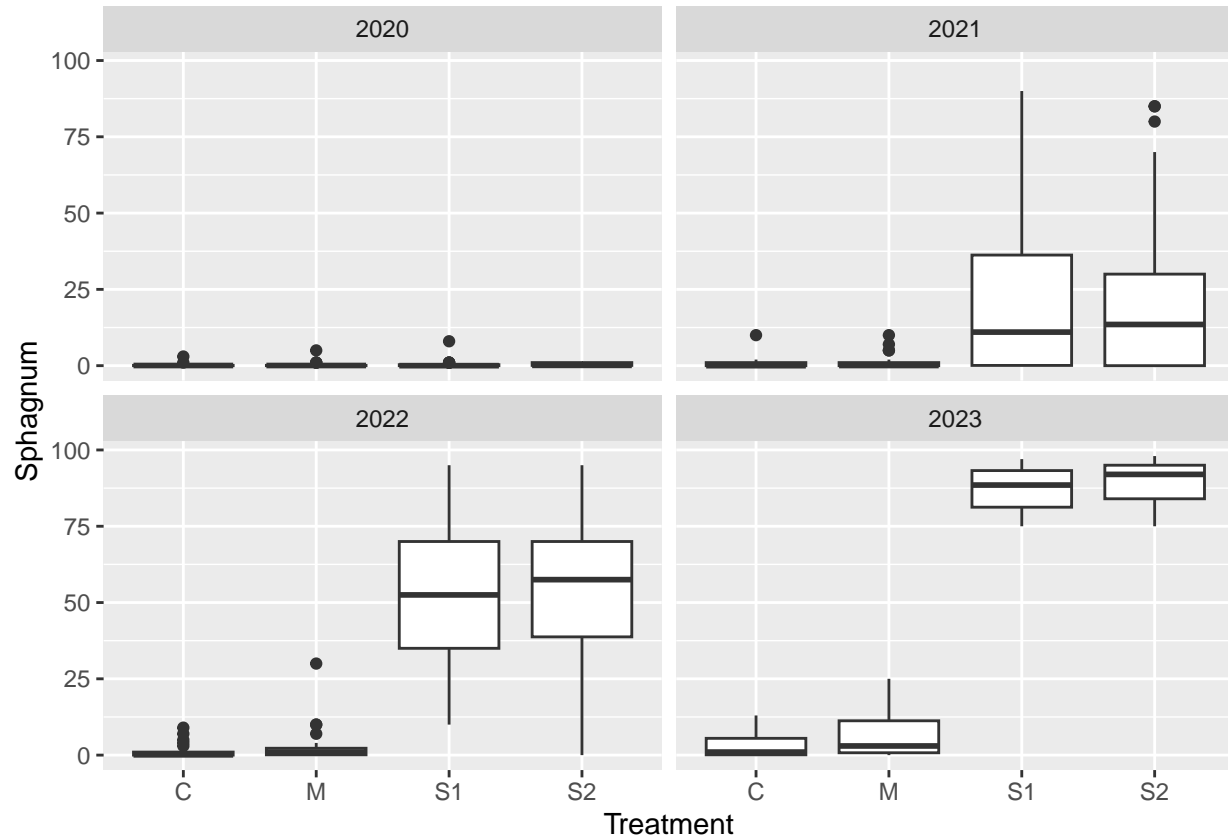
*Overall Sphagnum cover changes per location*

```
reveg%>%  
  filter(Treatment!='Ref1' & Treatment!='Ref2')%>%  
  ggplot(aes(x = Location, y = Sphagnum)) +  
  geom_boxplot() +  
  facet_wrap(vars(year))
```



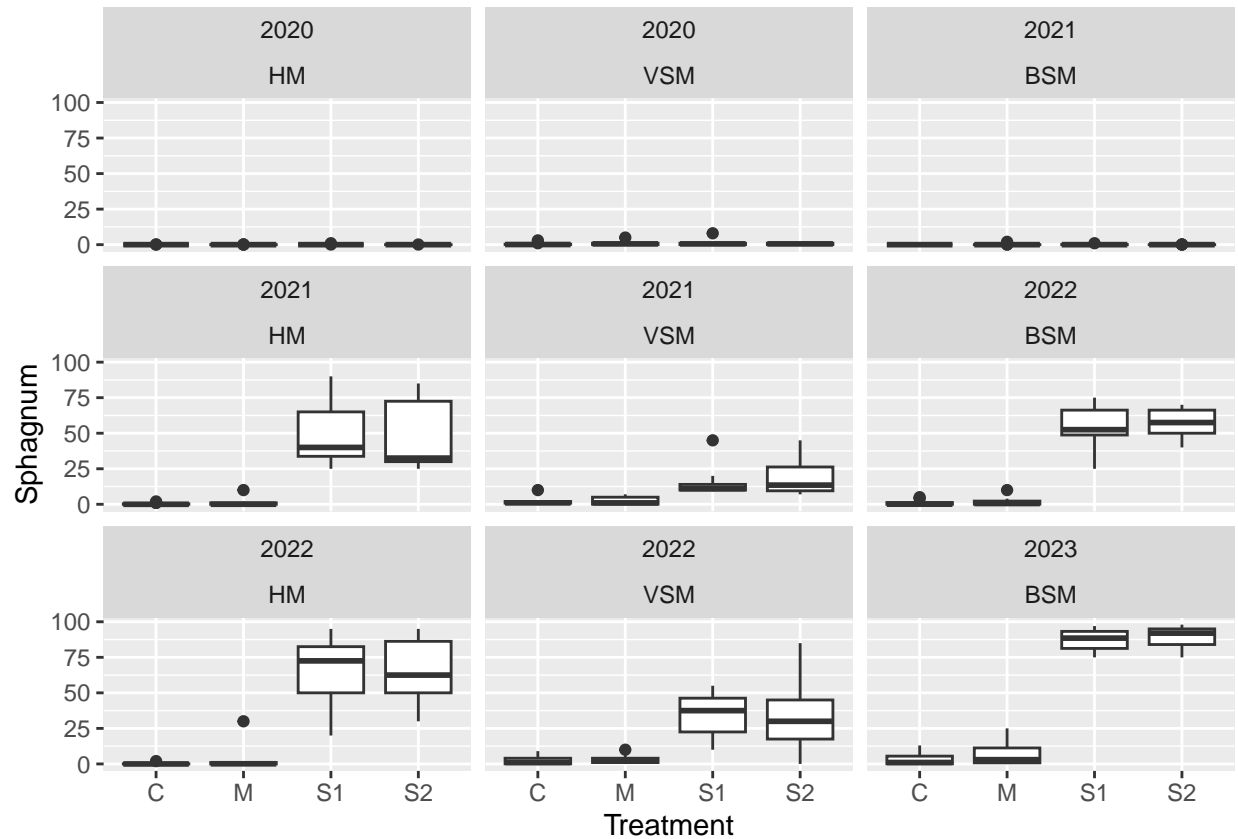
### *Sphagnum cover changes per treatment*

```
reveg%>%
  filter(Treatment!='Ref1' & Treatment!='Ref2')%>%
  ggplot(aes(x = Treatment, y = Sphagnum)) +
  geom_boxplot() +
  facet_wrap(vars(year))
```



### *Sphagnum cover changes per treatment and location*

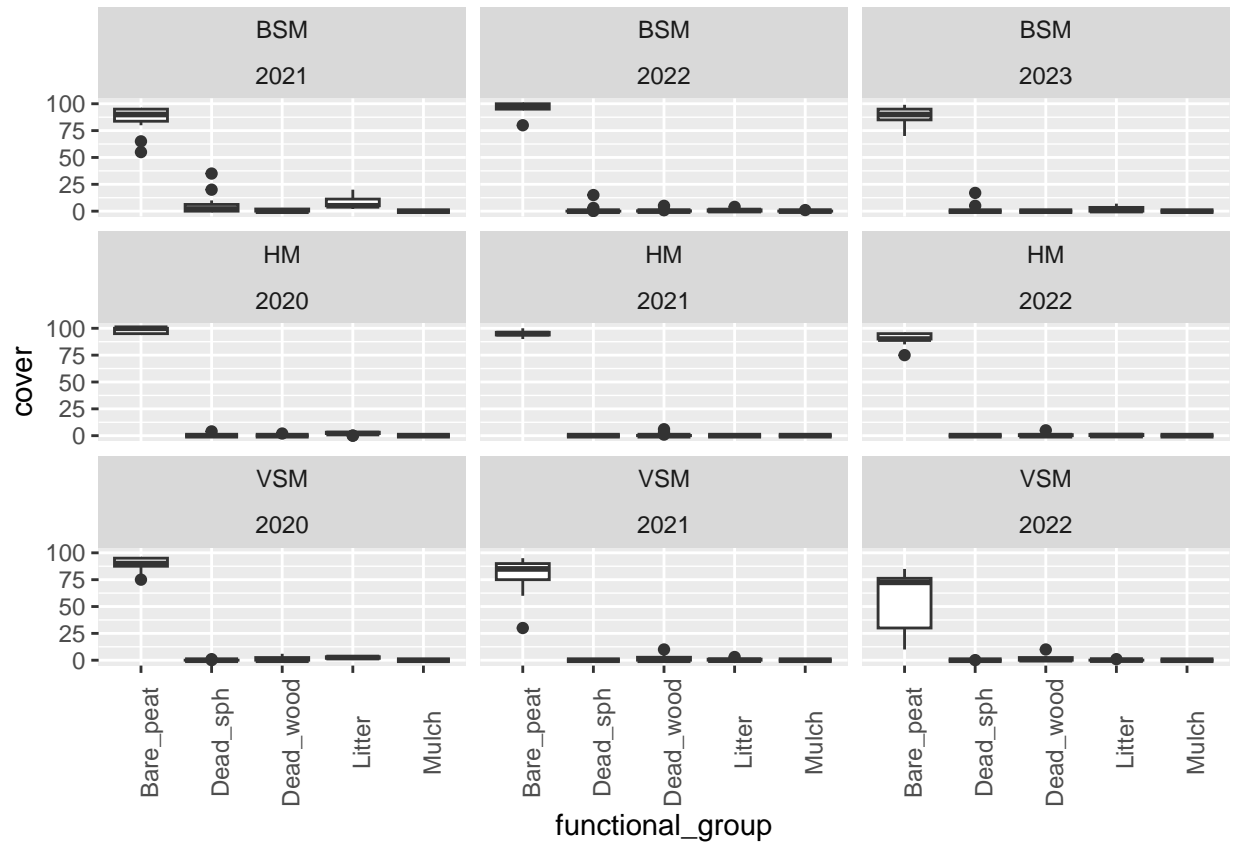
```
reveg%>%
  filter(Treatment!='Ref1' & Treatment!='Ref2')%>%
  ggplot(aes(x = Treatment, y = Sphagnum)) +
  geom_boxplot() +
  facet_wrap(vars(year, Location))
```



## Changes in other functional groups than plants

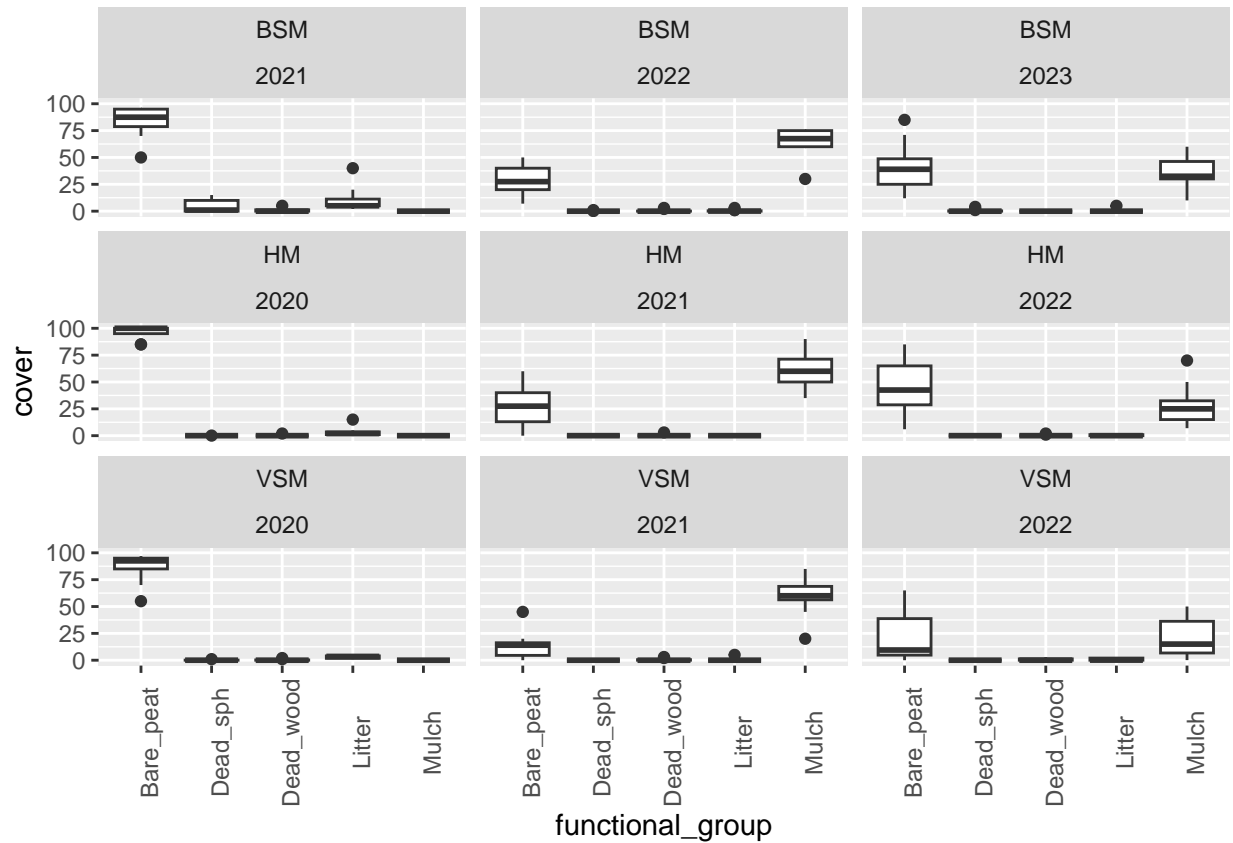
*Changes in cover in control plots per location*

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment=='C')%>%
  filter(functional_group %in% c('Dead_sph', 'Bare_peat', 'Litter', 'Mulch', 'Dead_wood'))%>%
  ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



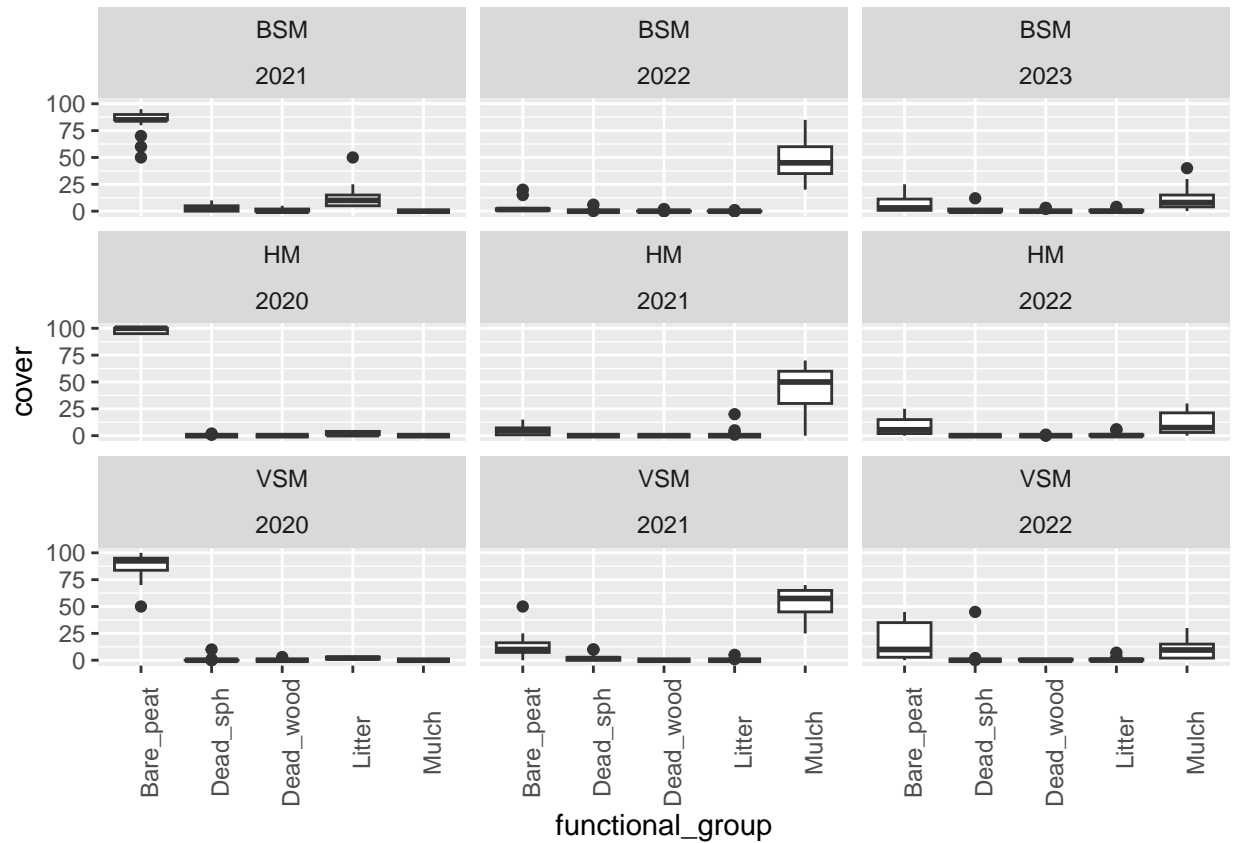
*Changes in cover in mulch plots per location*

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment=="M")%>%
  filter(functional_group %in% c('Dead_sph', 'Bare_peat', 'Litter', 'Mulch', 'Dead_wood'))%>%
ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



*Changes in cover in sphagnum plots per location*

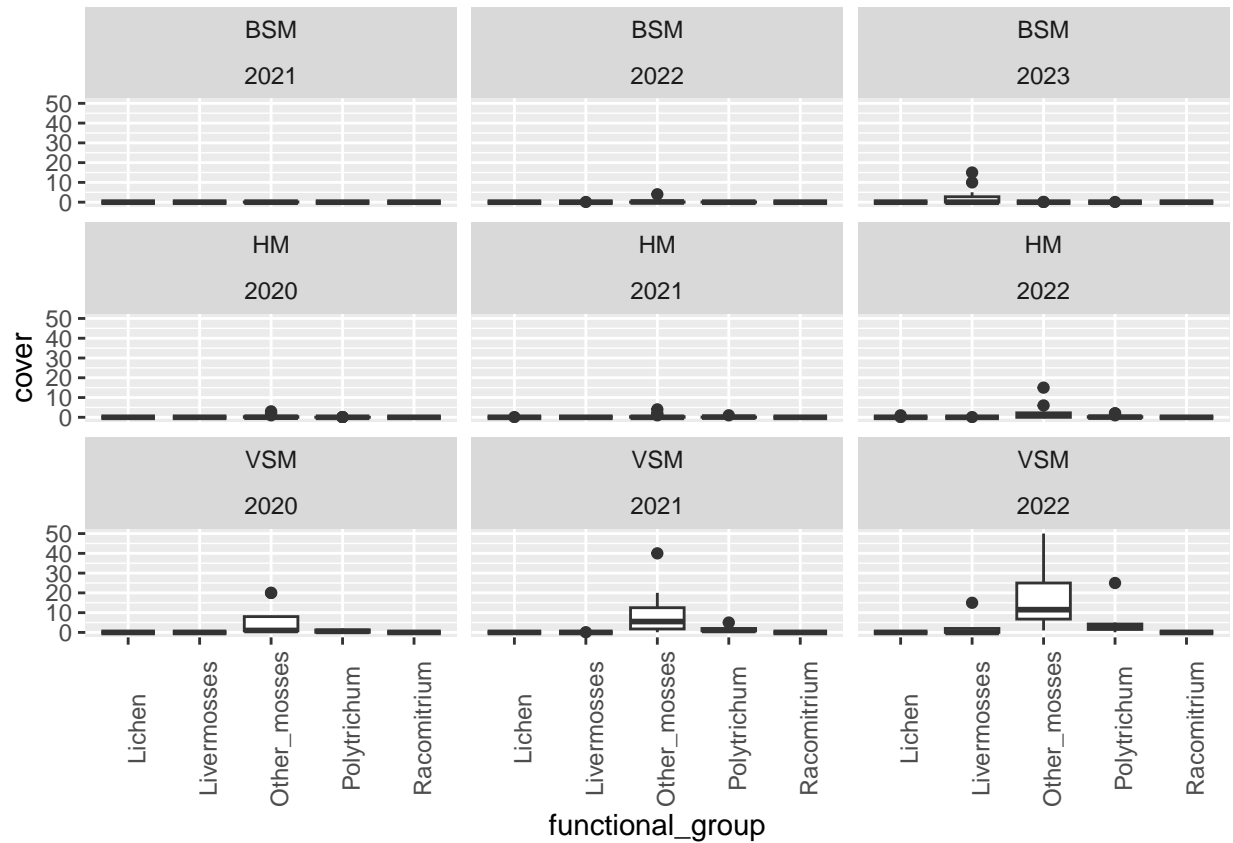
```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment %in% c('S1', 'S2'))%>%
  filter(functional_group %in% c('Dead_sph', 'Bare_peat', 'Litter', 'Mulch', 'Dead_wood'))%>%
  ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



## Changes in other functional plant groups - mosses and lichen

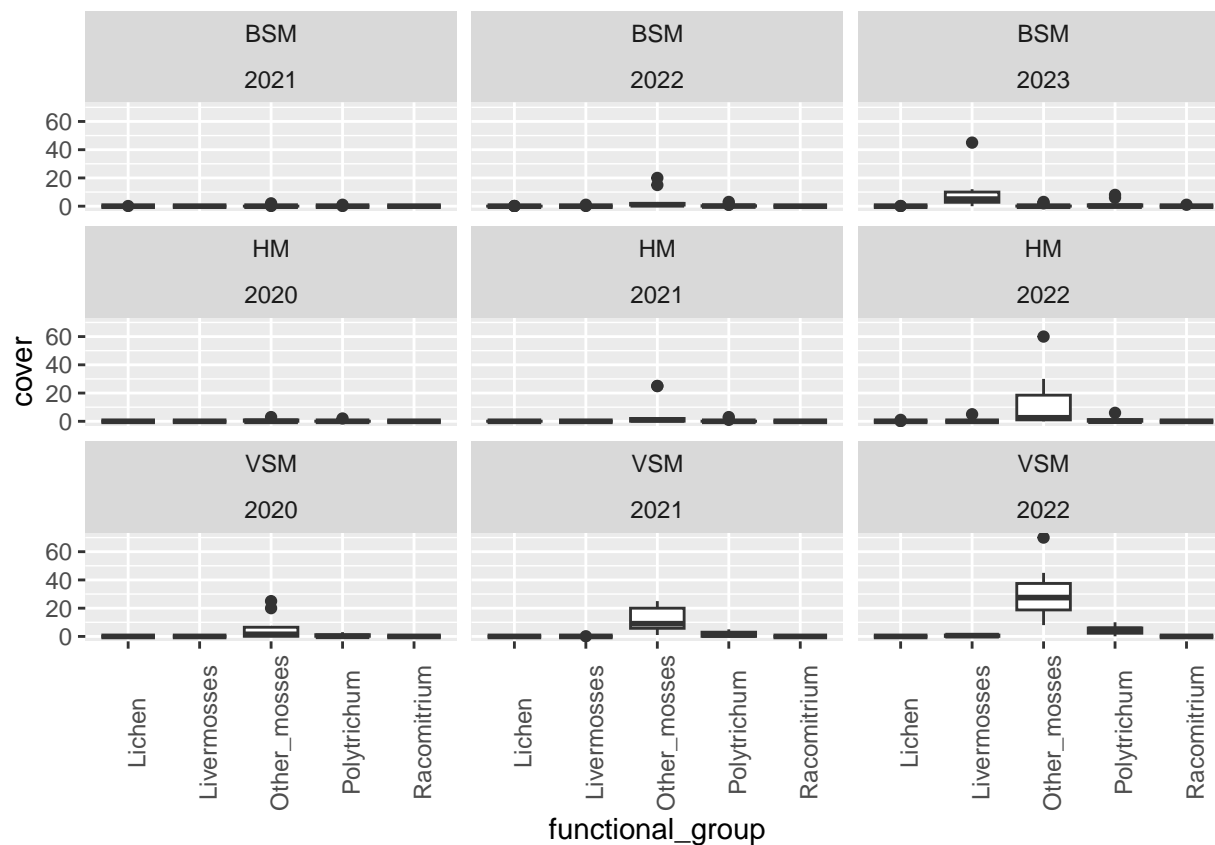
*Changes in cover in control plots per location*

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment=="C")%>%
  filter(functional_group %in% c('Polytrichum', 'Racomitrium', 'Other_mosses', 'Livermosses', 'Lichen'))
ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



*Changes in cover in mulch plots per location*

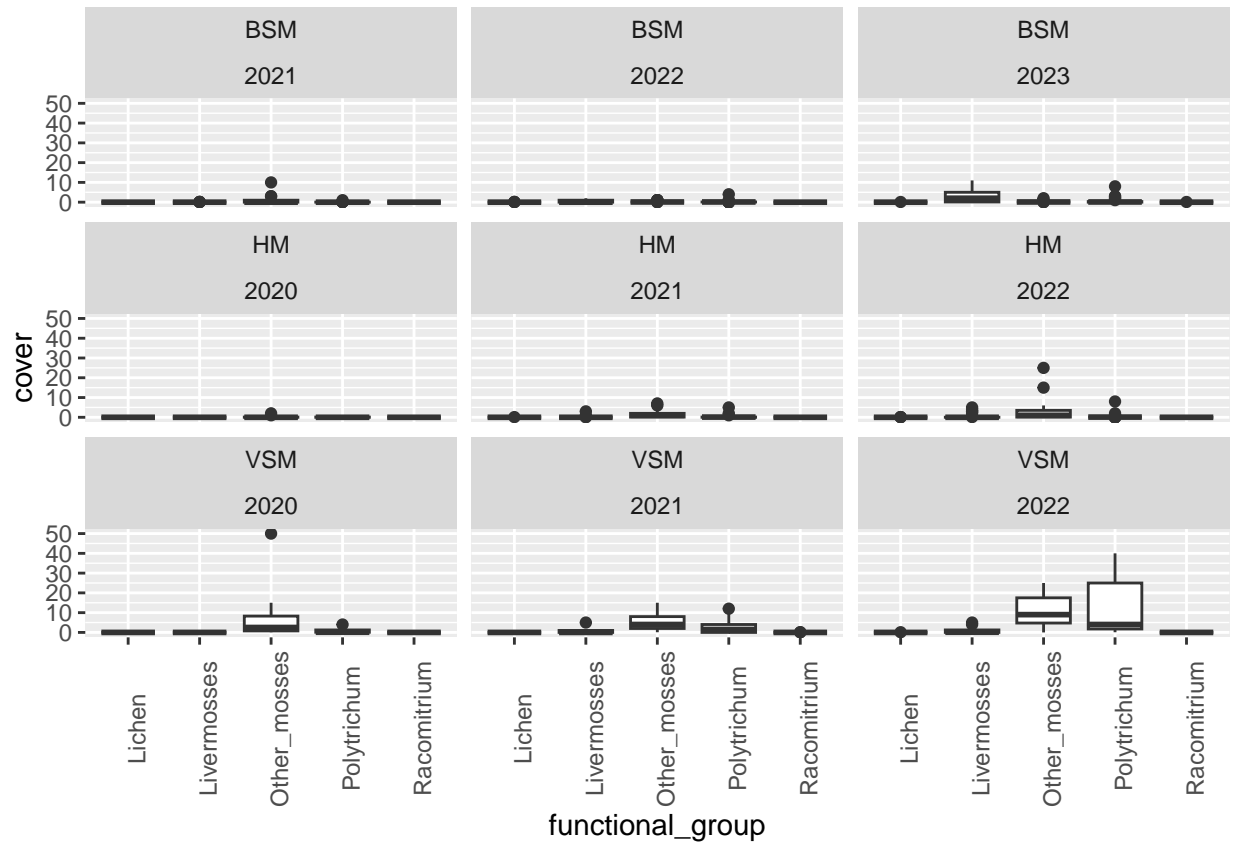
```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment=='M')%>%
  filter(functional_group %in% c('Polytrichum', 'Racomitrium', 'Other_mosses', 'Livermosses', 'Lichen'))
ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



*Changes in cover in sphagnum plots per location*

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment %in% c('S1', 'S2')) %>%
  filter(functional_group %in% c('Polytrichum', 'Racomitrium', 'Other_mosses', 'Livermosses', 'Lichen'))
ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```

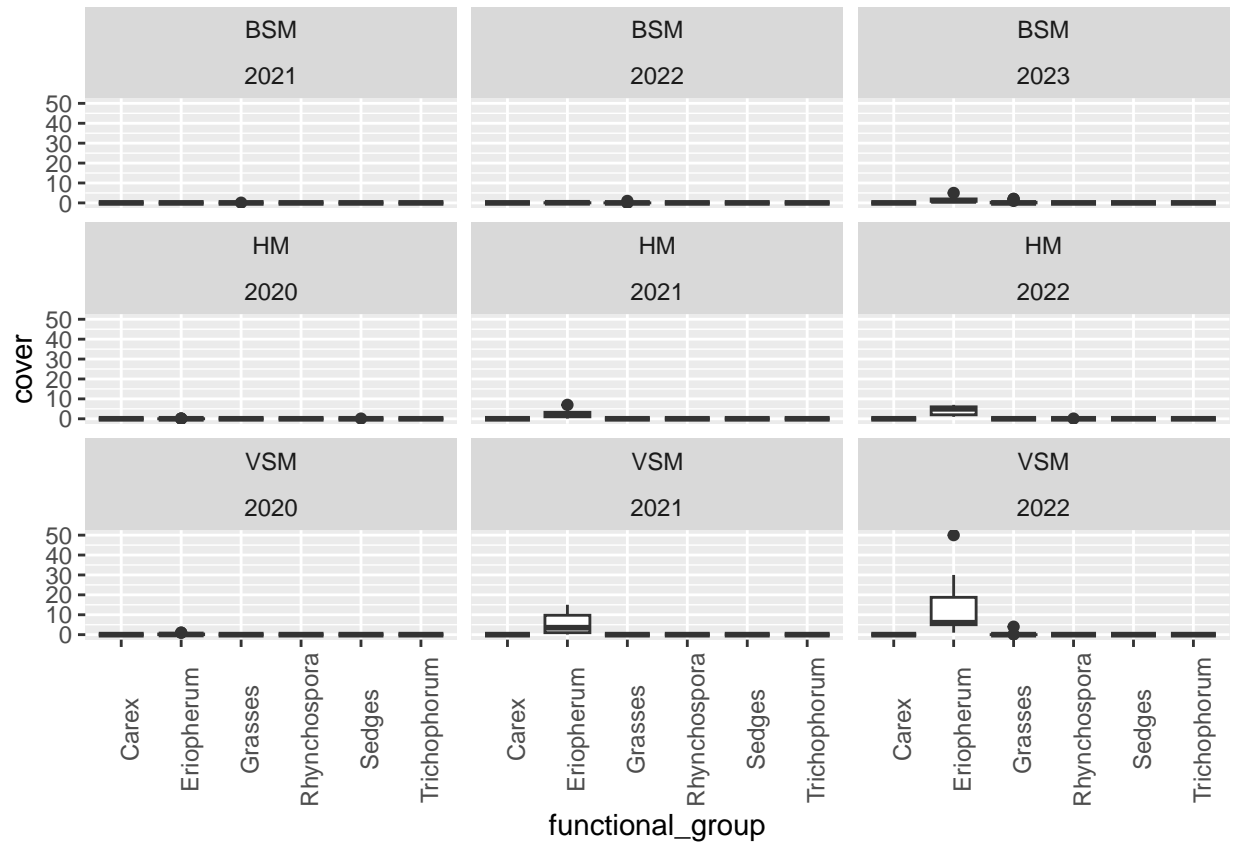




## Changes in other functional plant groups - graminoids

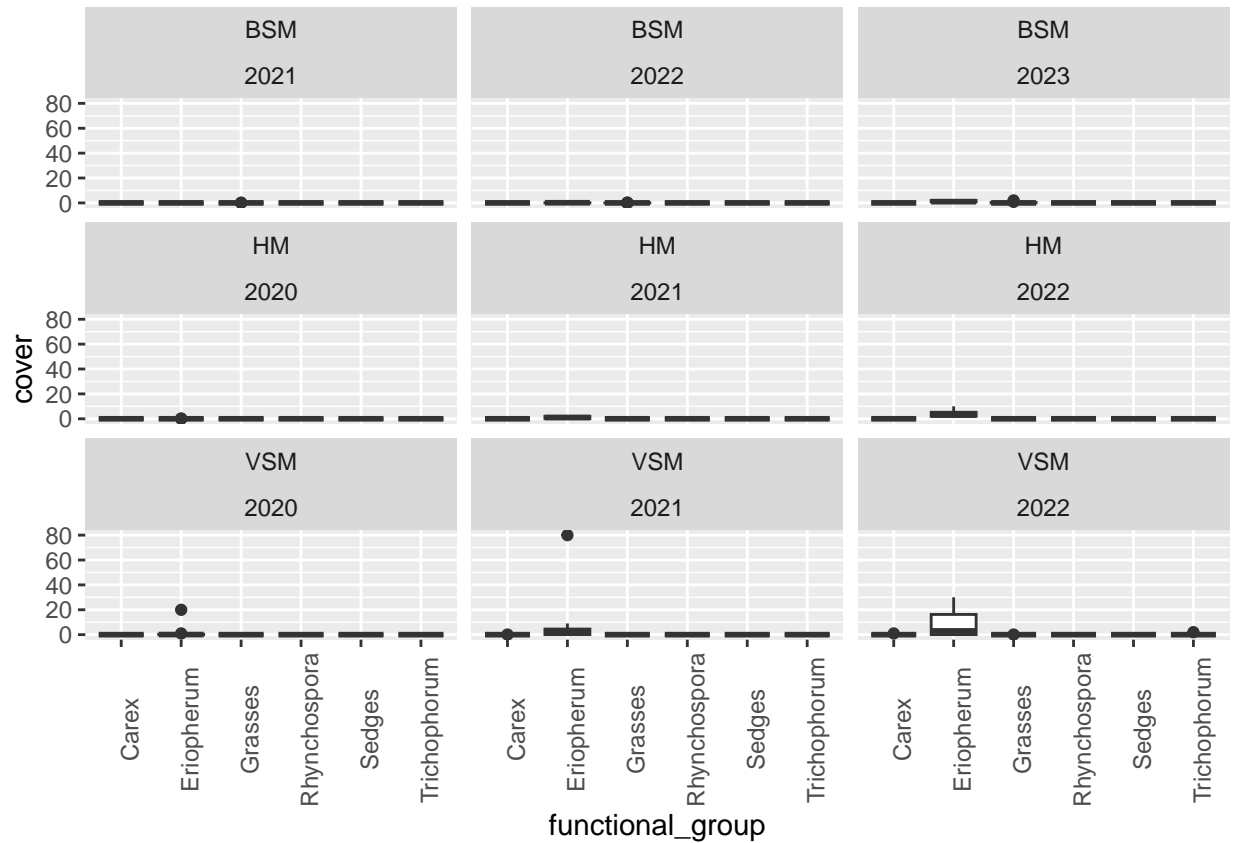
*Changes in cover in control plots per location*

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment=='C')%>%
  filter(functional_group %in% c('Carex', 'Trichophorum', 'Eriophorum', 'Sedges', 'Rhynchospora', 'Grass'))
ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```

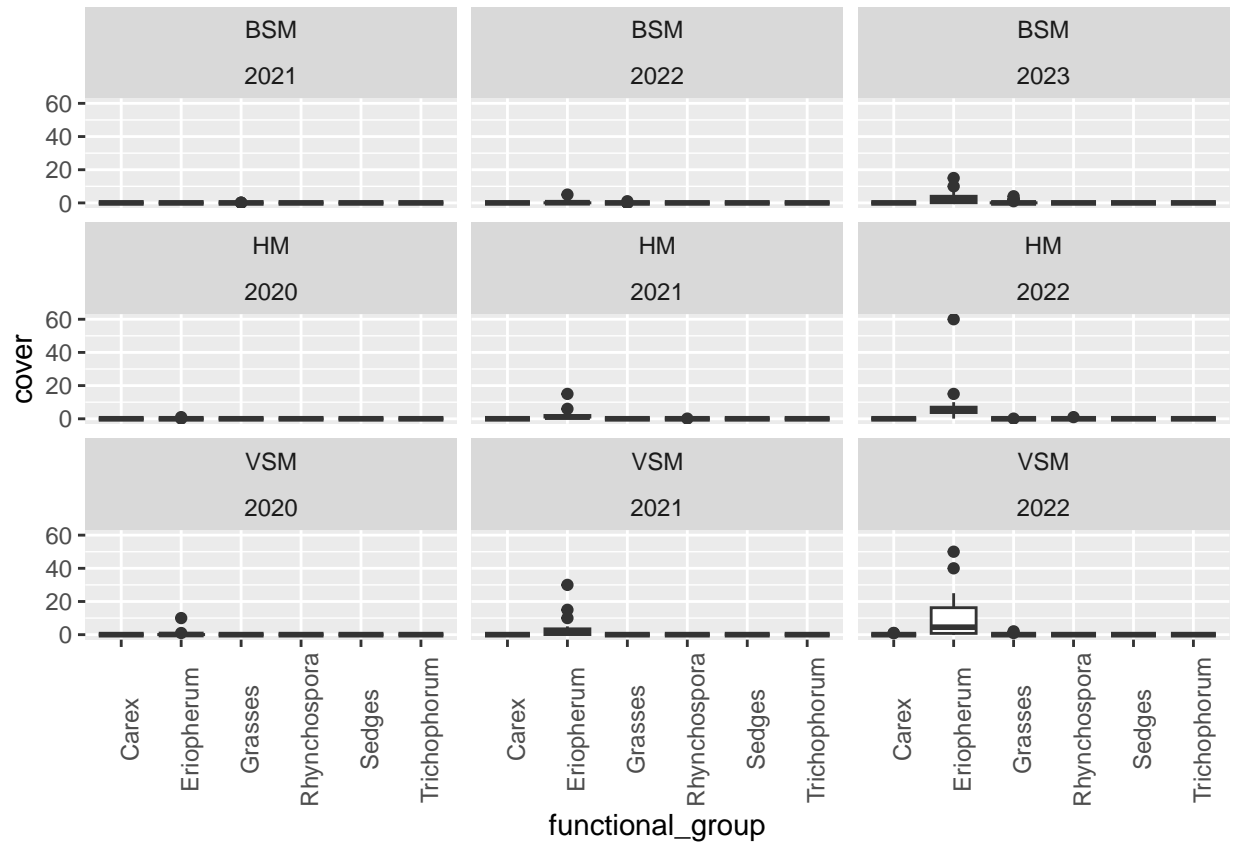


Changes in cover in mulch plots per location

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment=='M')%>%
  filter(functional_group %in% c('Carex', 'Trichophorum', 'Eriophorum', 'Sedges', 'Rhynchospora', 'Grasses'))
ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



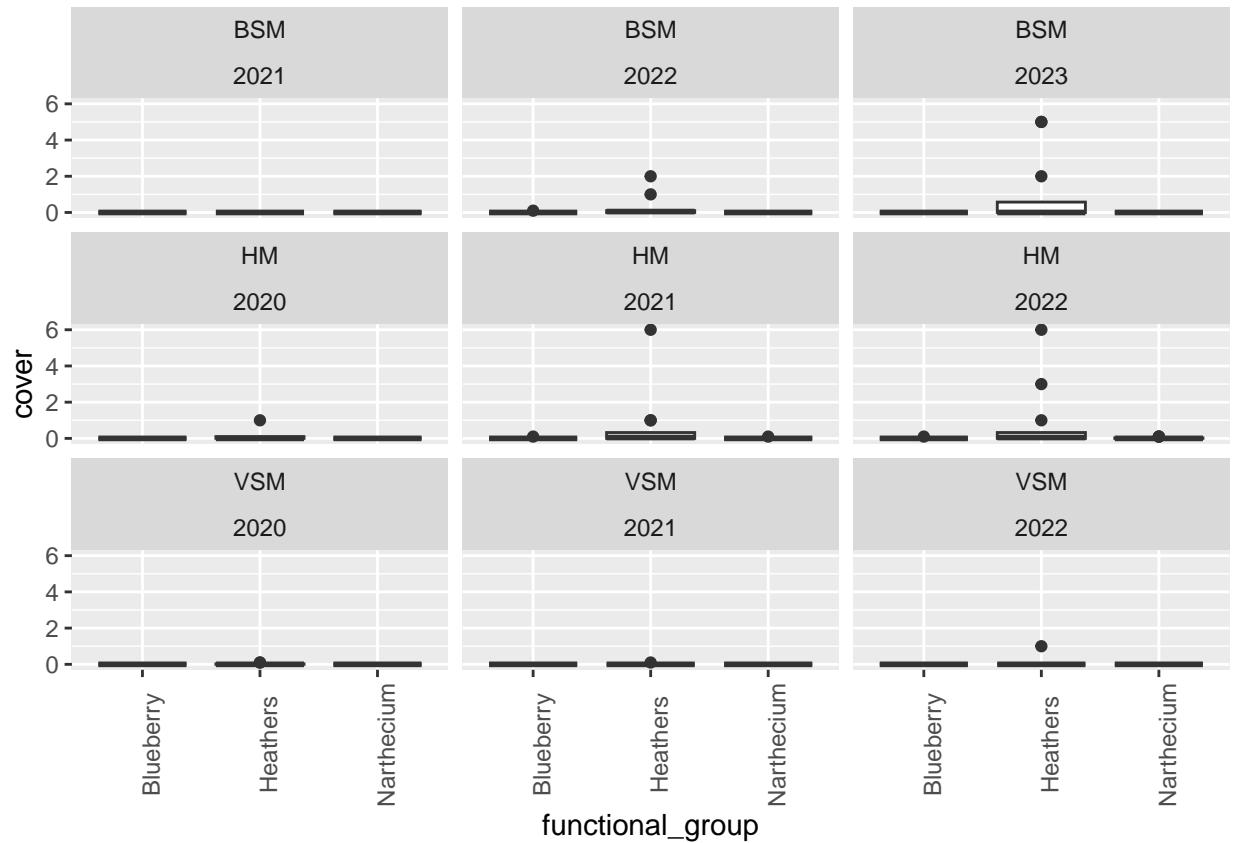
```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment %in% c('S1', 'S2')) %>%
  filter(functional_group %in% c('Carex', 'Trichophorum', 'Eriophorum', 'Sedges', 'Rhynchospora', 'Grasses'))
ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



## Changes in other functional plant groups - heather/vitis-idea, vaccinium-bushes, narthecium

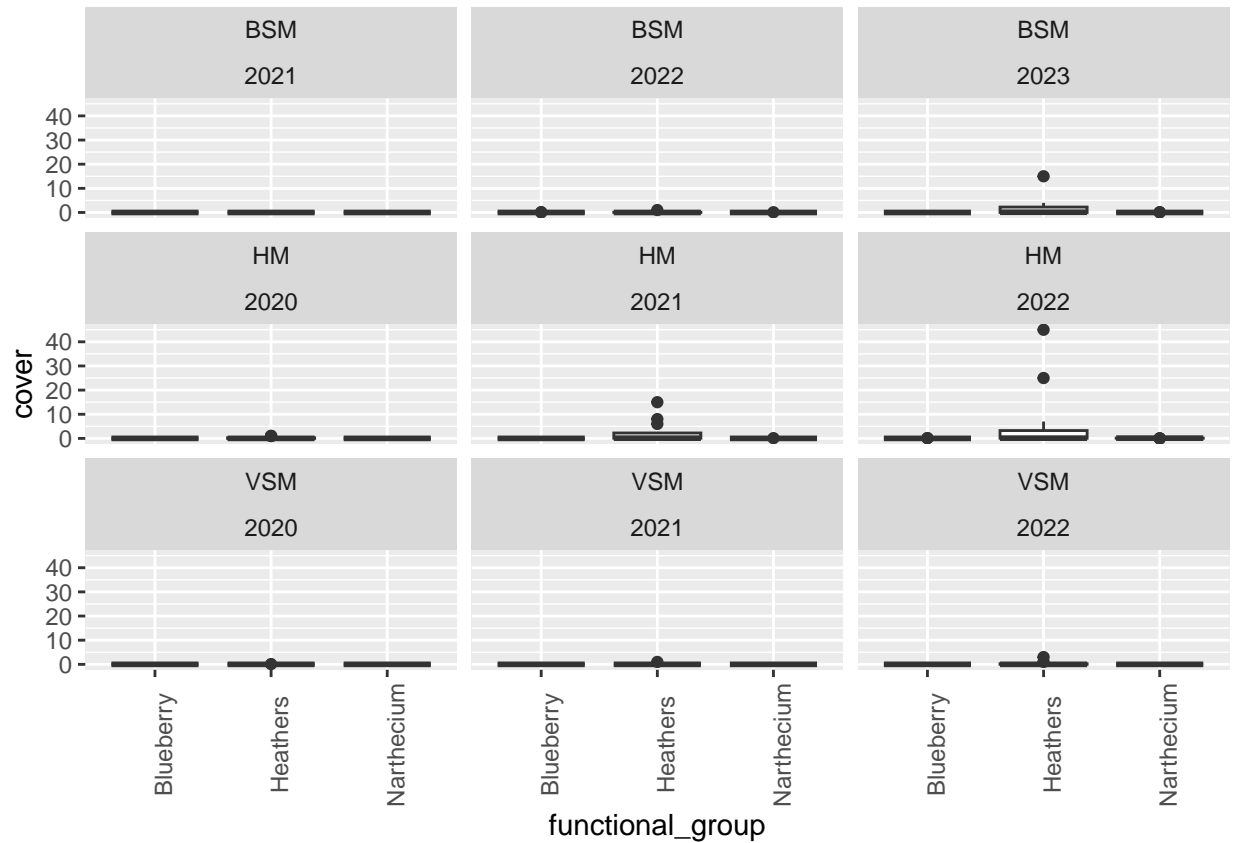
*Changes in cover in control plots per location*

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment=='C')%>%
  filter(functional_group %in% c('Heathers', 'Blueberry', 'Narthecium'))%>%
  ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



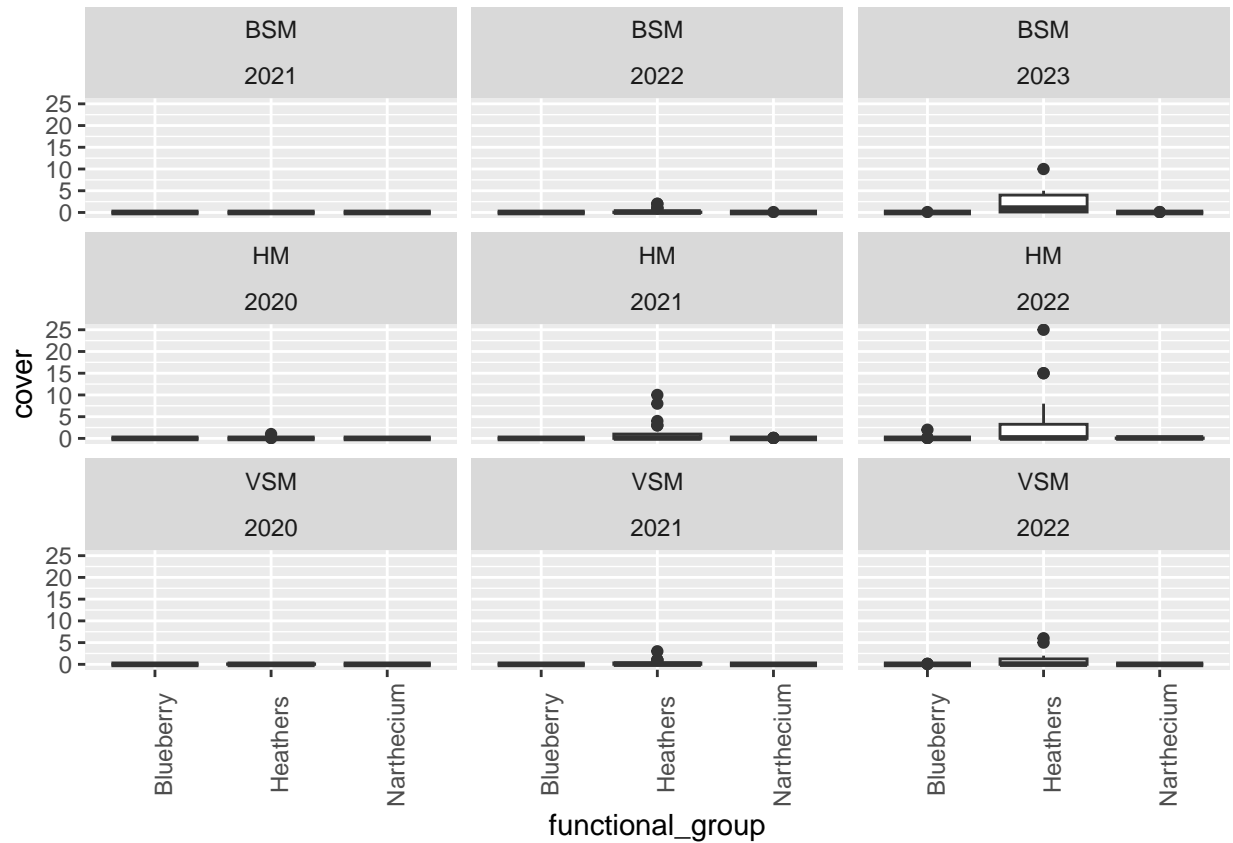
*Changes in cover in mulch plots per location*

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment=='M')%>%
  filter(functional_group %in% c('Heathers', 'Blueberry', 'Narthecium'))%>%
  ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



*Changes in cover in sphagnum plots per location*

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment %in% c('S1', 'S2'))%>%
  filter(functional_group %in% c('Heathers', 'Blueberry', 'Narthecium'))%>%
  ggplot(aes(x = functional_group, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```



*Changes in cover in bare peat only per location*

```
reveg%>%
  pivot_longer(Sphagnum:Temp_water, names_to = 'functional_group', values_to = "cover") %>%
  filter(Treatment!='Ref1' & Treatment!='Ref2')%>%
  filter(functional_group == 'Bare_peat') %>%
ggplot(aes(x = Treatment, y = cover)) +
  geom_boxplot() + theme(axis.text.x = element_text(angle = 90)) +
  facet_wrap(vars(Location, year))
```

