

Microbial diversity

Jonas Gehrlein

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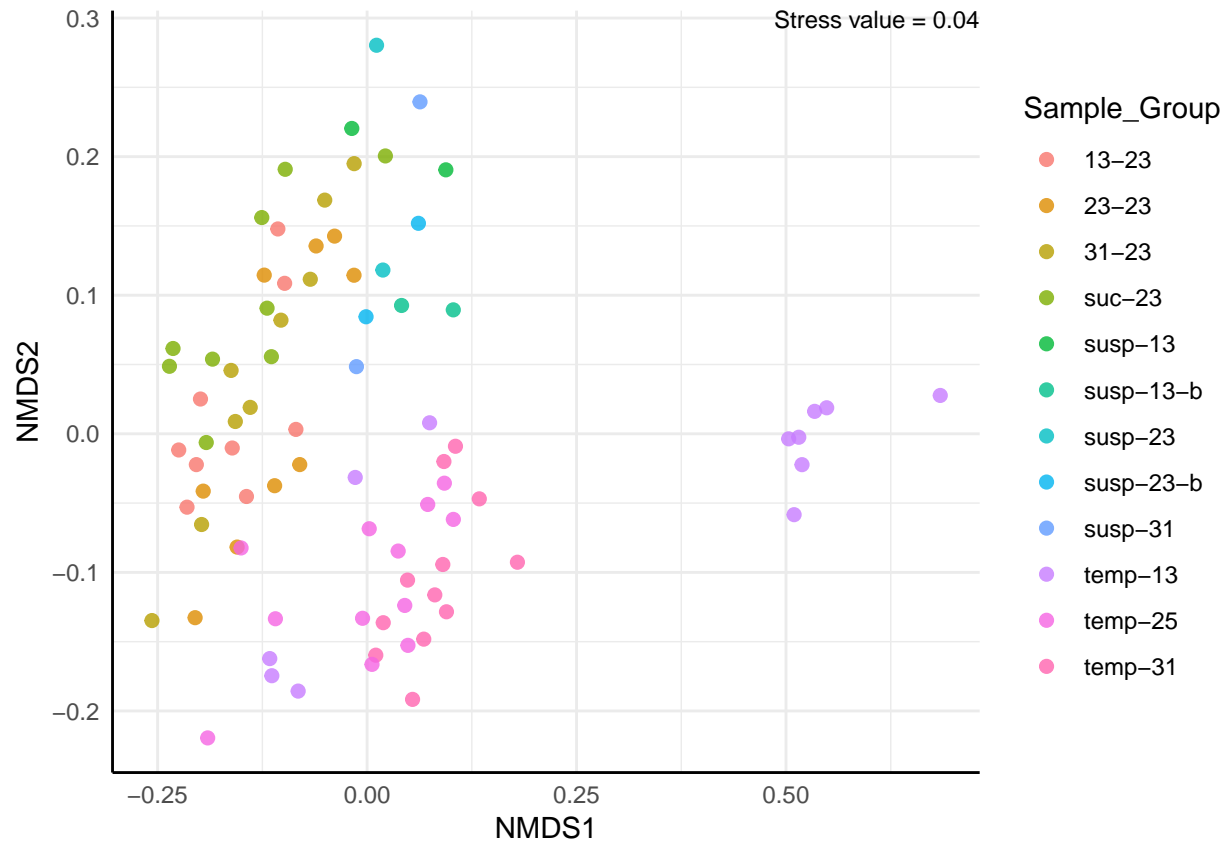
R Markdown

```
otutable <- read.delim(here('data','Fly_paper','otutable.txt'),header = TRUE, check.names = FALSE)
metadata <- read.table(here('data','Fly_paper','metadata.txt'),check.names = FALSE, sep = '\t', header = TRUE)
unifrac <- read.table(here('data','Fly_paper','beta_div_OTUS','OTUS.unweighted_unifrac.txt'))
wunifrac <- read.table(here('data','Fly_paper','beta_div_OTUS','OTUS.weighted_unifrac.txt'))
```

```
data <- amp_load(otutable = otutable, metadata = metadata)
col_v <- c(colnames(metadata[,5:10]))
data$abund <- unifrac
NMDS_u <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
                      detailed_output = TRUE, transform = 'none',
                      k = 10, try = 20, trymax = 50,
                      filter_species = 0, sample_color_by = col_v[1])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

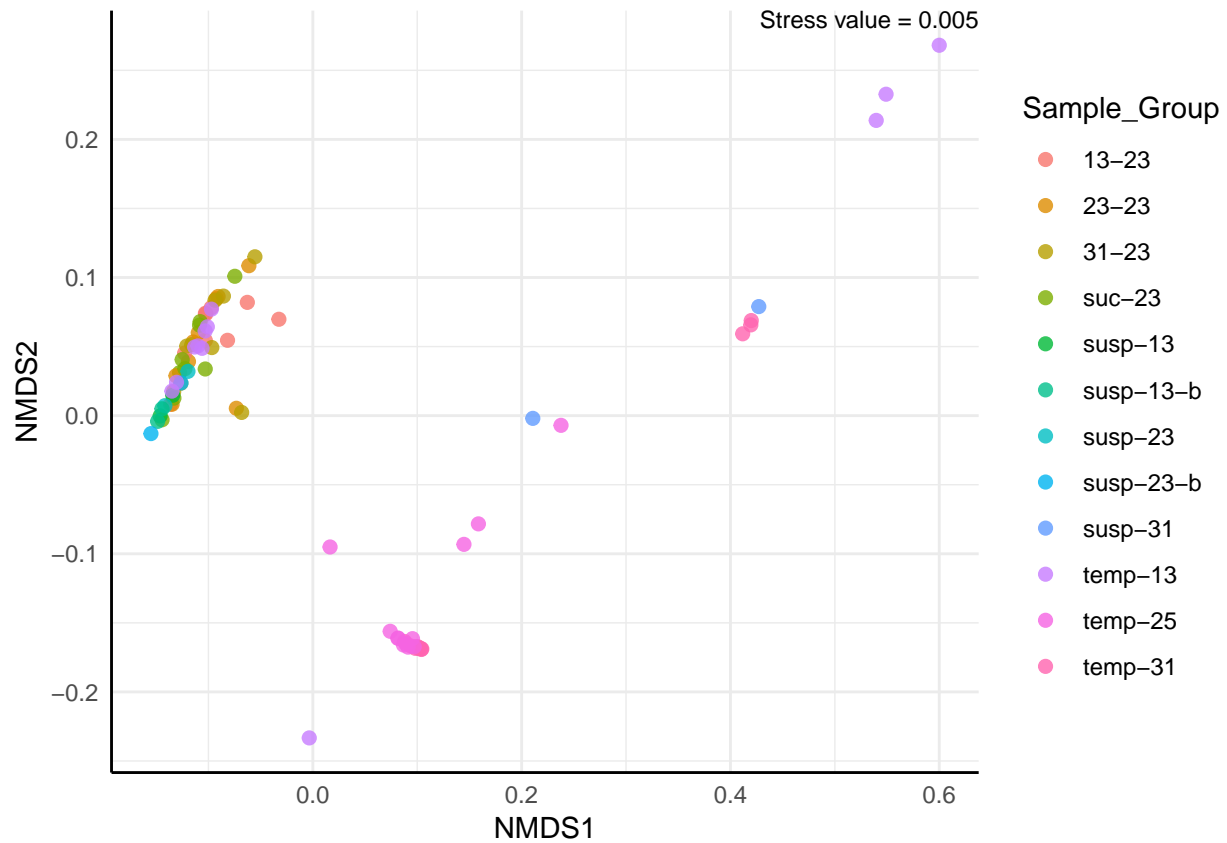
```
NMDS_u$plot
```



```
data$abund <- wunifrac
NMDS_w <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
  detailed_output = TRUE, transform = 'none',
  k = 10, try = 20, trymax = 50,
  sample_color_by = col_v[1])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

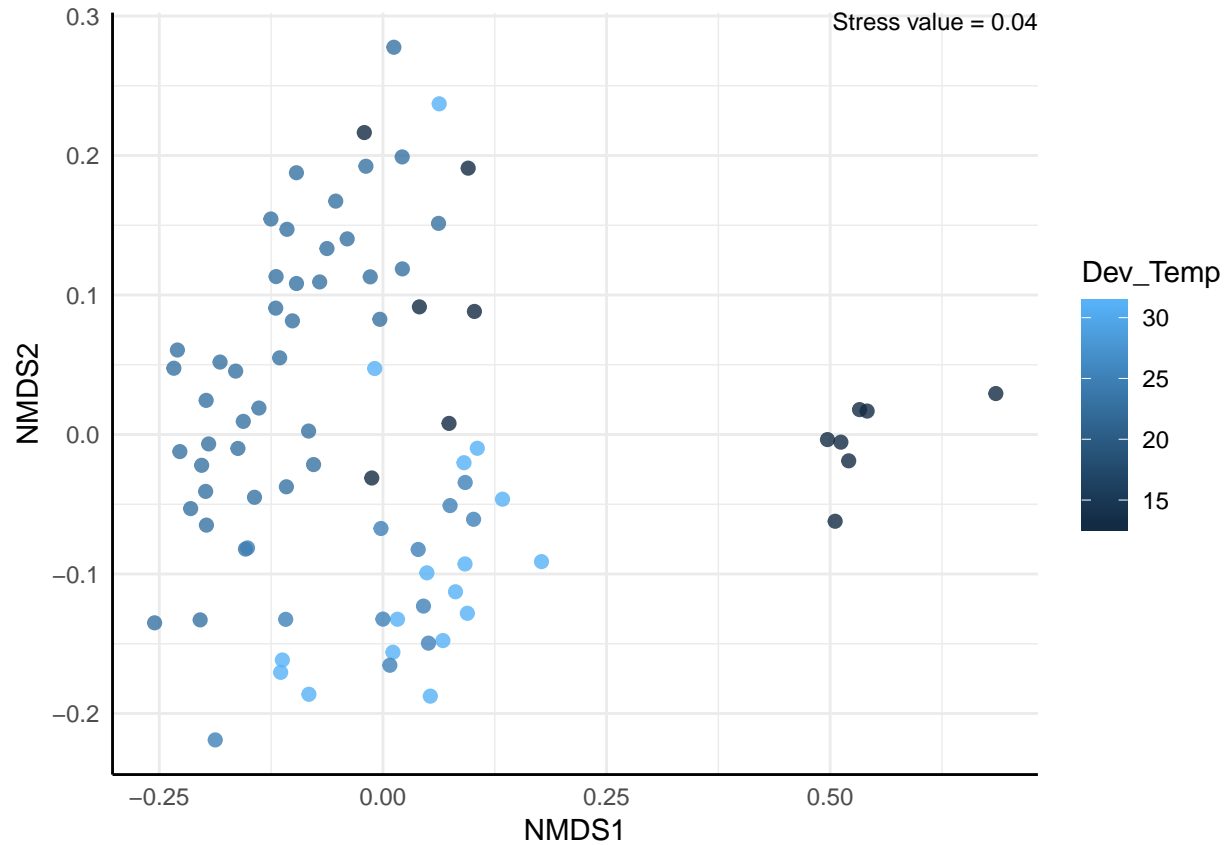
```
NMDS_w$plot
```



```
data$abund <- unifracs
NMDS <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
  detailed_output = TRUE, transform = 'none',
  k = 10, try = 20, trymax = 50,
  filter_species = 0, sample_color_by = col_v[2])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

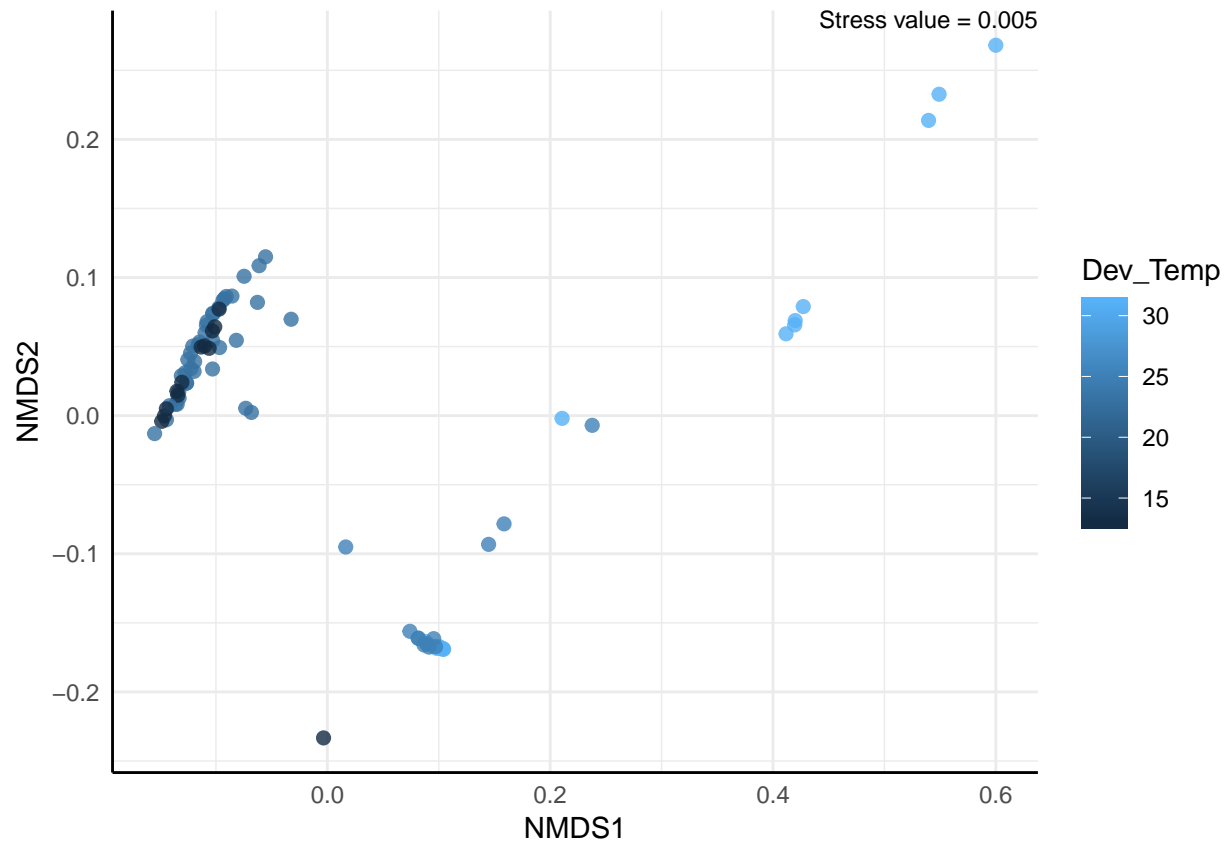
```
NMDS$plot
```



```
data$abund <- wunifrac
NMDS <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
  detailed_output = TRUE, transform = 'none',
  k = 10, try = 20, trymax = 50,
  filter_species = 0, sample_color_by = col_v[2])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

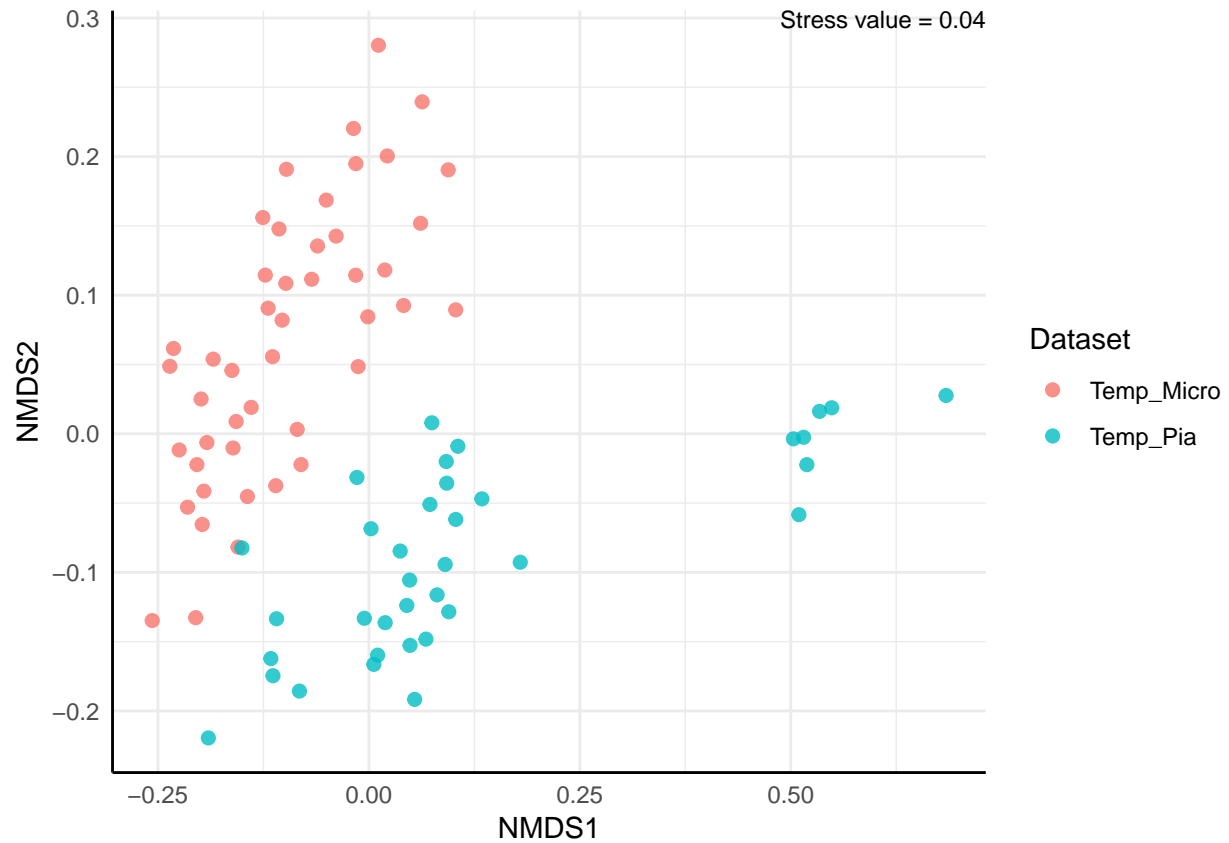
```
NMDS$plot
```



```
data$abund <- unifrac
NMDS <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
  detailed_output = TRUE, transform = 'none',
  k = 10, try = 20, trymax = 50,
  filter_species = 0, sample_color_by = col_v[3])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

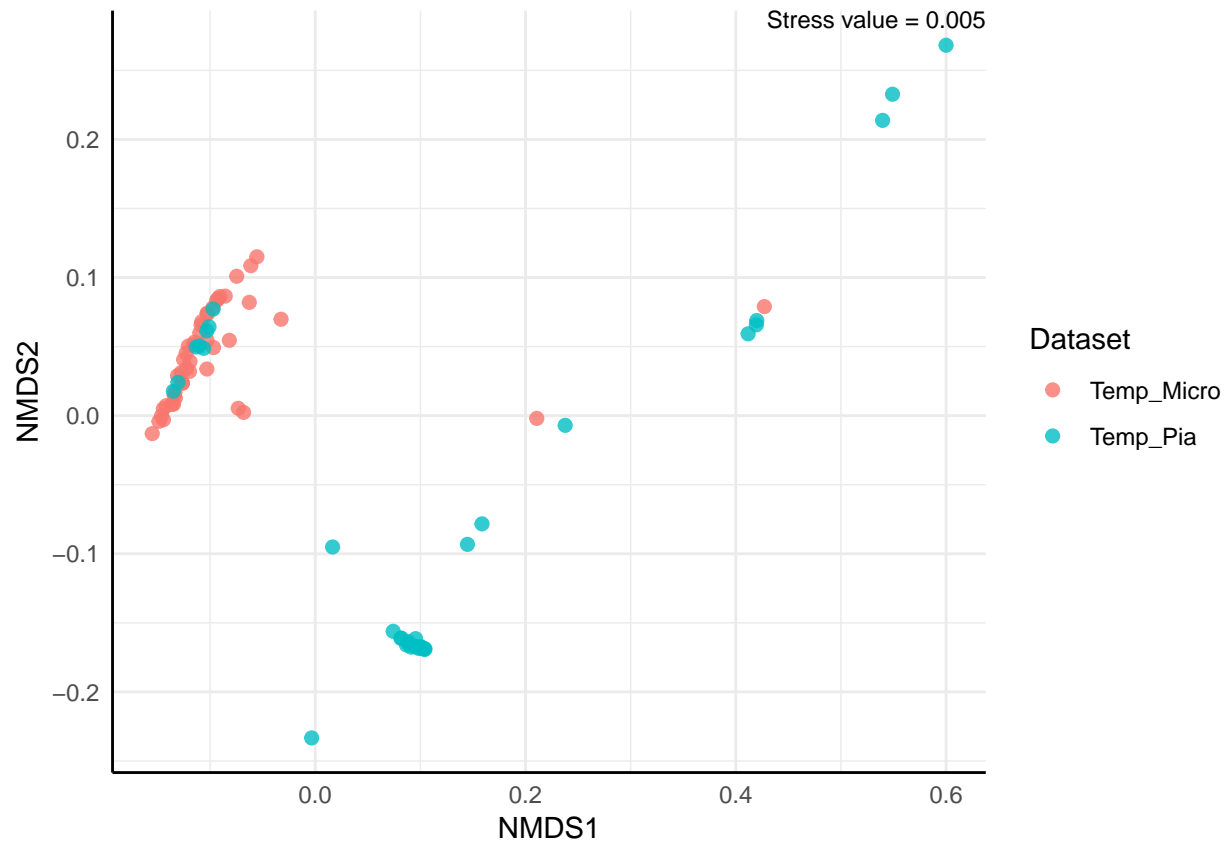
```
NMDS$plot
```



```
data$abund <- wunifrac
NMDS <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
  detailed_output = TRUE, transform = 'none',
  k = 10, try = 20, trymax = 50,
  filter_species = 0, sample_color_by = col_v[3])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

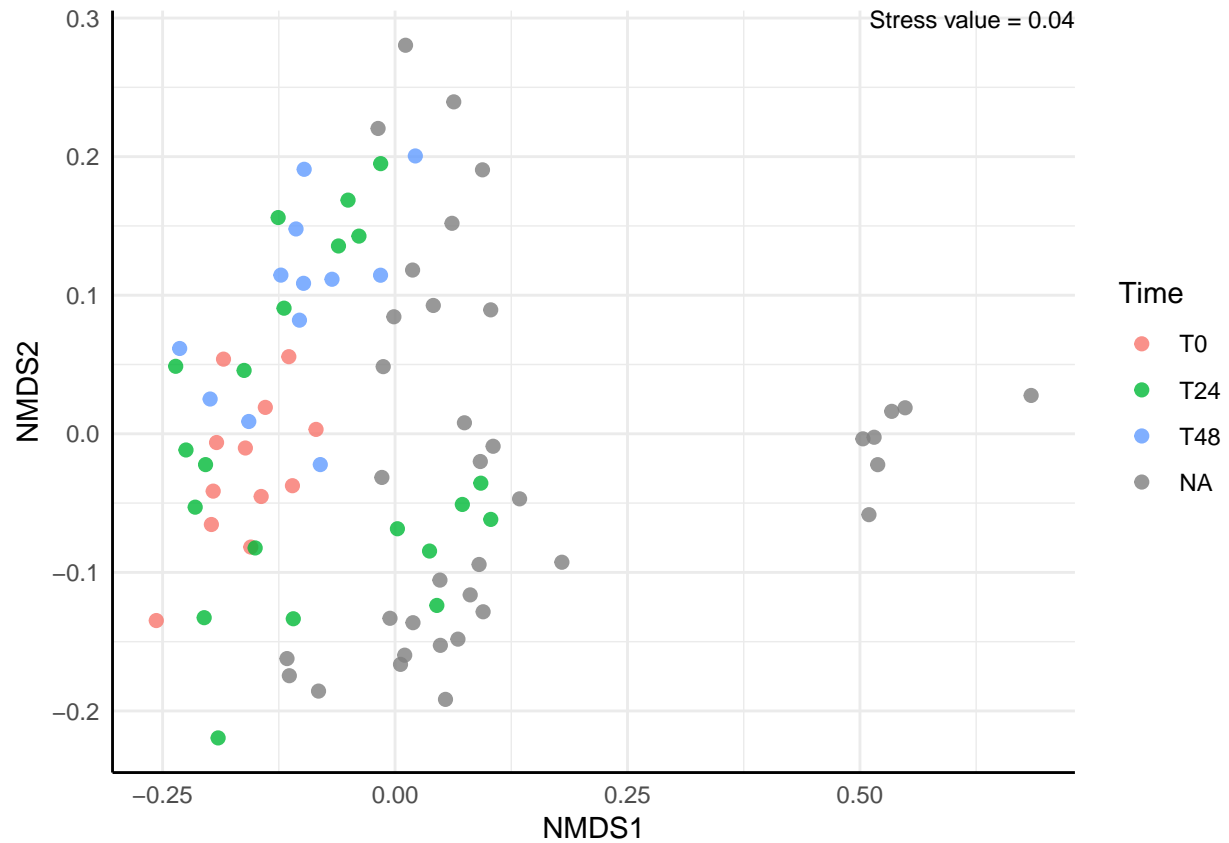
```
NMDS$plot
```



```
data$abund <- unifracs
NMDS <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
  detailed_output = TRUE, transform = 'none',
  k = 10, try = 20, trymax = 50,
  filter_species = 0, sample_color_by = col_v[4])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

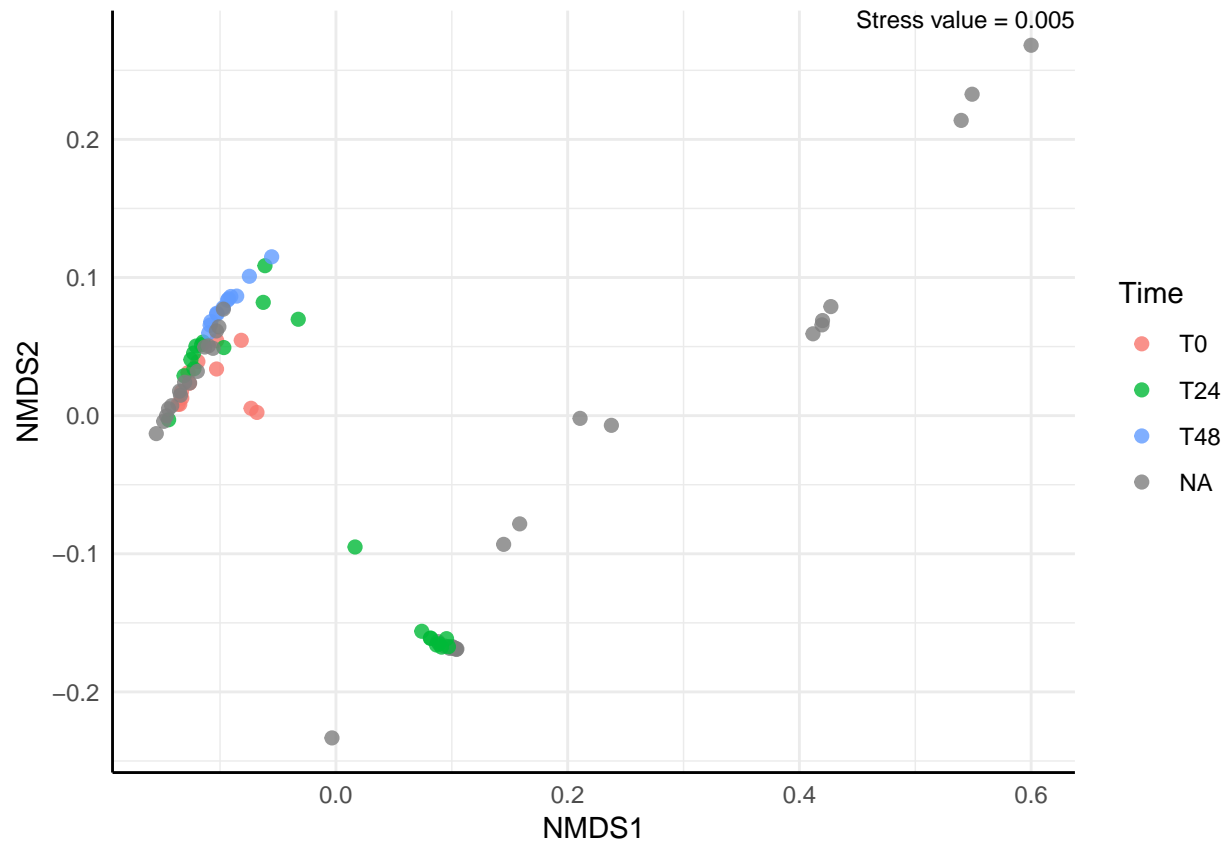
```
NMDS$plot
```



```
data$abund <- wunifrac
NMDS <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
  detailed_output = TRUE, transform = 'none',
  k = 10, try = 20, trymax = 50,
  filter_species = 0, sample_color_by = col_v[4])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

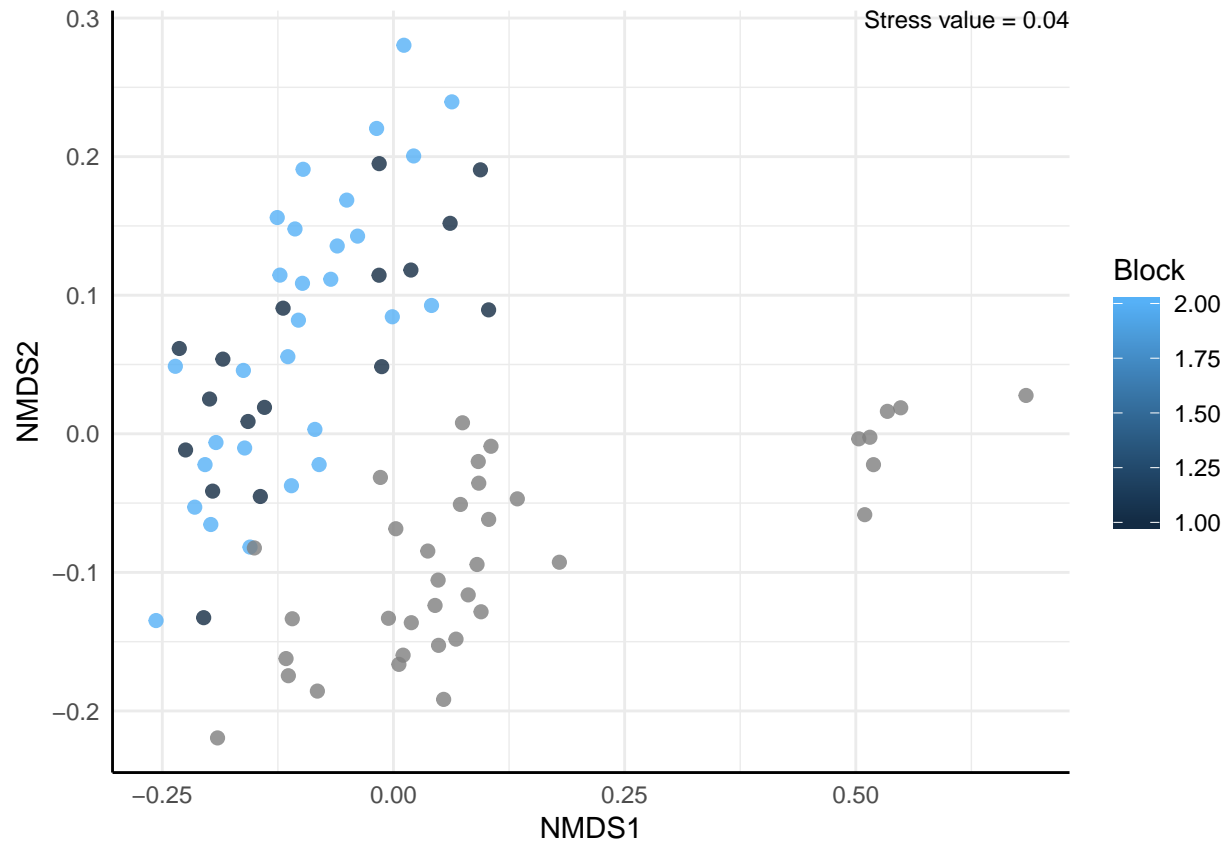
```
NMDS$plot
```

```
data$abund <- unifrac
NMDS <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
  detailed_output = TRUE, transform = 'none',
  k = 10, try = 20, trymax = 50,
  filter_species = 0, sample_color_by = col_v[5])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

```
NMDS$plot
```



```
data$abund <- wunifrac
NMDS <- amp_ordinate(data, type = 'NMDS', distmeasure = 'none',
  detailed_output = TRUE, transform = 'none',
  k = 10, try = 20, trymax = 50,
  filter_species = 0, sample_color_by = col_v[5])
```

```
## Warning: No distance measure selected, using raw data. If this is not
## deliberate, please provide one with the argument: distmeasure.
```

```
NMDS$plot
```

