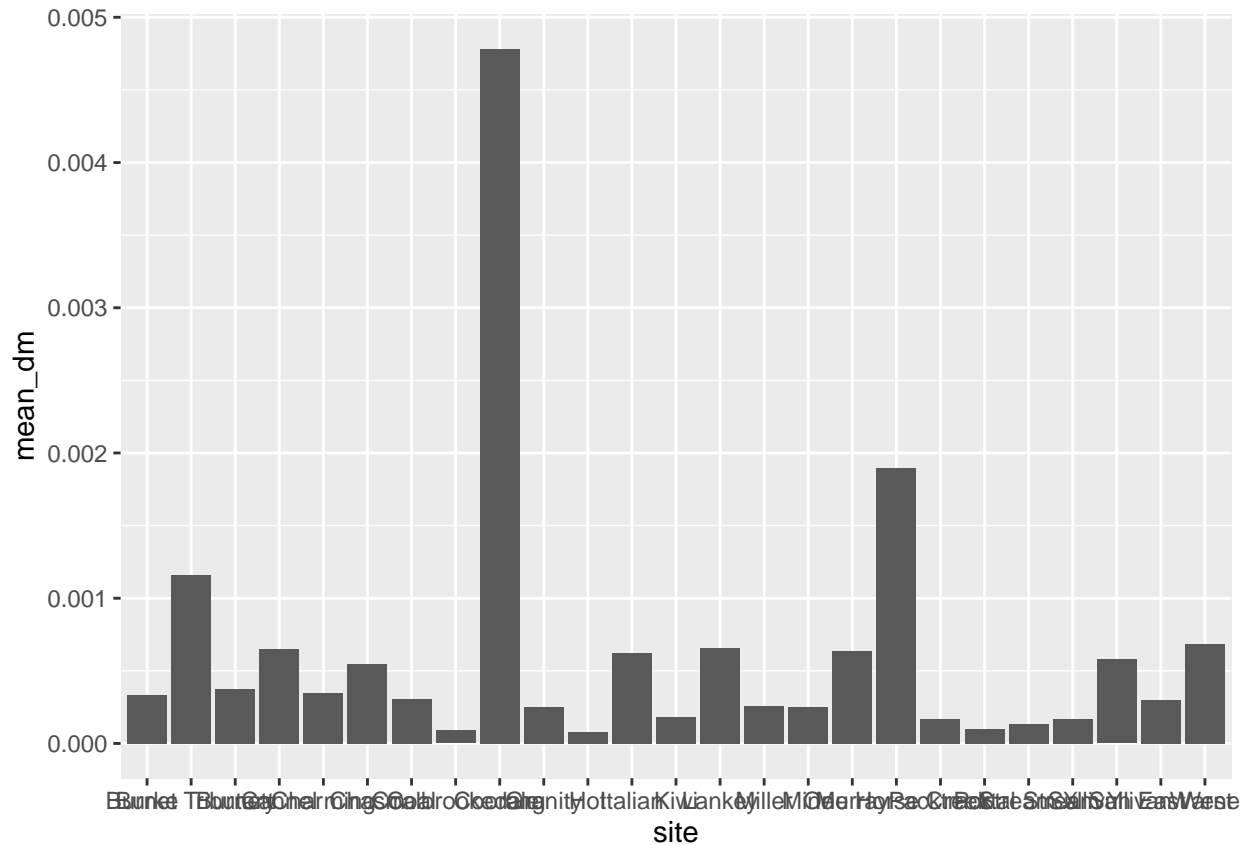
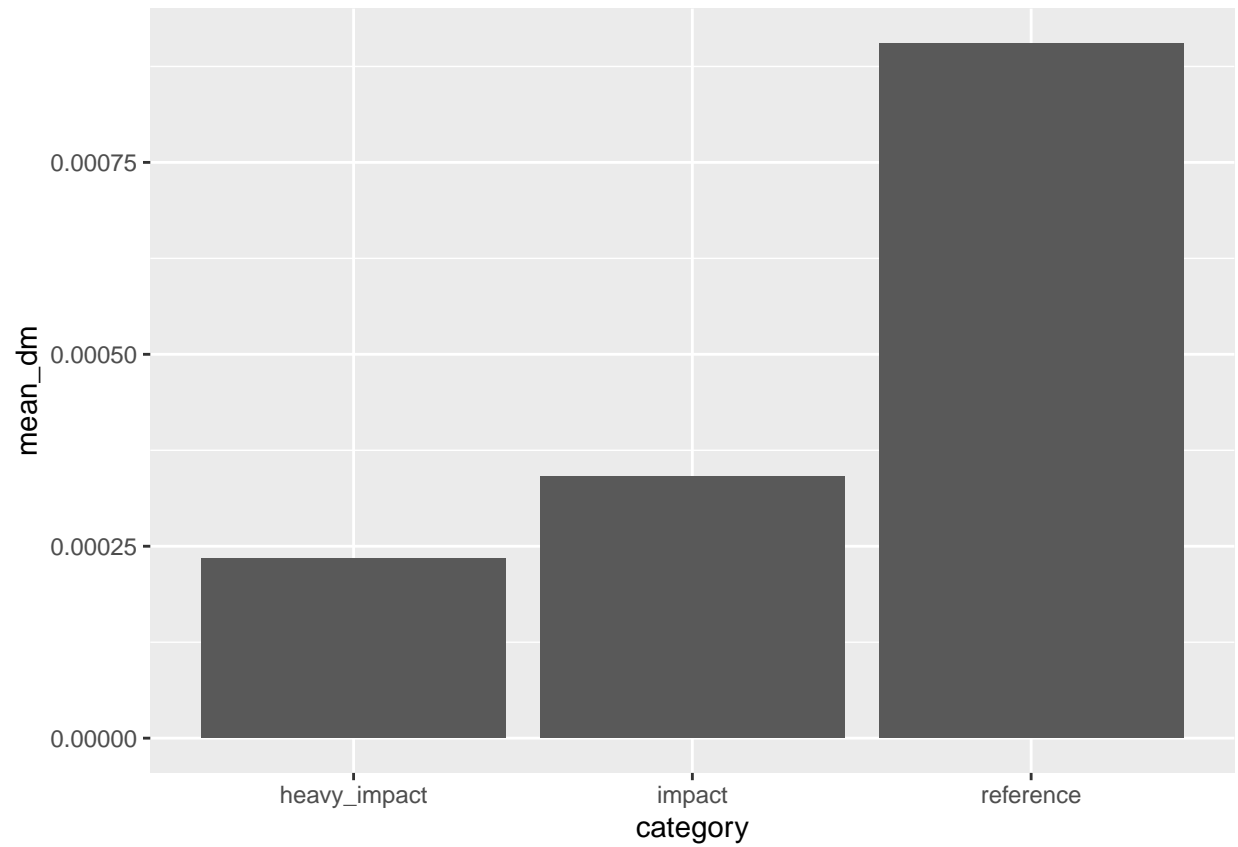


##	site	taxa	mean_dm_g	pca1	category
## 1	Burke	Acari	7.25e-06	-2.444464	reference
## 2	Burke	Aoteapsyche	2.16e-05	-2.444464	reference
## 3	Burke	Austroperla	2.44e-04	-2.444464	reference
## 4	Burke	Austrosimulium	1.18e-04	-2.444464	reference
## 5	Burke	Ceratopogonidae	2.47e-04	-2.444464	reference
## 6	Burke	Chironominae	1.79e-04	-2.444464	reference

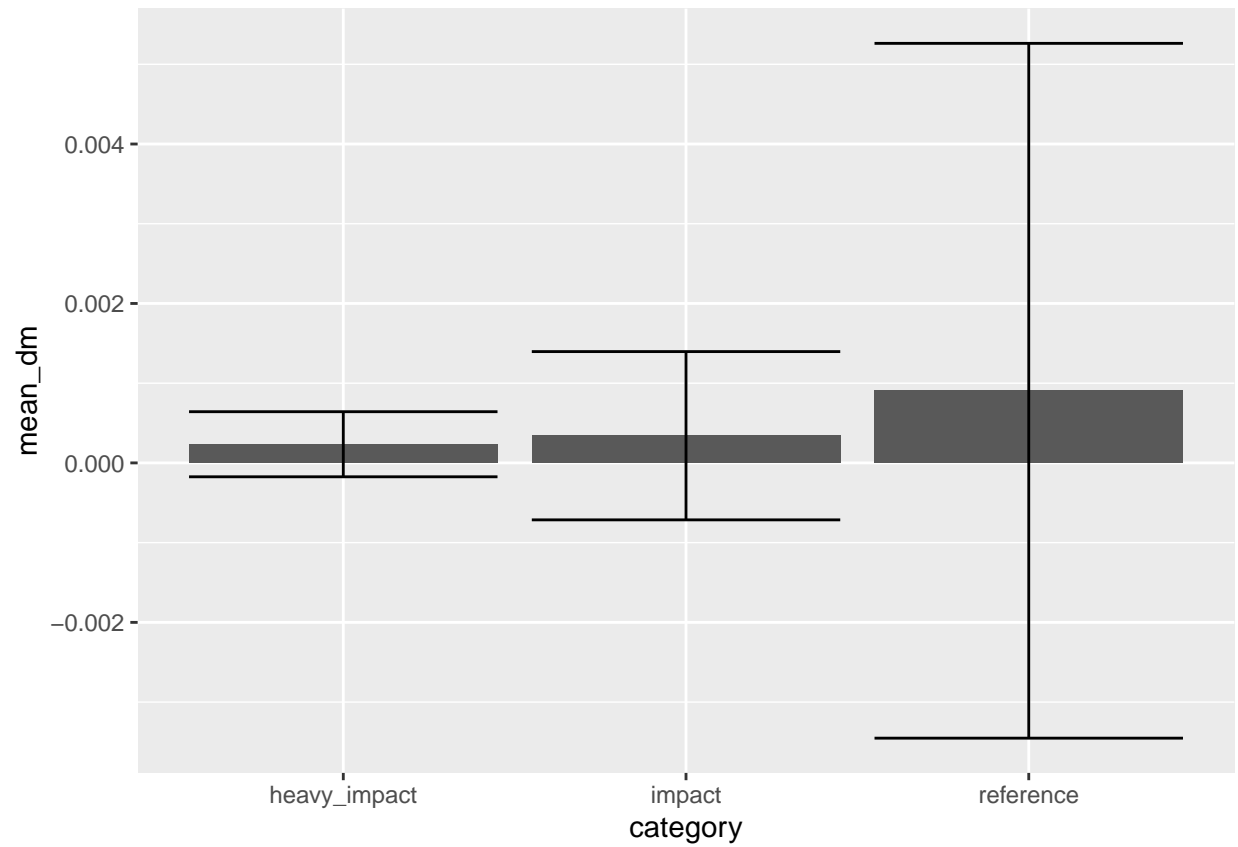
1. Summarize the data to get an average `mean_dm_g` for every site, and plot the data as a bar chart.



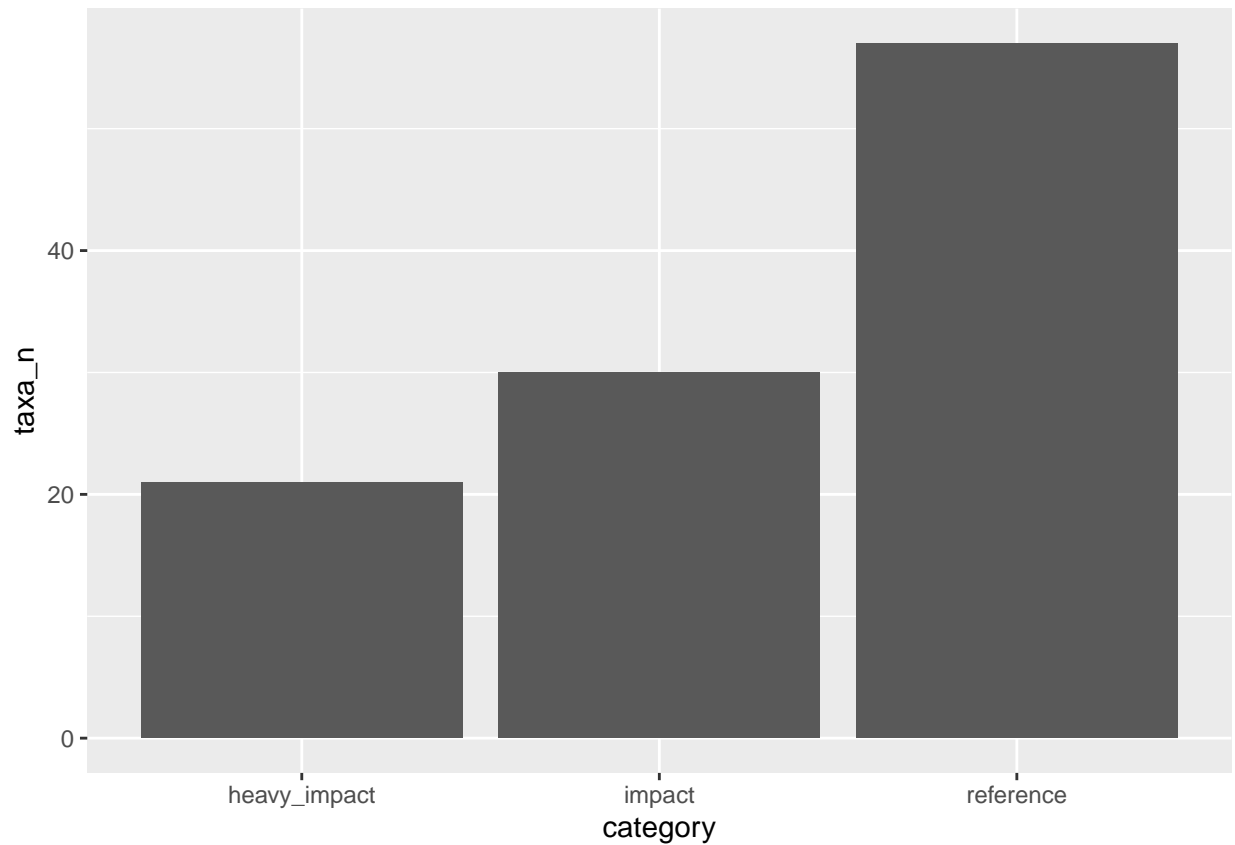
2. Summarize the data to get an average `mean_dm_g` for each category, and plot the data as a bar chart.



3. Summarize the data to get an average and a standard deviation (SD) `mean_dm_g` for each category, and plot the data as a bar chart with an errorbar.

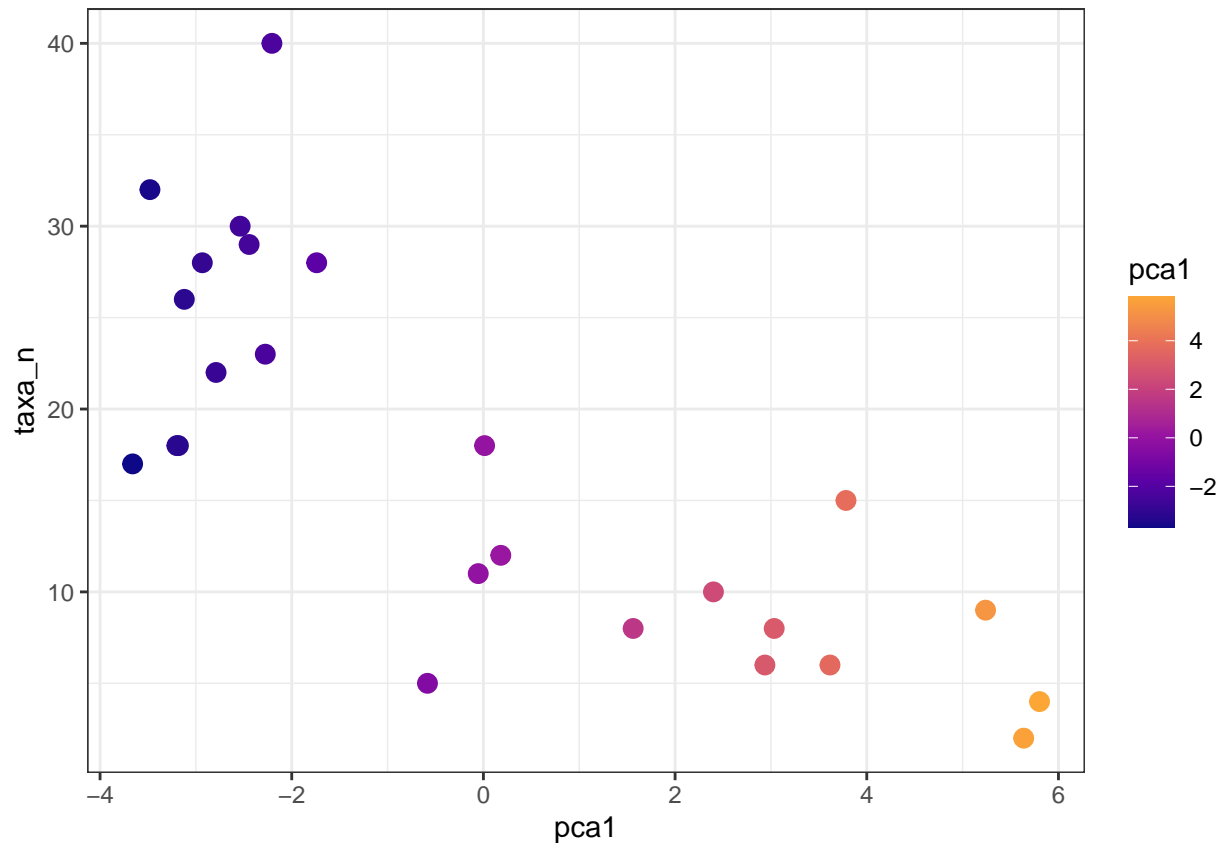


4. Modify the data to make a bar chart of the number of `taxa` in each category.



5. Modify the data to make a scatter point graph of the number of `taxa` for each values in the `pca1` column.

- Make the size of the points = 3
- Map color to `pca1` and use `scale_color_viridis_c()`
- run `?scale_color_viridis_c` to see what color option's are available and choose one



6. Modify the data to make a scatter point graph of the number of `taxa` for each values in the `pca1` column. This time, modify the code to include the `category` variable in your summary.

- Make the size of the points = 3
- Map color to `category` and use `scale_color_viridis_d()`
- `scale_color_viridis_d` has the same color options. Choose the same option you used above.
- set `direction = -1` to make the color palette match above.

```
## 'summarise()' has grouped output by 'pca1'. You can override using the '.groups'
## argument.
```

