

Class5

```
library(ggplot2)
```

Hiii

```
ggplot2222hii
```

```
sss
```

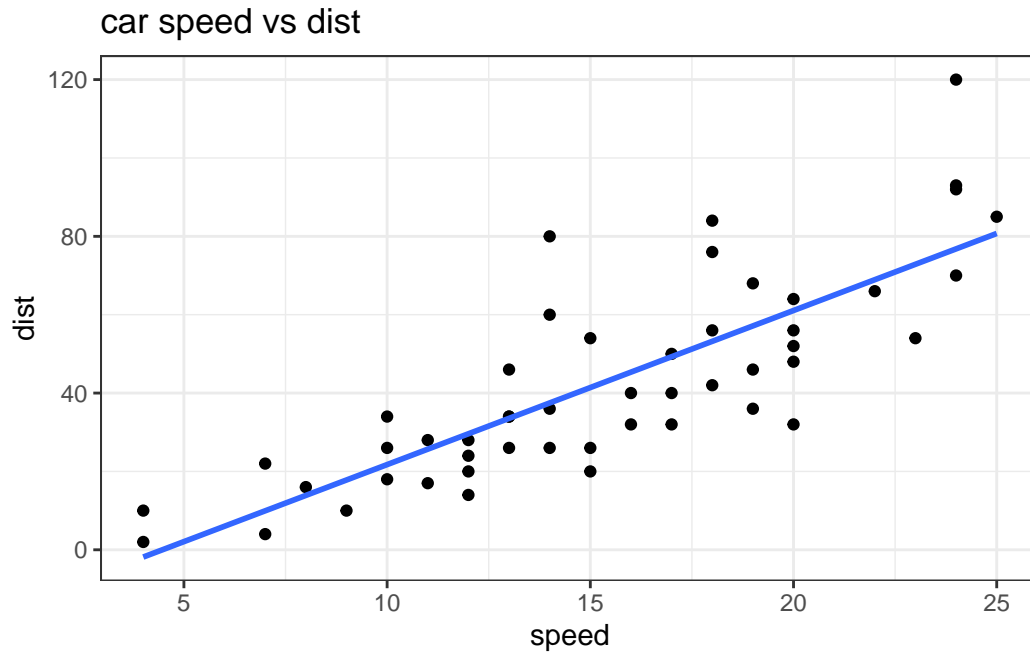
```
# Head  
cars
```

	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10
7	10	18
8	10	26
9	10	34
10	11	17
11	11	28
12	12	14
13	12	20
14	12	24
15	12	28
16	13	26
17	13	34
18	13	34

19	13	46
20	14	26
21	14	36
22	14	60
23	14	80
24	15	20
25	15	26
26	15	54
27	16	32
28	16	40
29	17	32
30	17	40
31	17	50
32	18	42
33	18	56
34	18	76
35	18	84
36	19	36
37	19	46
38	19	68
39	20	32
40	20	48
41	20	52
42	20	56
43	20	64
44	22	66
45	23	54
46	24	70
47	24	92
48	24	93
49	24	120
50	25	85

```
ggplot(cars) + aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method='lm', se=FALSE) + labs(title='car speed vs dist') + theme_minimal()
```

`geom_smooth()` using formula 'y ~ x'



```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

	Gene	Condition1	Condition2	State
1	A4GNT	-3.6808610	-3.4401355	unchanging
2	AAAS	4.5479580	4.3864126	unchanging
3	AASDH	3.7190695	3.4787276	unchanging
4	AATF	5.0784720	5.0151916	unchanging
5	AATK	0.4711421	0.5598642	unchanging
6	AB015752.4	-3.6808610	-3.5921390	unchanging

```
nrow(genes)
```

```
[1] 5196
```

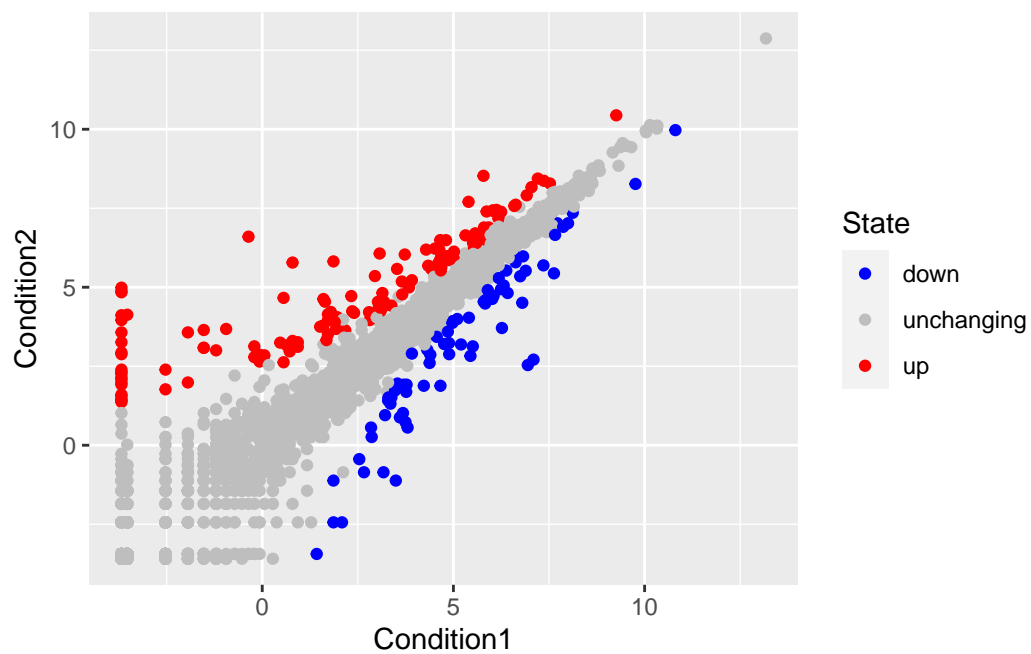
```
colnames(genes)
```

```
[1] "Gene"      "Condition1" "Condition2" "State"
```

```
table(genes$State)
```

```
down  unchanging    up
   72      4997    127
```

```
ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point() +
  scale_colour_manual( values=c("blue","gray","red") )
```



```
library(gapminder)
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

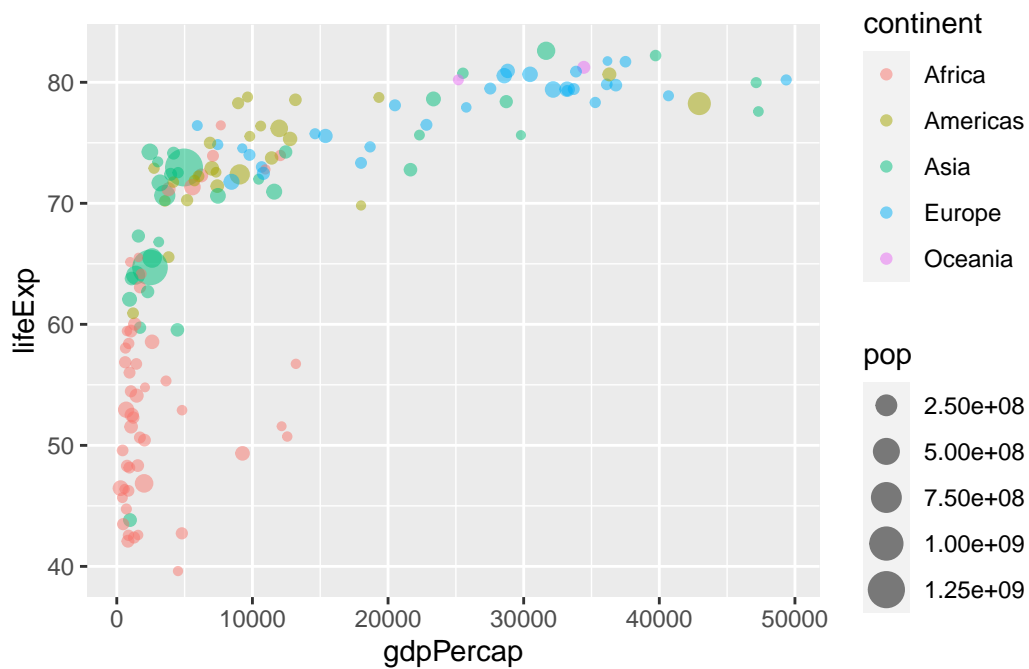
filter, lag

The following objects are masked from 'package:base':

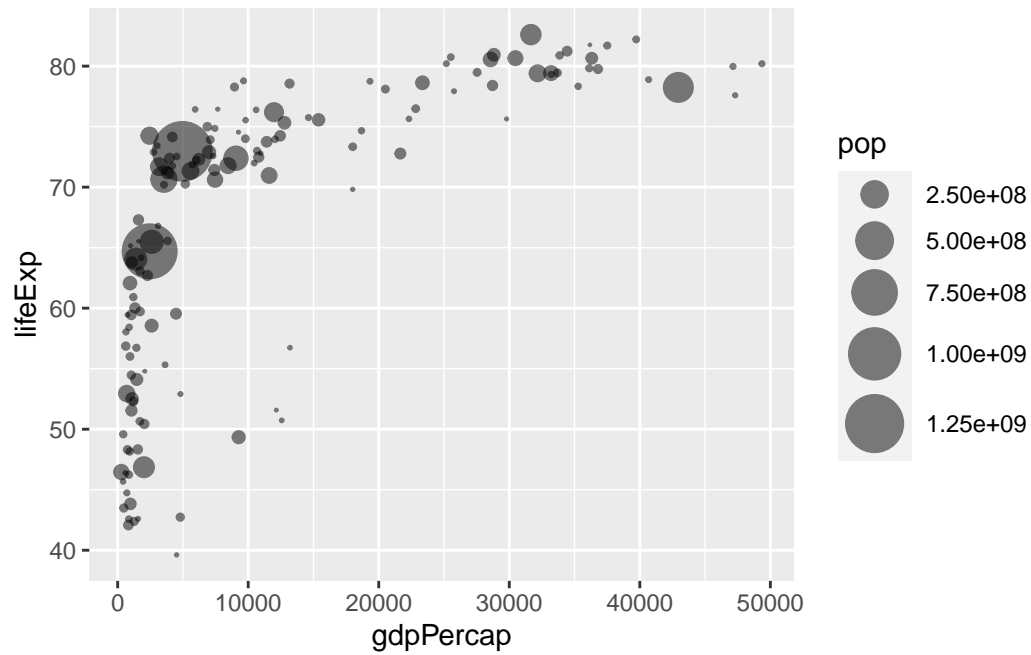
```
intersect, setdiff, setequal, union
```

```
gapminder_2007 = gapminder %>% filter(year==2007)
```

```
ggplot(gapminder_2007) +  
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +  
  geom_point(alpha=0.5)
```

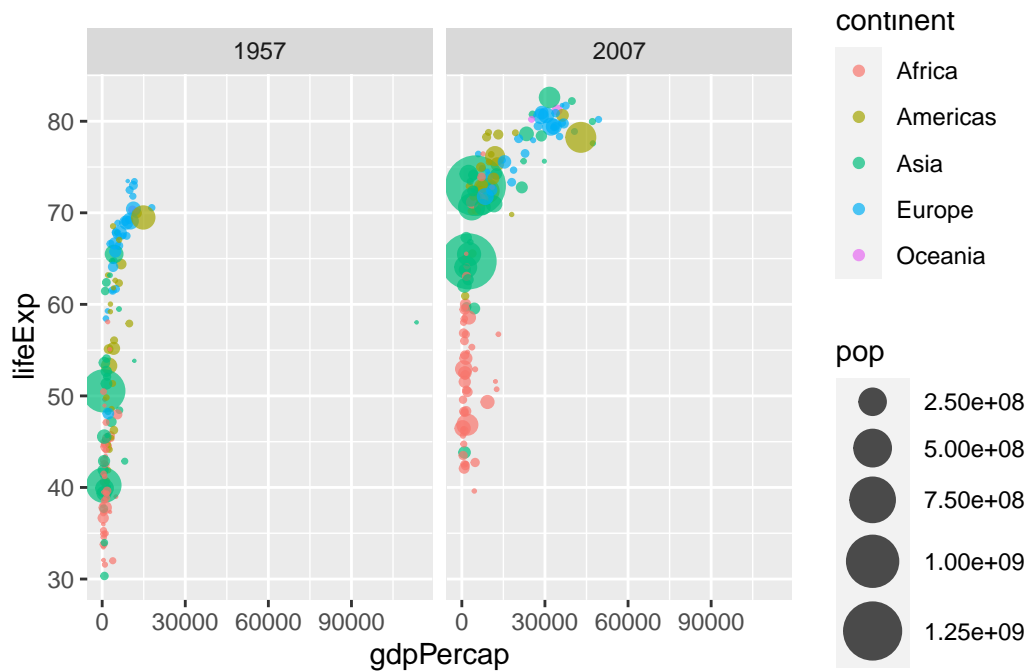


```
ggplot(gapminder_2007) +  
  geom_point(aes(x = gdpPercap, y = lifeExp,  
                 size = pop), alpha=0.5) +  
  scale_size_area(max_size = 10)
```



```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)

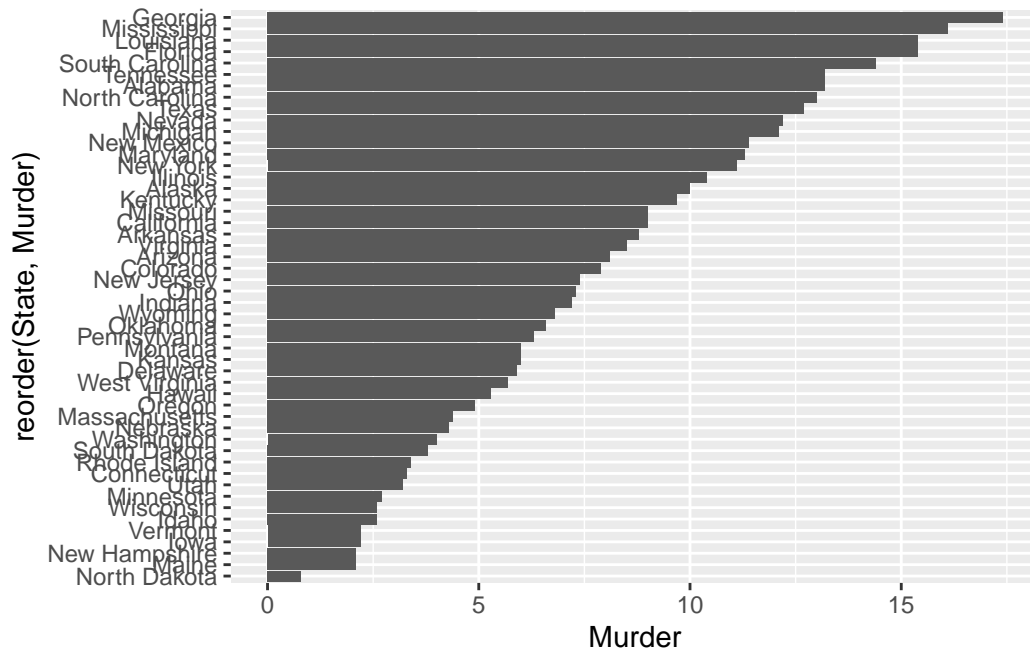
ggplot(gapminder_1957) +
  geom_point(aes(x = gdpPercap, y = lifeExp, color=continent,
                 size = pop), alpha=0.7) +
  scale_size_area(max_size = 10) +
  facet_wrap(~year)
```



```
head(USArrests)
```

	Murder	Assault	UrbanPop	Rape
Alabama	13.2	236	58	21.2
Alaska	10.0	263	48	44.5
Arizona	8.1	294	80	31.0
Arkansas	8.8	190	50	19.5
California	9.0	276	91	40.6
Colorado	7.9	204	78	38.7

```
USArrests$State <- rownames(USArrests)
ggplot(USArrests) +
  aes(x=reorder(State,Murder), y=Murder) +
  geom_col() +
  coord_flip()
```



```
sessionInfo()
```

```
R version 4.1.1 (2021-08-10)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Big Sur 10.16

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base

other attached packages:
[1] dplyr_1.0.7    gapminder_0.3.0 ggplot2_3.3.5

loaded via a namespace (and not attached):
[1] pillar_1.6.4    compiler_4.1.1  tools_4.1.1     digest_0.6.28
[5] lattice_0.20-45 nlme_3.1-153    jsonlite_1.7.2  evaluate_0.14
```


[9]	lifecycle_1.0.1	tibble_3.1.6	gtable_0.3.0	mgcv_1.8-38
[13]	pkgconfig_2.0.3	rlang_0.4.12	Matrix_1.3-4	yaml_2.2.1
[17]	xfun_0.33	fastmap_1.1.0	withr_2.4.2	stringr_1.4.0
[21]	knitr_1.36	generics_0.1.1	vctrs_0.3.8	grid_4.1.1
[25]	tidyselect_1.1.1	glue_1.5.0	R6_2.5.1	fansi_0.5.0
[29]	rmarkdown_2.11	farver_2.1.0	purrr_0.3.4	magrittr_2.0.1
[33]	scales_1.1.1	ellipsis_0.3.2	htmltools_0.5.2	splines_4.1.1
[37]	colorspace_2.0-2	labeling_0.4.2	utf8_1.2.2	stringi_1.7.5
[41]	munsell_0.5.0	crayon_1.4.2		