

# Application to Bioproduct-Types Submodel, version 9

## Set up packages.

```
In [1]: require(abind)
require(data.table)
require(deSolve)
require(LaplacesDemon)
require(magrittr)
require(np)
require(rTensor)

require(ggplot2)
require(GGally)

Loading required package: abind
Loading required package: data.table
Loading required package: deSolve
Loading required package: LaplacesDemon
Loading required package: magrittr
Loading required package: np
Nonparametric Kernel Methods for Mixed Datatypes (version 0.60-9)
[vignette("np_faq",package="np") provides answers to frequently asked
questions]
[vignette("np",package="np") an overview]
[vignette("entropy_np",package="np") an overview of entropy-based met
hods]
Loading required package: rTensor
Loading required package: ggplot2
Loading required package: GGally
Registered S3 method overwritten by 'GGally':
  method from
    +.gg      ggplot2
```

## Read results.

```
In [2]: xs = fread("framework/xs-v9.tsv")
xs %>% dim
```

```
21347  18
```

```
In [3]: xs[!is.na(s)] %>% dim
```

```
7601  18
```

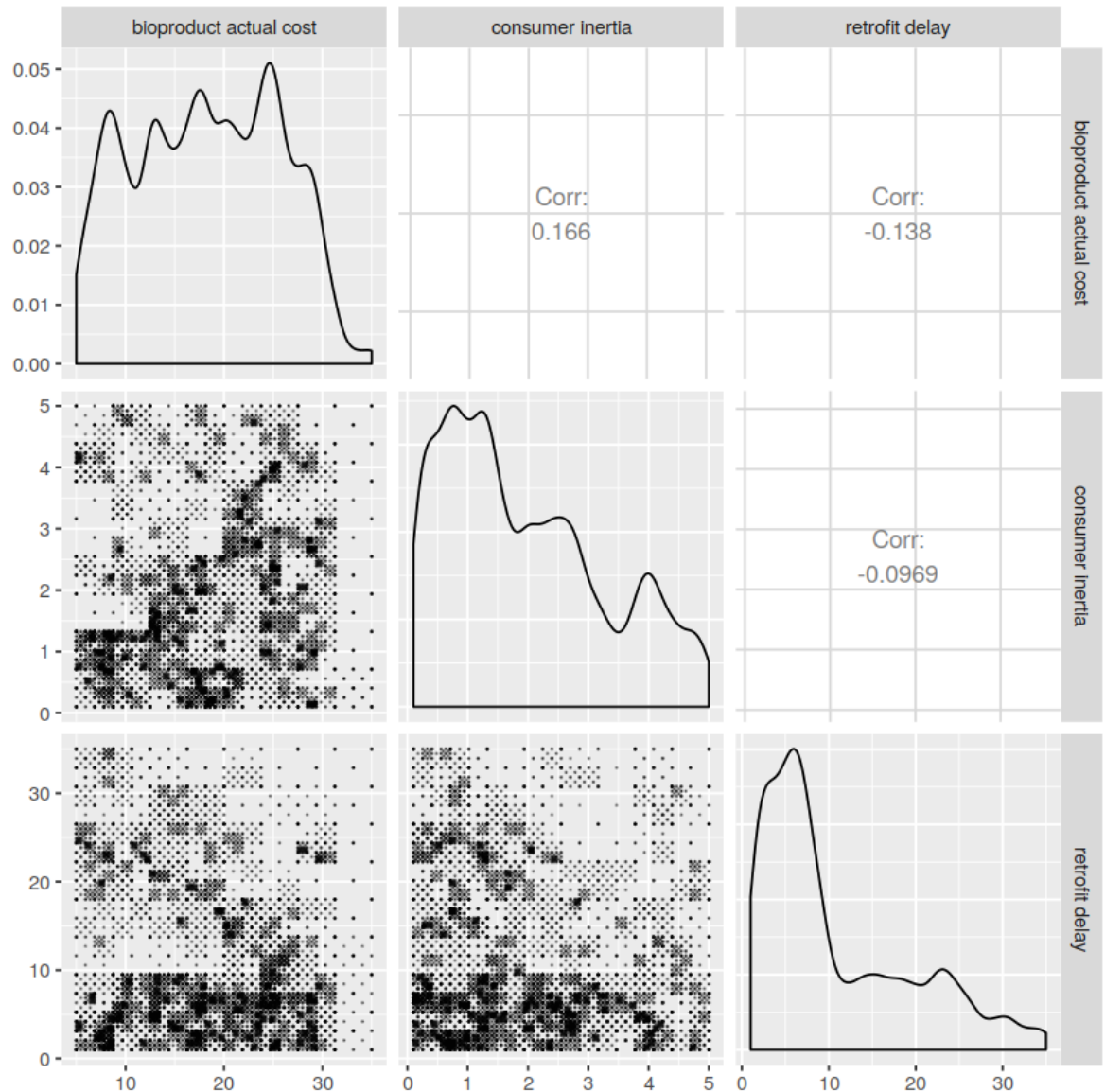
```
In [4]: ys = fread("framework/ys-v9.tsv")
ys %>% summary
```

sequence	Year	Adopters	NonAdopters
Min. : 1	Min. :2015	Min. : 0.0	Min. : 0.0
1st Qu.: 4805	1st Qu.:2022	1st Qu.: 800.3	1st Qu.: 158.2
Median :10124	Median :2032	Median : 7799.3	Median : 62099.5
Mean :10275	Mean :2032	Mean : 38534.1	Mean : 51377.2
3rd Qu.:15648	3rd Qu.:2042	3rd Qu.:101244.0	3rd Qu.: 95802.8
Max. :21319	Max. :2050	Max. :103500.0	Max. :102720.0
Potential Adopters			
Min. : 0.00			
1st Qu.: 46.54			
Median : 2251.11			
Mean : 11838.63			
3rd Qu.: 16766.80			
Max. :100003.00			

```
In [5]: xys = merge(xs, ys, by="sequence")[, .(
  `sequence`,
  `bioproduct actual cost`,
  `consumer inertia`,
  `retrofit delay`,
  `Year`,
  `NonAdopters`,
  `Potential Adopters`,
  `Adopters`
)]
```

**Plot sampling pattern.**

```
In [6]: ggpairs(
  xs,
  16:18,
  # mapping = aes(color=!probed),
  lower = list(continuous = wrap("points", alpha = 0.2, size=0.1))
)
```



List modes of marginal distributions of sampling pattern.

Bioproduct actual cost.

```
In [7]: Modes(xs[!is.na(s), `bioproduct actual cost`])$modes
24.7565682862267 17.6038340212242 8.37680681937094 13.5983028328228
```

### Consumer inertia.

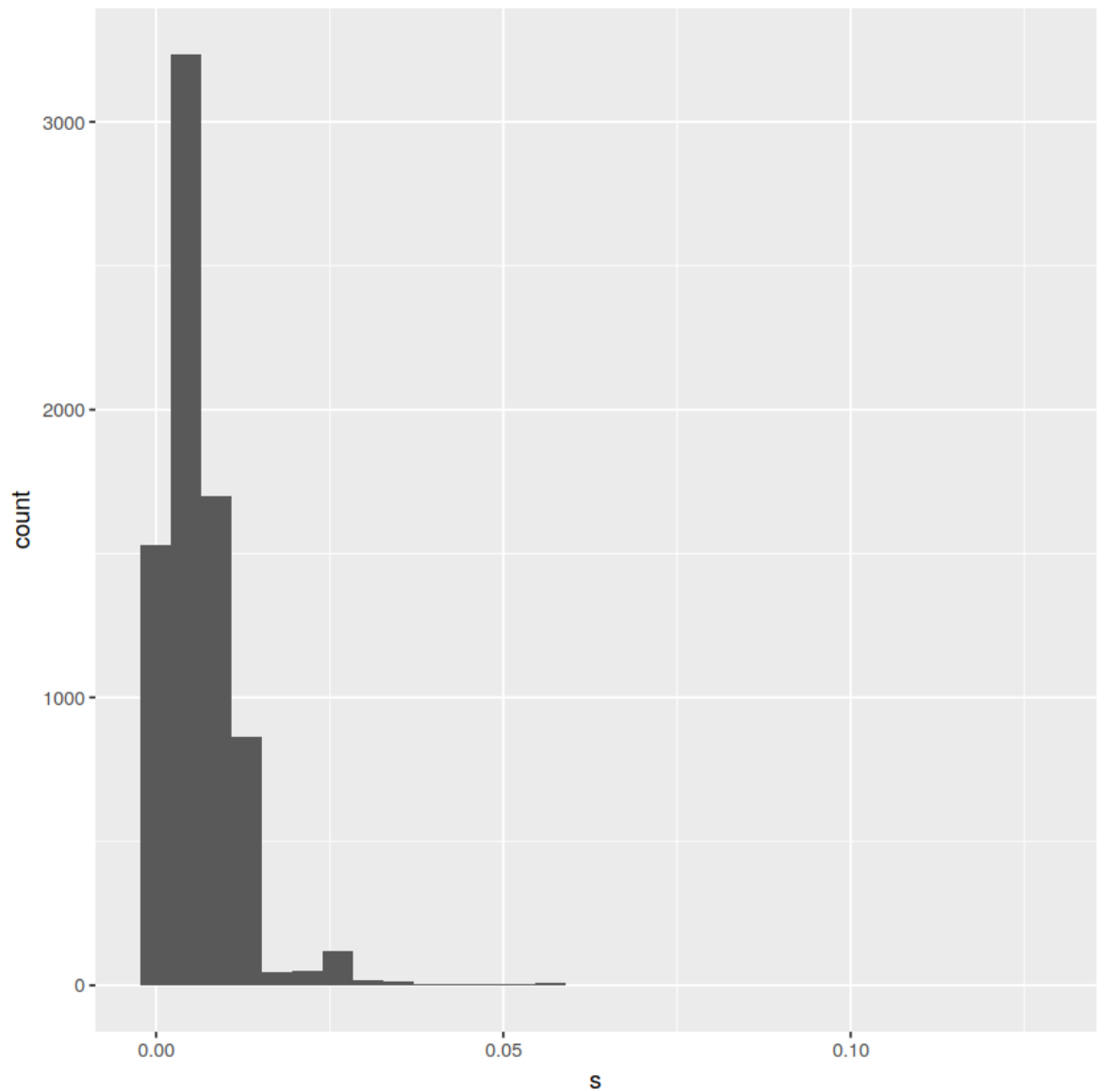
```
In [8]: Modes(xs[!is.na(s), `consumer inertia`])$modes  
0.838242929184577 2.26967741349016 4.02318465676449
```

### Retrofit delay.

```
In [9]: Modes(xs[!is.na(s), `retrofit delay`])$modes  
5.8637897005515 15.3439270388412 23.4347339051402
```

### Plot distribution of nonlinearity measure.

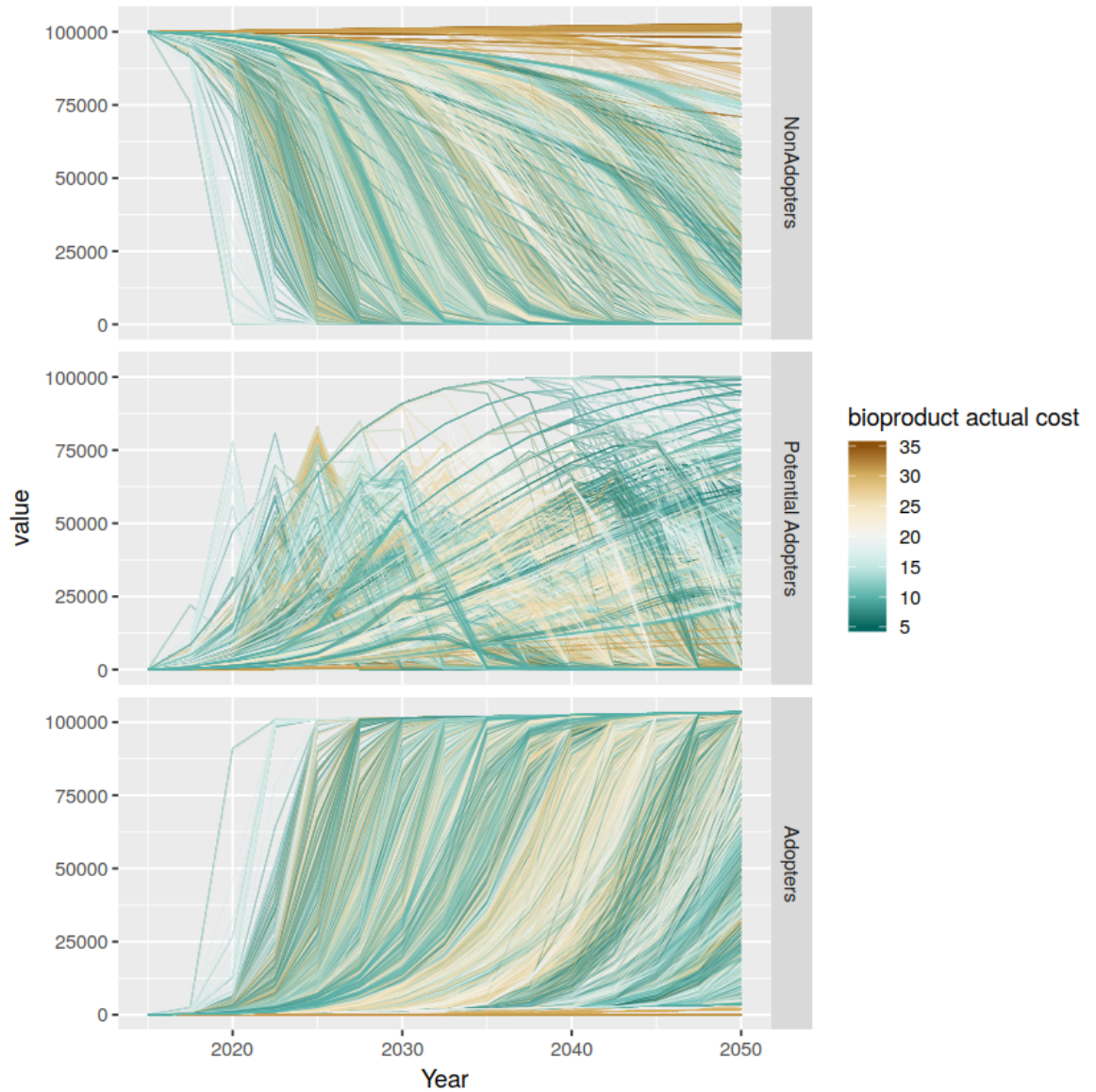
```
In [10]: ggplot(xs[!is.na(s)], aes(x=s)) + geom_histogram(bins=30)
```



**Plot response variables.**

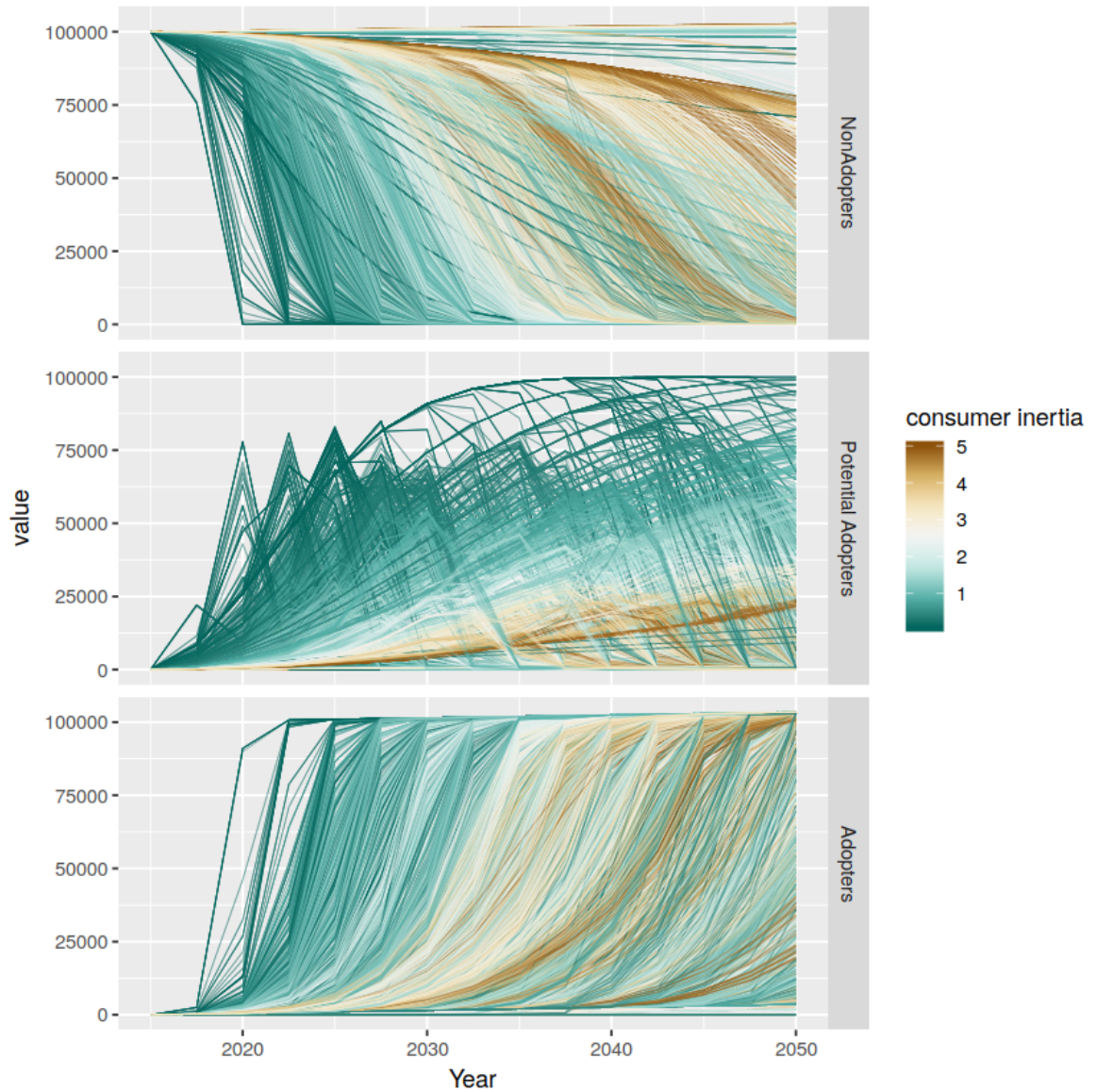
**As a function of bioproduct actual cost.**

```
In [11]: ggplot(
  melt(xys, id.vars=c("sequence", "Year", "bioproduct actual cost",
    "consumer inertia", "retrofit delay")),
  aes(x=Year, y=value, group=sequence, color=`bioproduct actual cos
t`)) +
  geom_line(alpha=0.25, size=0.25) +
  scale_color_distiller(type="div") +
  facet_grid(variable ~ .)
```



**As a function of consumer inertia.**

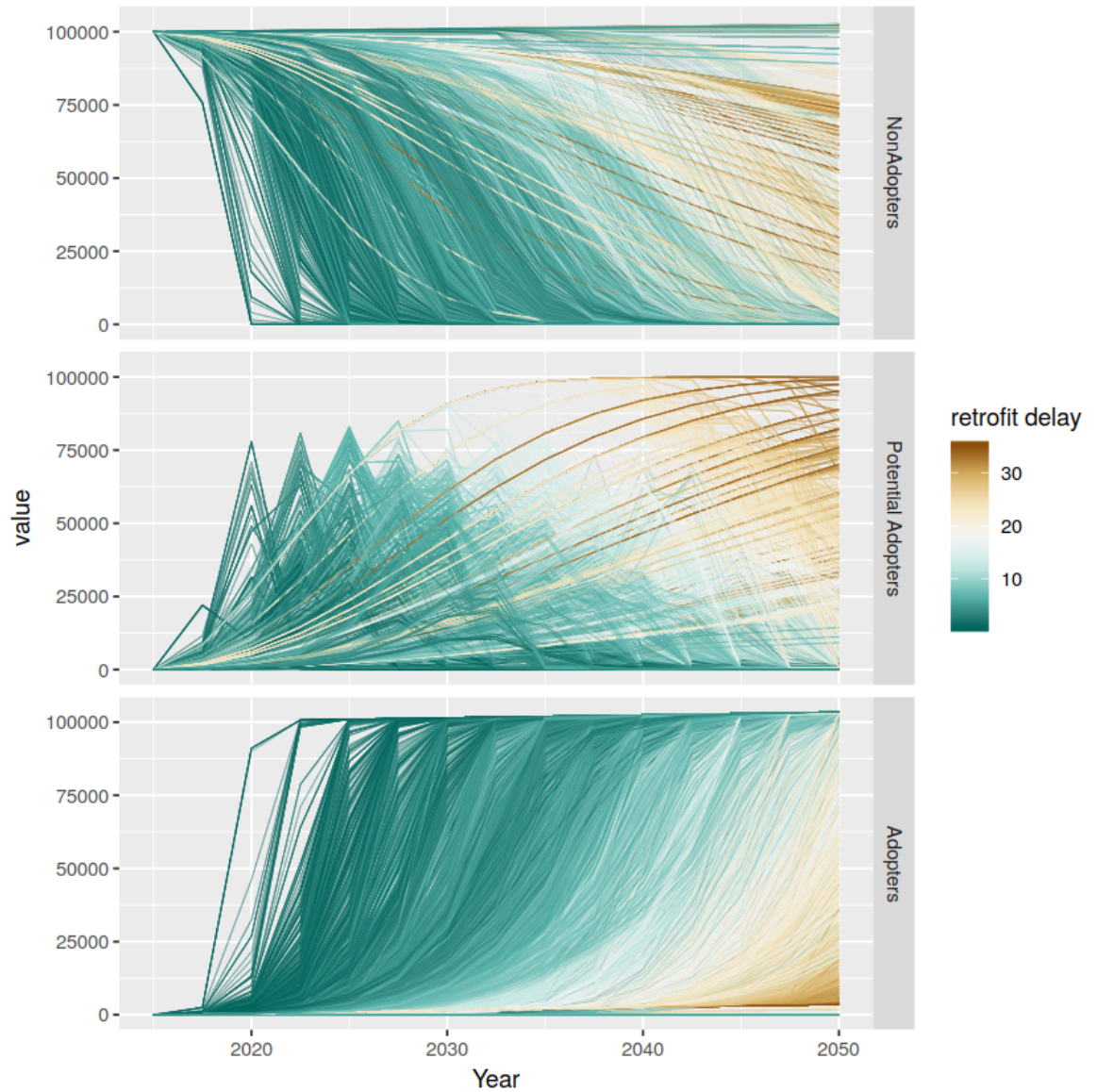
```
In [12]: ggplot(
  melt(xys, id.vars=c("sequence", "Year", "bioproduct actual cost",
    "consumer inertia", "retrofit delay")),
  aes(x=Year, y=value, group=sequence, color=`consumer inertia`)) +
  geom_line(alpha=0.25, size=0.25) +
  scale_color_distiller(type="div") +
  facet_grid(variable ~ .)
```



**As a function of retrofit delay.**



```
In [13]: ggplot(
  melt(xys, id.vars=c("sequence", "Year", "bioproduct actual cost",
    "consumer inertia", "retrofit delay")),
  aes(x=Year, y=value, group=sequence, color=`retrofit delay`)) +
  geom_line(alpha=0.25, size=0.25) +
  scale_color_distiller(type="div") +
  facet_grid(variable ~ .)
```



**Distribution of output at final year.**



```
In [14]: ggpairs(
  xys[Year == 2050],
  6:8,
  # mapping = aes(color=!probed),
  lower = list(continuous = wrap("points", alpha = 0.2, size=0.1))
)
```

