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 q
uestions]
[vignette("np",package="np") an overview]
[vignette("entropy_np",package="np") an overview of entropy-based metho
ds]
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(cmd="xzcat xs-v9.tsv.xz")
        xs %>% dim
```

105156 18

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

38041 18

```
In [4]:  ys = fread(cmd="xzcat ys-v9.tsv.xz")
         ys %>% summary
```

```
     sequence              Year            Adopters           NonAdopters
  Min.   :     1    Min.   :2015    Min.   :      0.0    Min.   :      0.0
  1st Qu.: 23733    1st Qu.:2022    1st Qu.:    996.9    1st Qu.:    296.1
  Median : 49898    Median :2032    Median :   8731.5    Median : 59991.1
  Mean   : 50647    Mean   :2032    Mean   :  38509.9    Mean   : 50965.8
  3rd Qu.: 77030    3rd Qu.:2042    3rd Qu.:100925.0    3rd Qu.: 95284.9
  Max.   :105122    Max.   :2050    Max.   :103500.0    Max.   :102720.0
  Potential Adopters
  Min.   :      0.0
  1st Qu.:    156.9
  Median :   2576.4
  Mean   :  12274.4
  3rd Qu.:  17507.4
  Max.   :100003.0
```

```
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 = 0.075, size=0.1))
        )
```
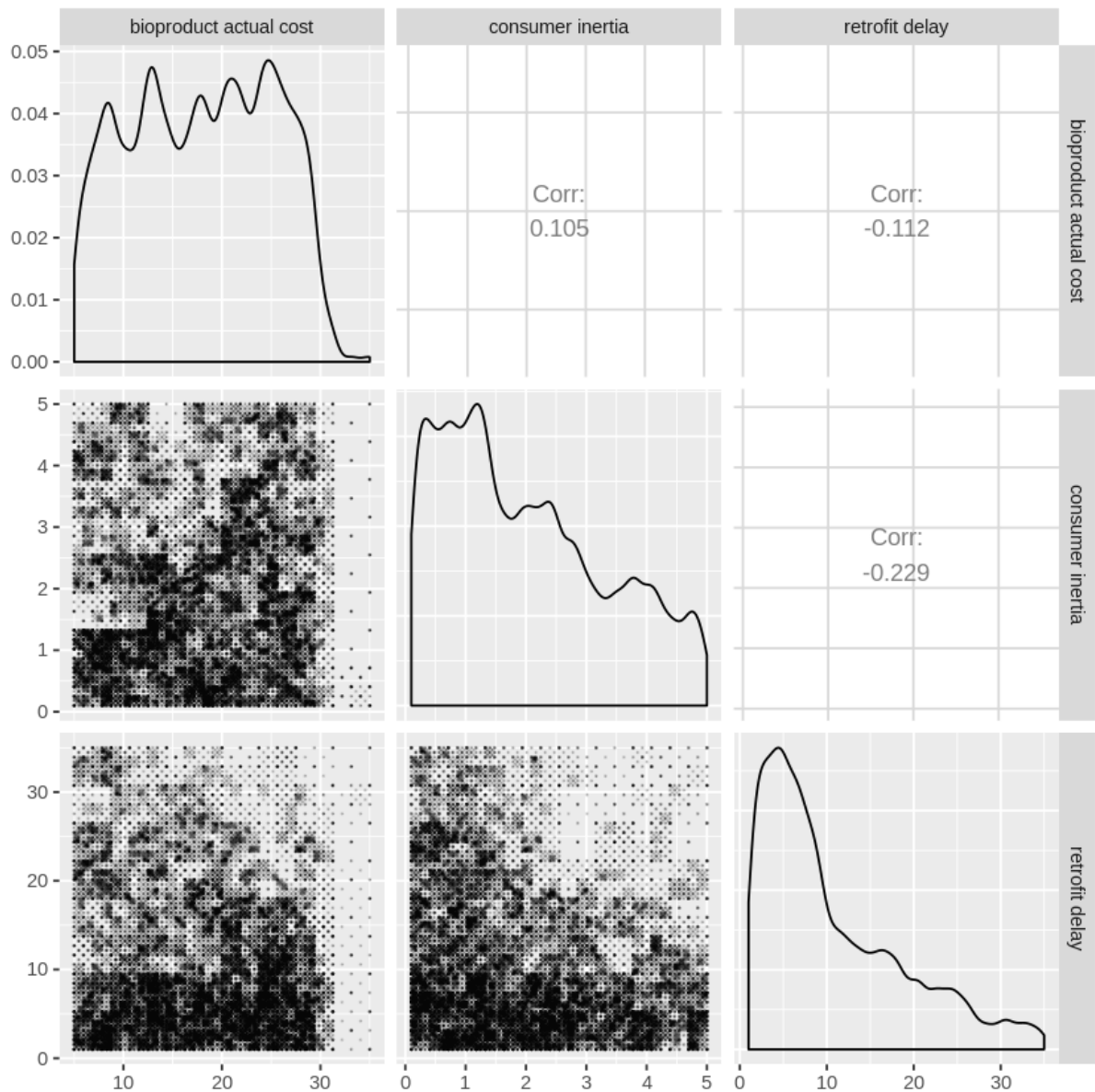

List modes of marginal distributions of sampling pattern.

Bioproduct actual cost.

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

24.8470237649743   13.051469427834   21.1185439457633   17.7968073795571
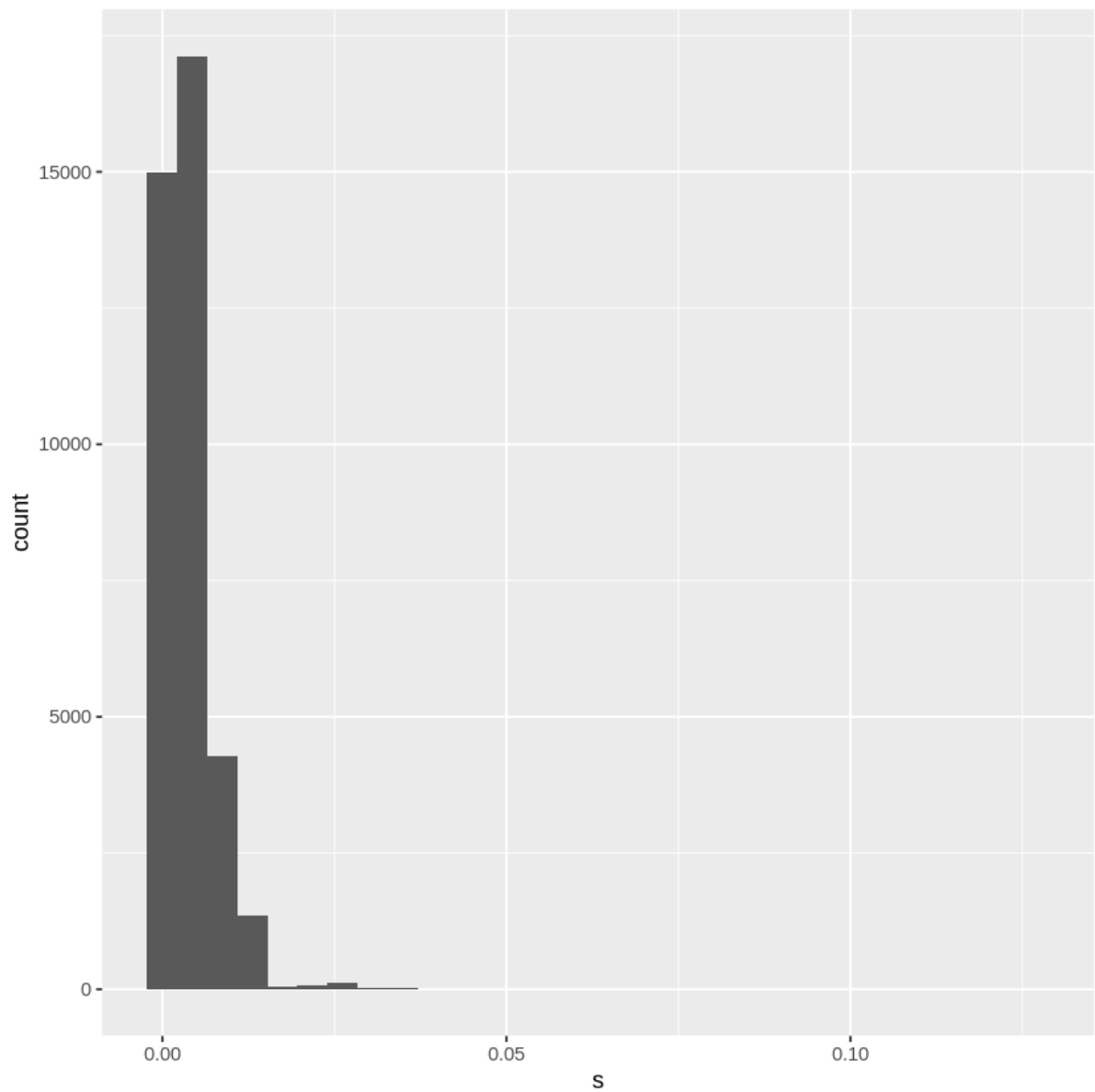8.30613147611093

Consumer inertia.

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

1.15351729694458   0.395911296096708   2.32950273109651   3.7768694192835

Retrofit delay.

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

4.10564224855375   16.037085193009
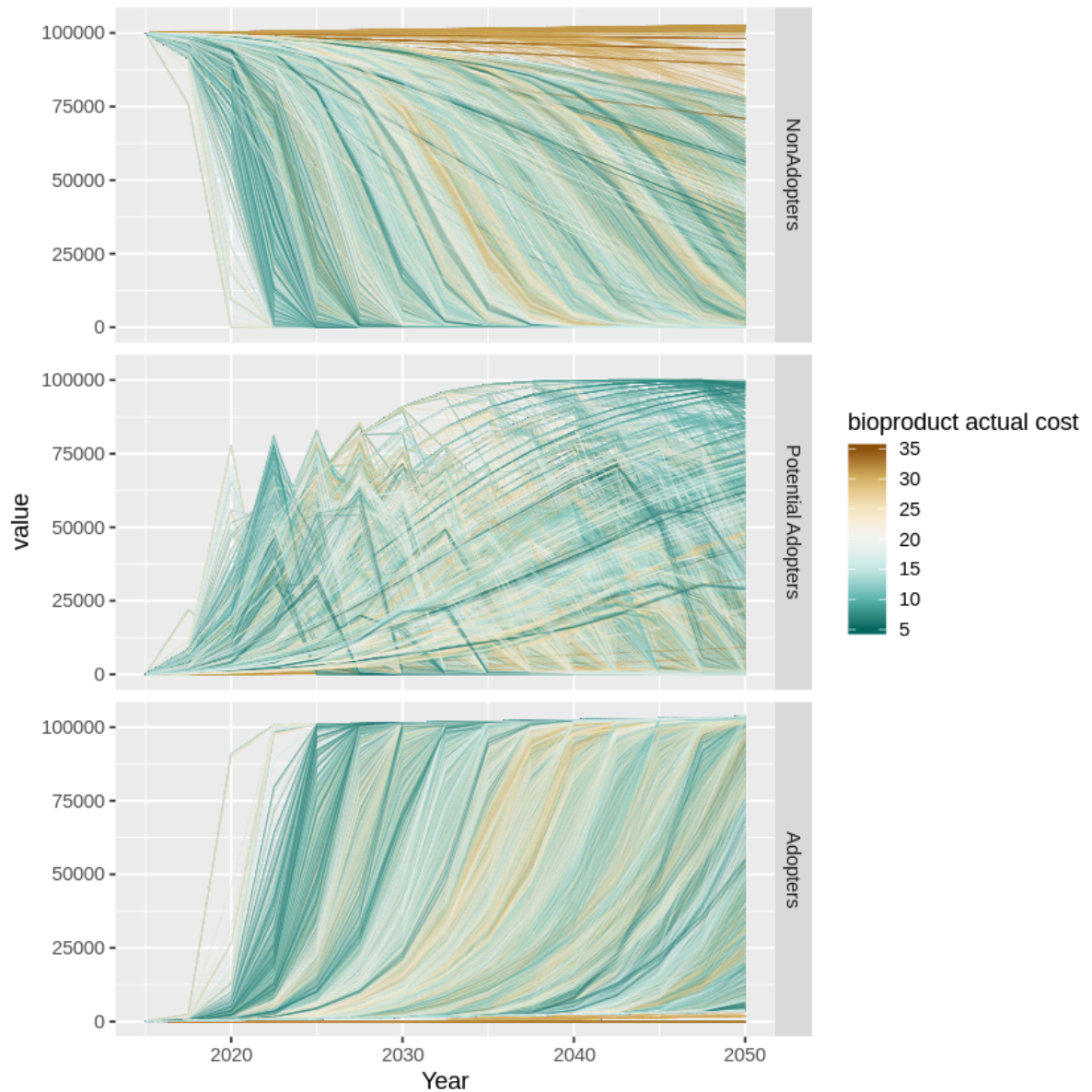
Plot distribution of nonlinearity measure.

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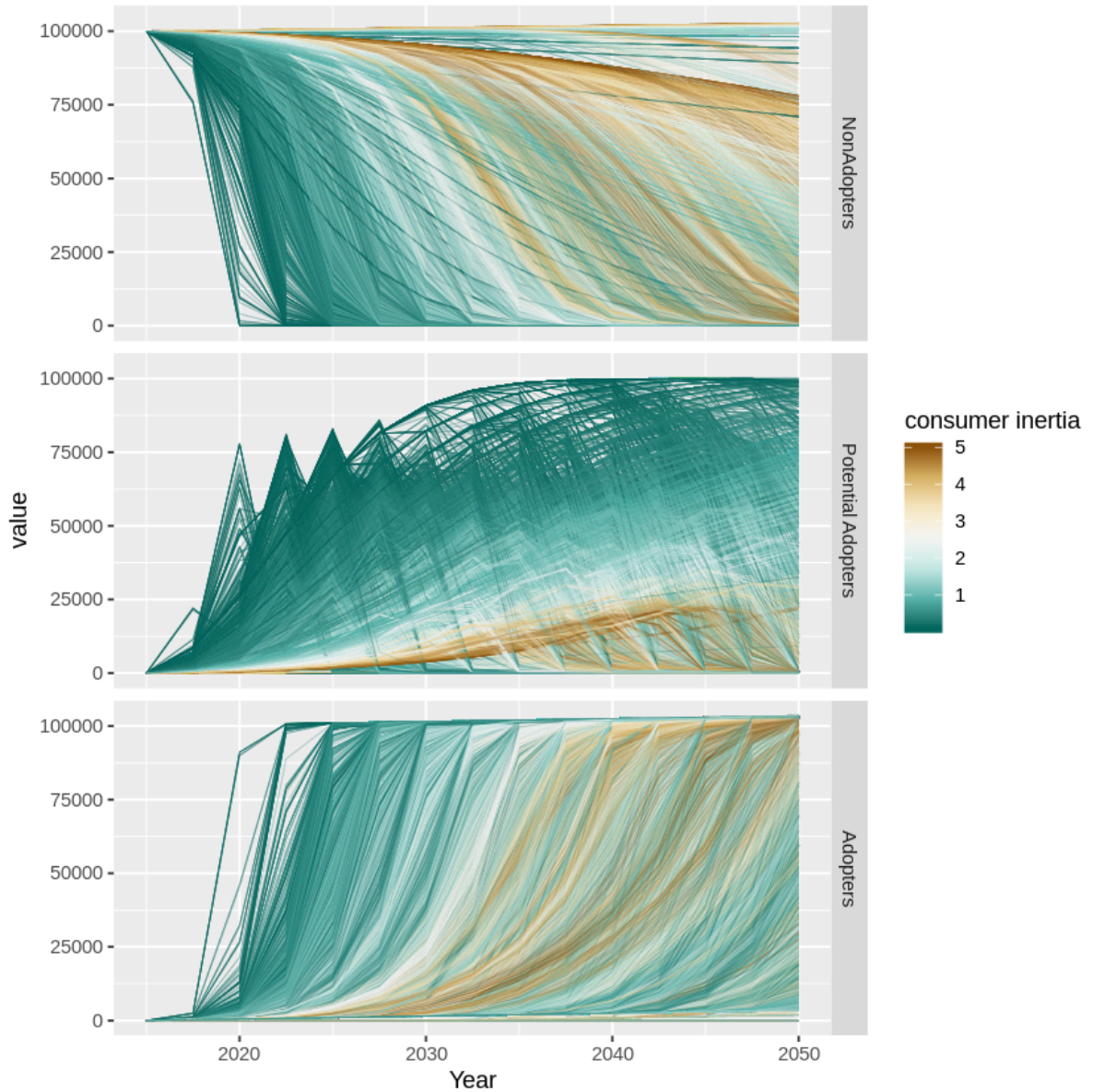

Plot response variables.

## As a function of bioproduct actual cost.

As a function of consumer inertia.

```
In [12]:  ggplot(
              melt(xys, id.vars=c("sequence", "Year", "bioproduct actual cost", "c
          onsumer inertia", "retrofit delay")),
              aes(x=Year, y=value, group=sequence, color=`consumer inertia`)) +
          geom_line(alpha=0.125, size=0.25) +
          scale_color_distiller(type="div") +
          facet_grid(variable ~ .)
```


As a function of retrofit delay.

```
ggplot(
    melt(xys, id.vars=c("sequence", "Year", "bioproduct actual cost", "c
onsumer inertia", "retrofit delay")),
    aes(x=Year, y=value, group=sequence, color=`retrofit delay`)) +
geom_line(alpha=0.125, size=0.25) +
scale_color_distiller(type="div") +
facet_grid(variable ~ .)
```
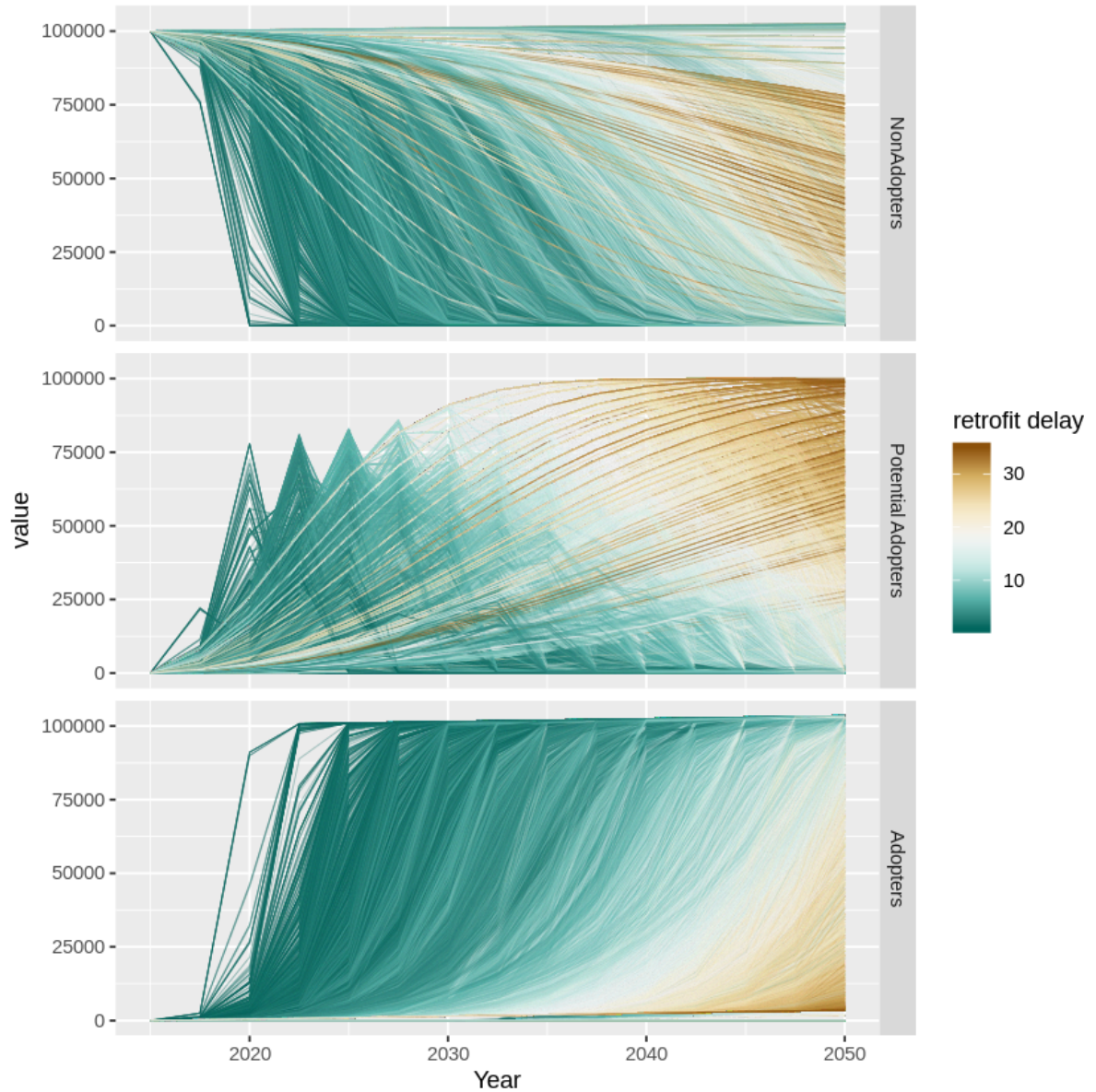

Distribution of output at final year.

```
In [15]: ggpairs(
             xys[Year == 2050],
             6:8,
         #   mapping = aes(color=!probed),
             lower = list(continuous = wrap("points", alpha = 0.1, size=0.1))
         )
```