

```
> soybean <- na.omit(soybean_df)
> nrow(soybean)
[1] 562
> head(soybean)
  class date plant.stand precip temp hail crop.hist area.dam sever seed.tmt germ plant.growth leaves
1 diaporthe-stem-canker 6 0 2 1 0 1 1 1 1 0 0 1 1
2 diaporthe-stem-canker 4 0 2 1 0 2 0 2 1 1 1 1
3 diaporthe-stem-canker 3 0 2 1 0 1 0 2 1 2 1 1
4 diaporthe-stem-canker 3 0 2 1 0 1 0 2 0 1 1 1
5 diaporthe-stem-canker 6 0 2 1 0 2 0 1 0 2 1 1
6 diaporthe-stem-canker 5 0 2 1 0 3 0 1 0 1 1 1
  leaf.halo leaf.marg leaf.size leaf.shread leaf.malf leaf.mild stem lodging stem.cankers canker.lesion fruiting.bodies
1 0 2 2 0 0 0 1 1 3 1 1
2 0 2 2 0 0 0 1 0 3 1 1
3 0 2 2 0 0 0 1 0 3 0 1
4 0 2 2 0 0 0 1 0 3 0 1
5 0 2 2 0 0 0 1 0 3 1 1
6 0 2 2 0 0 0 1 0 3 0 1
  ext.decay mycelium int.discolor sclerotia fruit.pods fruit.spots seed mold.growth seed.discolor seed.size shriveling
1 1 0 0 0 0 4 0 0 0 0 0
2 1 0 0 0 0 4 0 0 0 0 0
3 1 0 0 0 0 4 0 0 0 0 0
4 1 0 0 0 0 4 0 0 0 0 0
5 1 0 0 0 0 4 0 0 0 0 0
6 1 0 0 0 0 4 0 0 0 0 0
  roots
1 0
2 0
3 0
4 0
5 0
6 0
> preproc <- preProcess(soybean[, -1], method = c("center", "scale"))
> soybean[, -1] <- predict(preproc, soybean[, -1])
> set.seed(123)
```

```
> soybean_df <- read.csv("D:\\S5\\ML\\exp5\\Soybean.csv")
> nrow(soybean_df)
[1] 683
> head(soybean_df)
  class date plant.stand precip temp hail crop.hist area.dam sever seed.tmt germ plant.growth leaves
1 diaporthe-stem-canker 6 0 2 1 0 1 1 1 1 0 0 1 1
2 diaporthe-stem-canker 4 0 2 1 0 2 0 2 1 1 1 1
3 diaporthe-stem-canker 3 0 2 1 0 1 0 2 1 2 1 1
4 diaporthe-stem-canker 3 0 2 1 0 1 0 2 0 1 1 1
5 diaporthe-stem-canker 6 0 2 1 0 2 0 1 0 2 1 1
6 diaporthe-stem-canker 5 0 2 1 0 3 0 1 0 1 1 1
  leaf.halo leaf.marg leaf.size leaf.shread leaf.malf leaf.mild stem lodging stem.cankers canker.lesion fruiting.bodies
1 0 2 2 0 0 0 1 1 3 1 1
2 0 2 2 0 0 0 1 0 3 1 1
3 0 2 2 0 0 0 1 0 3 0 1
4 0 2 2 0 0 0 1 0 3 0 1
5 0 2 2 0 0 0 1 0 3 1 1
6 0 2 2 0 0 0 1 0 3 0 1
  ext.decay mycelium int.discolor sclerotia fruit.pods fruit.spots seed mold.growth seed.discolor seed.size shriveling
1 1 0 0 0 0 4 0 0 0 0 0
2 1 0 0 0 0 4 0 0 0 0 0
3 1 0 0 0 0 4 0 0 0 0 0
4 1 0 0 0 0 4 0 0 0 0 0
5 1 0 0 0 0 4 0 0 0 0 0
6 1 0 0 0 0 4 0 0 0 0 0
  roots
1 0
2 0
3 0
4 0
5 0
6 0
> sum(is.na(soybean_df))
[1] 2337
```

```
> testing_data <- soybean[-splitIndex, ]
> nrow(testing_data)
[1] 110
> head(testing_data)
  class date plant.stand precip temp hail crop.hist area.dam sever
1 diaporthe-stem-canker 1.3586630 -0.7864439 0.5799624 -0.2411884 -0.5398468 -0.8970066 -0.5709737 0.447054
5 diaporthe-stem-canker 1.3586630 -0.7864439 0.5799624 -0.2411884 -0.5398468 0.1255445 -1.4723422 0.447054
16 charcoal-rot 0.7560043 -0.7864439 -2.2298555 1.3724766 1.8490814 1.1480957 1.2317634 0.447054
19 charcoal-rot -0.4493132 -0.7864439 -2.2298555 1.3724766 -0.5398468 0.1255445 0.3303949 0.447054
26 rhizoctonia-root-rot -1.6546307 1.2692839 0.5799624 -1.8548534 -0.5398468 1.1480957 -0.5709737 2.122016
28 rhizoctonia-root-rot -1.0519719 1.2692839 0.5799624 -1.8548534 -0.5398468 0.1255445 -0.5709737 0.447054
  seed.tmt germ plant.growth leaves leaf.halo leaf.marg leaf.size leaf.shread leaf.malf leaf.mild
1 -0.8486412 -1.33723184 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796
5 -0.8486412 1.19742008 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796
16 0.7847025 1.19742008 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796
19 -0.8486412 1.19742008 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796
26 -0.8486412 1.19742008 1.76827 -2.8372815 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796
28 -0.8486412 -0.06990588 1.76827 -2.8372815 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796
  stem lodging stem.cankers canker.lesion fruiting.bodies ext.decay mycelium int.discolor sclerotia
1 1.002672 3.5155259 1.5289869 0.1077633 2.3032912 1.7768891 -0.103789 -0.335347 -0.1919237
5 1.002672 -0.2839463 1.5289869 0.1077633 2.3032912 1.7768891 -0.103789 -0.335347 -0.1919237
16 1.002672 -0.2839463 -0.7126408 1.9430043 -0.4333888 -0.5617799 -0.103789 4.151915 5.2011325
19 1.002672 -0.2839463 -0.7126408 1.9430043 -0.4333888 -0.5617799 -0.103789 4.151915 5.2011325
26 1.002672 -0.2839463 0.0345684 0.1077633 -0.4333888 1.7768891 -0.103789 -0.335347 -0.1919237
28 1.002672 -0.2839463 0.0345684 0.1077633 -0.4333888 1.7768891 -0.103789 -0.335347 -0.1919237
  fruit.pods fruit.spots seed mold.growth seed.discolor seed.size shriveling roots
1 -0.5102642 1.984213 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
5 -0.5102642 1.984213 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
16 -0.5102642 1.984213 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
19 -0.5102642 1.984213 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
26 3.1506098 1.984213 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
28 3.1506098 1.984213 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185

> splitIndex <- createDataPartition(soybean$class, p = 0.8, list = FALSE)
> training_data <- soybean[splitIndex, ]
> nrow(training_data)
[1] 452
> head(training_data)
  class date plant.stand precip temp hail crop.hist area.dam sever seed.tmt
2 diaporthe-stem-canker 0.1533456 -0.7864439 0.5799624 -0.2411884 -0.5398468 0.1255445 -1.472342 2.122016 0.7847025
3 diaporthe-stem-canker -0.4493132 -0.7864439 0.5799624 -0.2411884 -0.5398468 -0.8970066 -1.472342 2.122016 0.7847025
4 diaporthe-stem-canker -0.4493132 -0.7864439 0.5799624 -0.2411884 -0.5398468 -0.8970066 -1.472342 2.122016 -0.8486412
6 diaporthe-stem-canker 0.7560043 -0.7864439 0.5799624 -0.2411884 -0.5398468 1.1480957 -1.472342 0.447054 -0.8486412
7 diaporthe-stem-canker 0.7560043 -0.7864439 0.5799624 -0.2411884 1.8490814 -0.8970066 -1.472342 0.447054 -0.8486412
8 diaporthe-stem-canker 0.1533456 -0.7864439 0.5799624 -0.2411884 1.8490814 -0.8970066 -1.472342 0.447054 -0.8486412
  germ plant.growth leaves leaf.halo leaf.marg leaf.size leaf.shread leaf.malf leaf.mild stem lodging
2 -0.06990588 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796 1.002672 -0.2839463
3 1.19742008 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796 1.002672 -0.2839463
4 -0.06990588 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796 1.002672 -0.2839463
6 -0.06990588 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796 1.002672 -0.2839463
7 -1.33723184 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796 1.002672 3.5155259
8 1.19742008 1.76827 0.3518229 -1.361203 1.385862 1.249163 -0.4534777 -0.196845 -0.2613796 1.002672 -0.2839463
  stem.cankers canker.lesion fruiting.bodies ext.decay mycelium int.discolor sclerotia fruit.pods fruit.spots
2 1.528987 0.1077633 2.303291 1.776889 -0.103789 -0.335347 -0.1919237 -0.5102642 1.984213
3 1.528987 -0.8098572 2.303291 1.776889 -0.103789 -0.335347 -0.1919237 -0.5102642 1.984213
4 1.528987 -0.8098572 2.303291 1.776889 -0.103789 -0.335347 -0.1919237 -0.5102642 1.984213
6 1.528987 -0.8098572 2.303291 1.776889 -0.103789 -0.335347 -0.1919237 -0.5102642 1.984213
7 1.528987 0.1077633 2.303291 1.776889 -0.103789 -0.335347 -0.1919237 -0.5102642 1.984213
8 1.528987 0.1077633 2.303291 1.776889 -0.103789 -0.335347 -0.1919237 -0.5102642 1.984213
  seed mold.growth seed.discolor seed.size shriveling roots
2 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
3 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
4 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
6 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
7 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
8 -0.4333888 -0.3190288 -0.3087825 -0.2372565 -0.2063872 -0.1364185
```