Modeling Point Processes with Spatstat
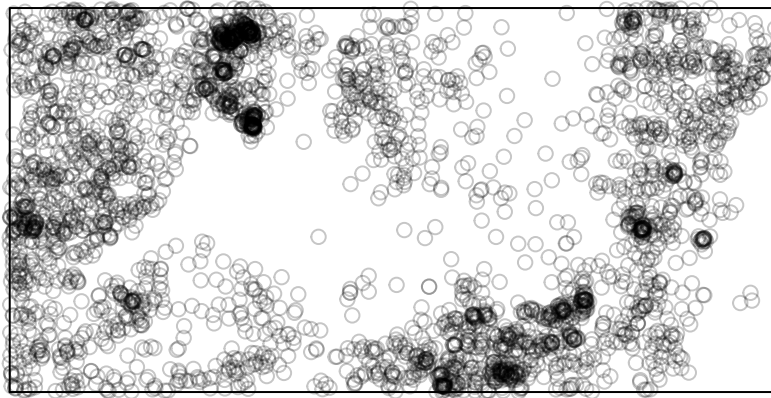
Model Fitting

The `ppm` function can be used for model fitting with a point process.
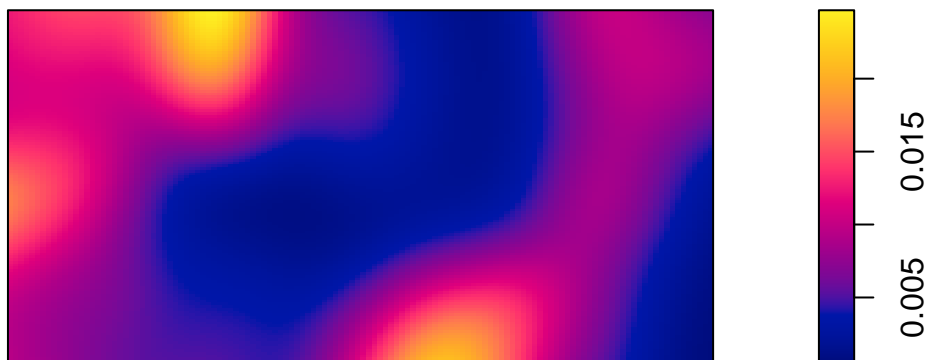
```
plot(bei)
```
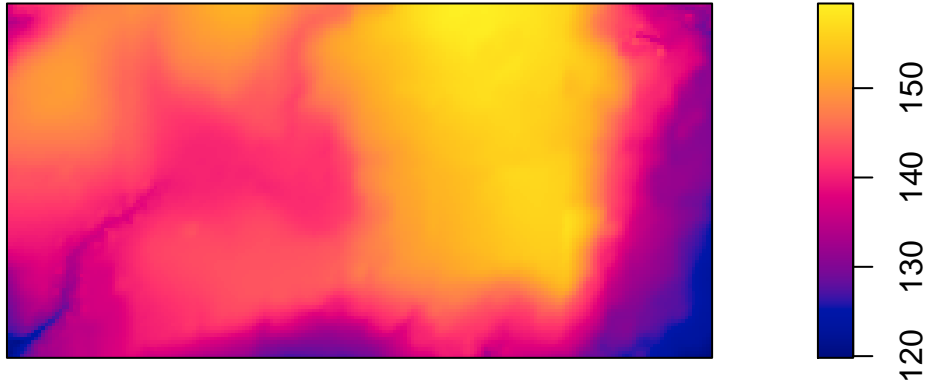
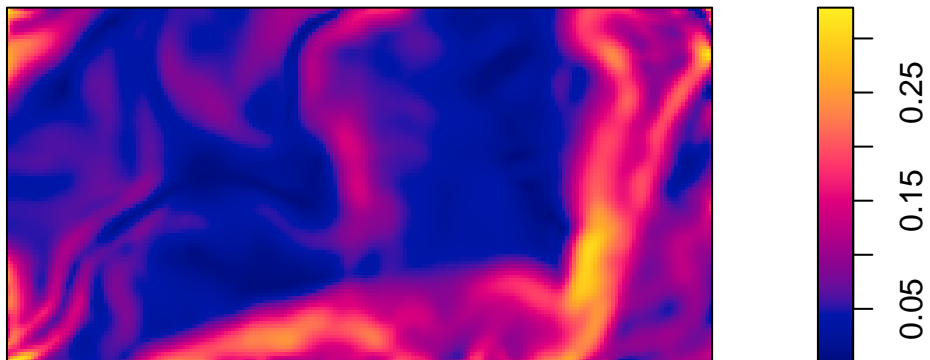**bei**


```
plot(density.ppp(bei))
```

density.ppp(bei)

```
elev <- bei.extra$elev
grad <- bei.extra$grad
plot(elev)
```

elev


```
plot(grad)
```

grad

The `ppm` function allows model fitting

```
tree.model <- ppm(bei ~ elev + grad);
tree.model
```

```
## Nonstationary Poisson process
##
## Log intensity:  ~elev + grad
##
## Fitted trend coefficients:
## (Intercept)        elev        grad
## -8.56355220  0.02143995  5.84646680
##
##                Estimate         S.E.       CI95.lo       CI95.hi Ztest        Zval
## (Intercept) -8.56355220 0.341113849 -9.23212306 -7.89498134   *** -25.104675
## elev         0.02143995 0.002287866  0.01695581  0.02592408   ***   9.371155
## grad         5.84646680 0.255781018  5.34514522  6.34778838   ***  22.857313
```

```
plot(tree.model)
```
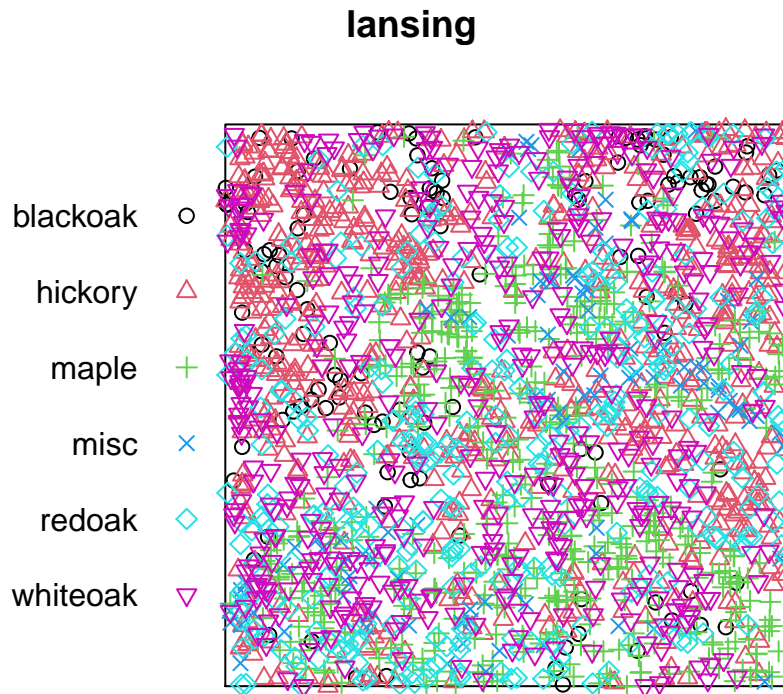
Fitted trend
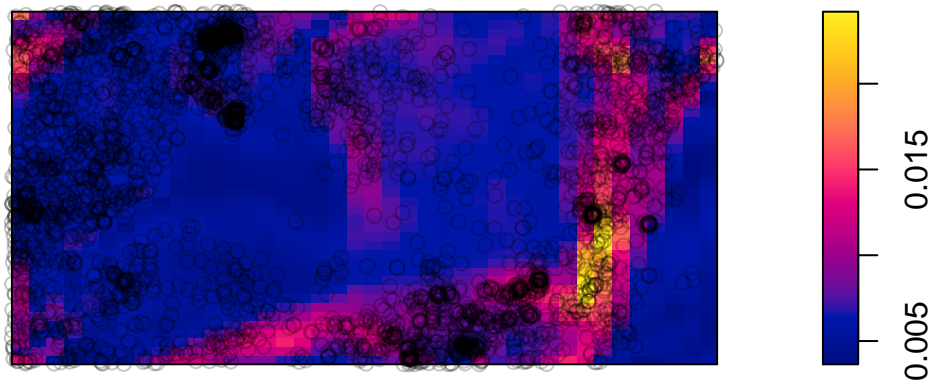
Estimated se
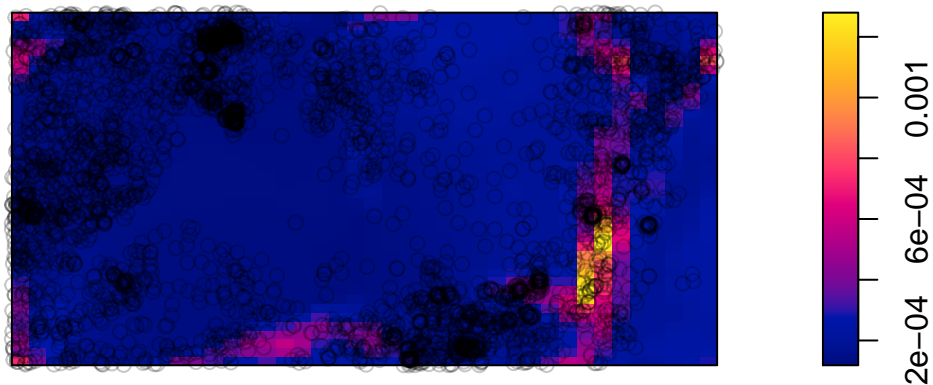
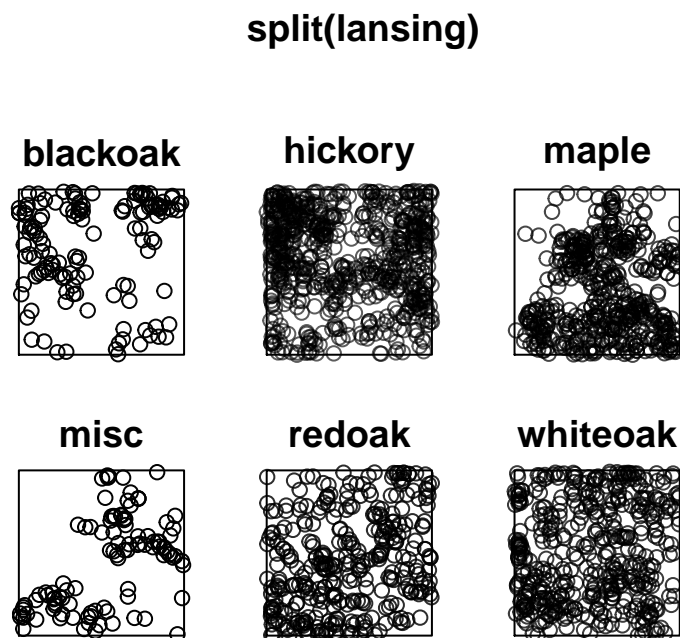For more complicated models, `kppm` can be used for clustering behavior.

Marked Point Patterns

The `lansing` data set contains locations of six types of trees.

```
plot(lansing, cols = 1:6)
```

lansing


```
plot(split(lansing))
```

split(lansing)

To analyze this data, consider the following model.

```
lansing.model <- ppm(lansing ~  marks - 1)
lansing.model
```

```
## Stationary multitype Poisson process
##
## Possible marks: 'blackoak', 'hickory', 'maple', 'misc', 'redoak' and 'whiteoak'
##
## Log intensity:  ~marks - 1
##
## Intensities:
## beta_blackoak  beta_hickory    beta_maple     beta_misc   beta_redoak
##           135           703           514           105           346
## beta_whiteoak
##           448
##
##               Estimate        S.E.  CI95.lo  CI95.hi Ztest      Zval
## marksblackoak 4.905275 0.08606630 4.736588 5.073962   *** 56.99414
## markshickory  6.555357 0.03771571 6.481435 6.629278   *** 173.80970
## marksmaple    6.242223 0.04410811 6.155773 6.328674   *** 141.52099
## marksmisc     4.653960 0.09759001 4.462687 4.845233   ***  47.68890
## marksredoak   5.846439 0.05376033 5.741070 5.951807   *** 108.75005
## markswhiteoak 6.104793 0.04724556 6.012194 6.197393   *** 129.21412
```
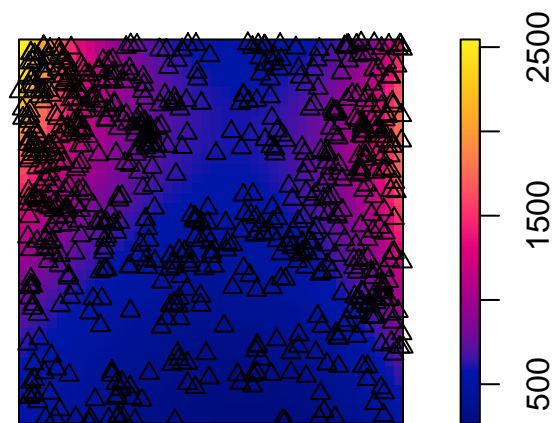
In contrast with this model, we can also include

```
lansing.model2 <- ppm(lansing ~  marks * polynom(x,y,3))
#lansing.model2
plot(lansing.model2)
```
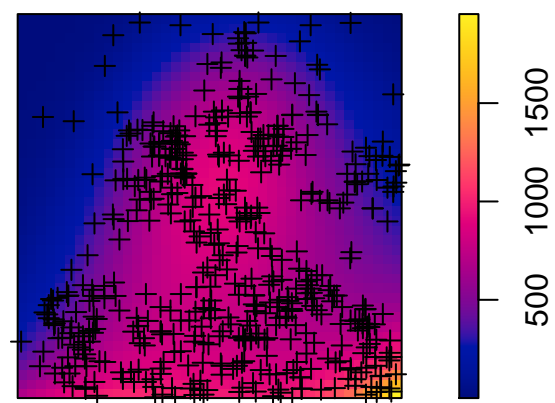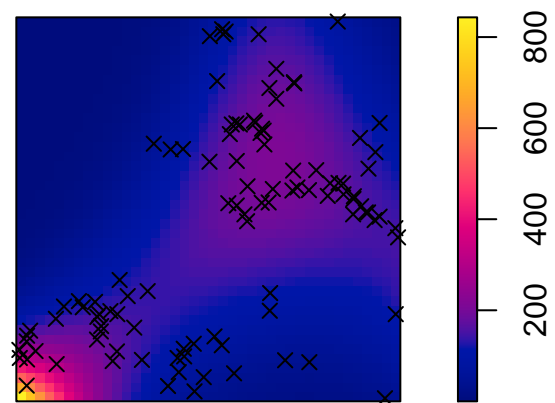
Fitted trend
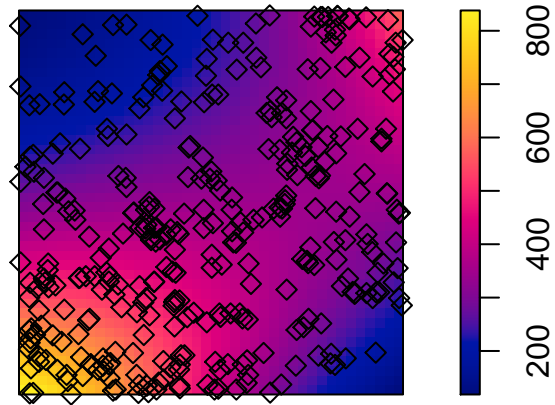## mark = blackoak
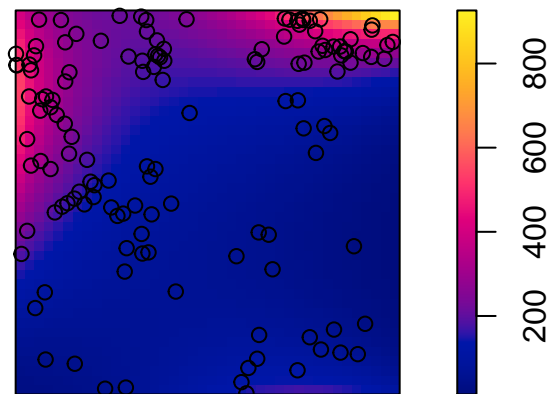
**Fitted trend
mark = hickory**

**Fitted trend
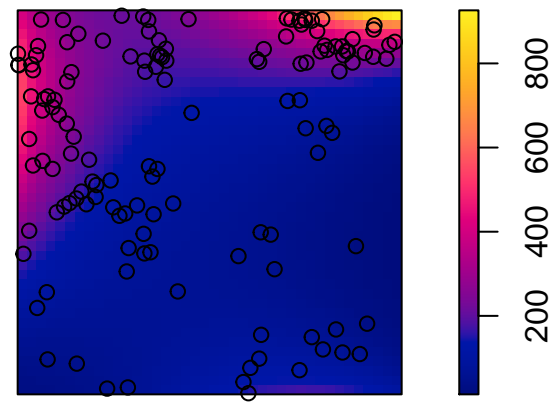mark = maple**

**Fitted trend
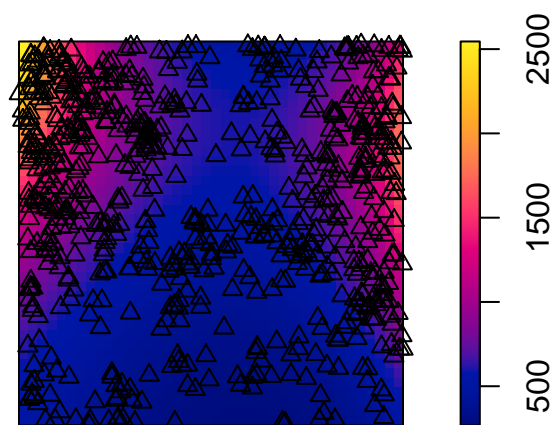mark = misc**

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Fitted trend
mark = redoak

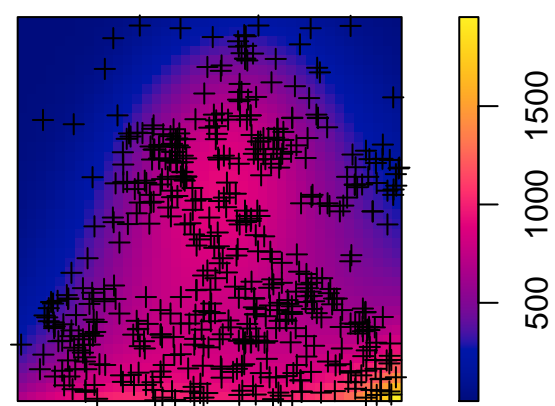**Fitted trend**
mark = whiteoak
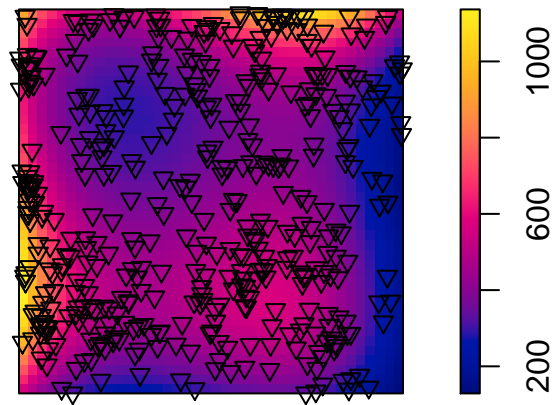
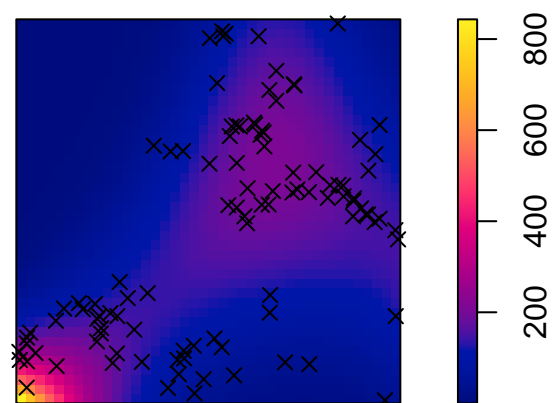**Estimated se**
mark = blackoak
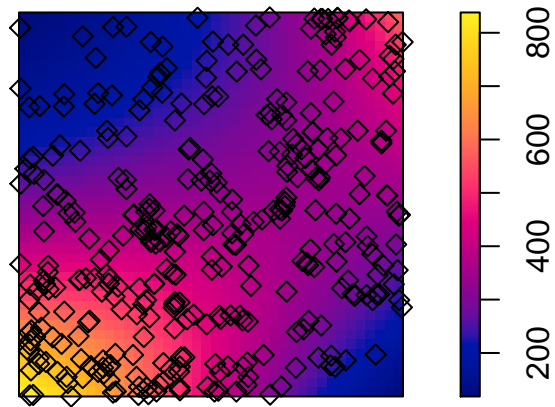
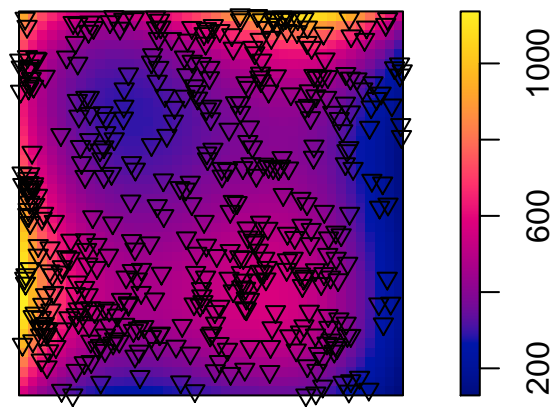**Estimated se
mark = hickory**

**Estimated se
mark = maple**

**Estimated se
mark = misc**

Estimated se
mark = redoak

Estimated se
mark = whiteoak

More advanced point pattern models

Cluster processes   Clustering is not well defined. In general the idea is that the point distances are shorter than expected. However, there "is a fundamental ambiguity between heterogeneity and clustering" (Diggle 2007).