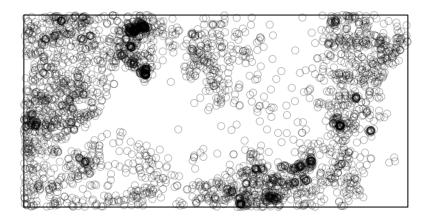
Modeling Point Processes with Spatstat

Model Fitting

The ppm function can be used for model fitting with a point process.

plot(bei)

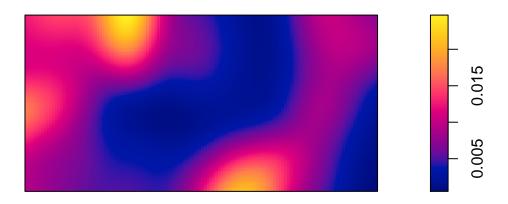
bei



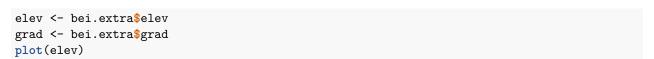
The bei dataset contains locations of trees in a tropical rain forest. The point pattern is clearly non-homogenous

plot(density.ppp(bei))

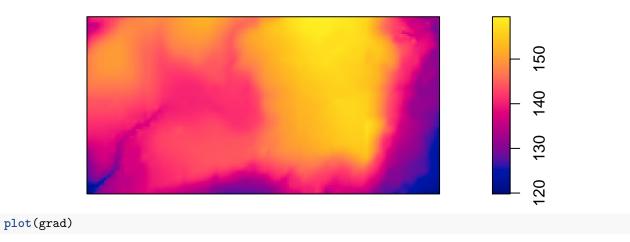
density.ppp(bei)



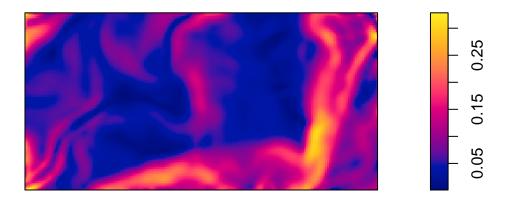
The pattern in the intensity of the trees may be related to elevation and the elevation gradient.



elev



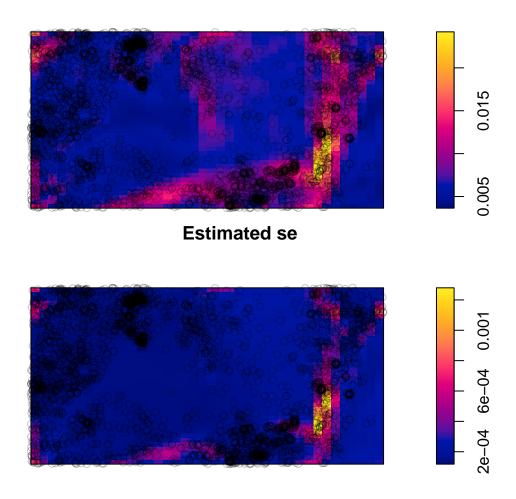
grad



The ppm function allows model fitting

```
tree.model <- ppm(bei ~ elev + grad);</pre>
tree.model
## Nonstationary Poisson process
##
## Log intensity: ~elev + grad
##
## Fitted trend coefficients:
## (Intercept)
                                    grad
## -8.56355220 0.02143995 5.84646680
##
##
                                             CI95.lo
                                   S.E.
                                                          CI95.hi Ztest
                                                                               Zval
                  Estimate
## (Intercept) -8.56355220 0.341113849 -9.23212306 -7.89498134
                                                                        -25.104675
## elev
                0.02143995\ 0.002287866 \quad 0.01695581 \quad 0.02592408
                                                                           9.371155
## grad
                5.84646680\ 0.255781018\ 5.34514522\ 6.34778838
                                                                          22.857313
plot(tree.model)
```

Fitted trend



For more complicated models, kppm can be used for clustering behavior.

Marked Point Patterns

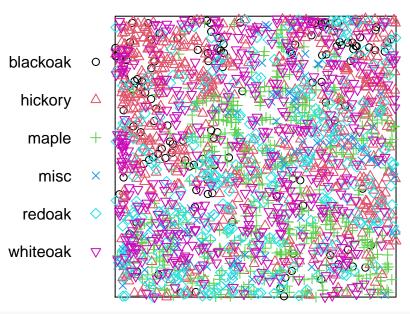
Marked point process data contains meta data for each point. Rather than just s, we have (s, m).

The marked information can either be categorical (multi-type) or continuous.

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

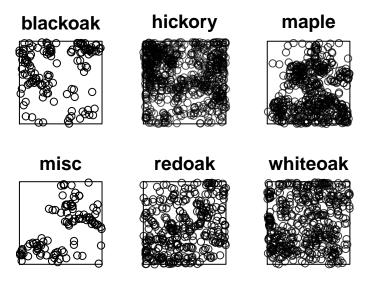
plot(lansing, cols = 1:6)

lansing



plot(split(lansing))

split(lansing)



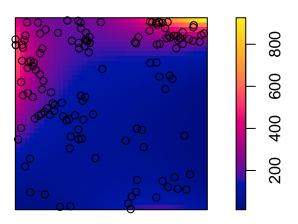
To analyze this data, consider the following model.

```
lansing.model <- ppm(lansing ~ marks - 1)</pre>
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
                                                                      346
             135
                           703
                                         514
                                                        105
##
## beta_whiteoak
##
             448
##
                                S.E. CI95.lo CI95.hi Ztest
##
                 Estimate
                                                                   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
```

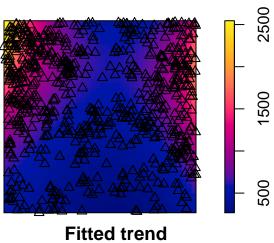
In contrast with this model, we can also include

```
lansing.model2 <- ppm(lansing ~ marks * polynom(x,y,3))
#lansing.model2
plot(lansing.model2)</pre>
```

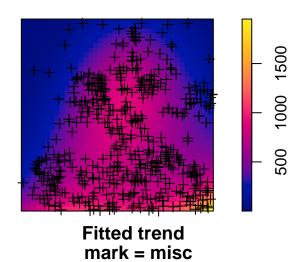
Fitted trend mark = blackoak



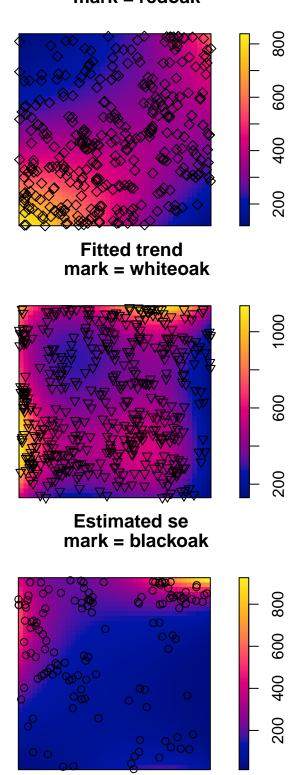
Fitted trend mark = hickory



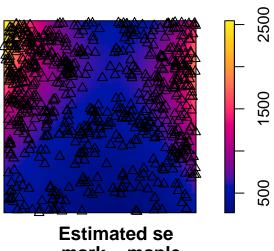
Fitted trend mark = maple



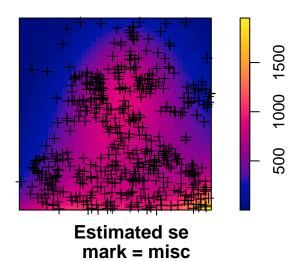
Fitted trend mark = redoak



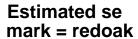
Estimated se mark = hickory

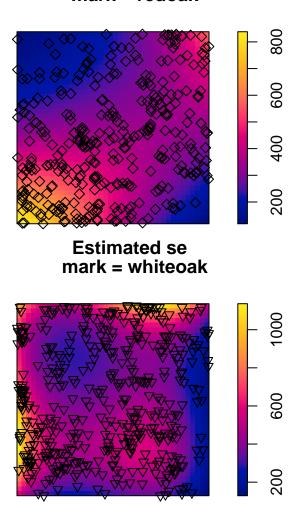


mark = maple



200





Similarly continuous marked data can be included as a predictor i the ppm framework, potentially with interactions with spatially referenced data.

Marked point process data can also be used for spatial-temporal point patterns, where the year corresponds to the mark.

| 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" (Diggi 2007). |
|---|
| Neyman-Scott Process: This is a two stage process. |
| 1. Generate parents |
| 2. For each parent, generate a set of offspring |
| The shot noise processes are variations on the Neyman-Scott process, also with a two stage process. |
| Strauss Process: contains a term that allows repulsion by adjusting the intensity in a vicinity of an existing point. The "hardcore" process will make the intensity 0 for any pair of points less than a specified distant d_0 . |