Practical session: R library spatstat

Examples of point pattern data:

- **amacrine** (rabbit amacrine cells, locations and 2 types)
- **anemones** (sea anemones data, locations and sizes)
- **ants** (ant nests data, locations and 2 types)
- **bei** (tropical rainforest trees, locations)
- **betacells** (cat retinal ganglia data, locations, 2 types and sizes)
- **bramblecanes** (Bramble Canes data, locations and 3 types)
- **cells** (biological cells data, locations)
- **chorley** (cancer data, locations and 2 types)
- **finpines** (Finnish Pines data, locations and 2 size measures)
- **hamster** (hamster tumour data, locations and 2 types)
- **japanesepines** (Japanese Pines data, locations)
- **lansing** (Lansing Woods data, locations and 6 types)
- **longleaf** (Longleaf Pines data, locations and sizes)
- **nztrees** (trees data, locations)
- **ponderosa** (ponderosa pine trees data, locations)
- **redwood** (redwood saplings data, locations)
- **spruces** (Spruce trees in Saxonia, locations and sizes)
- **swedishpines** (Swedish pines data, locations)
- **urkiola** (Urkiola Woods data, locations and 2 types)

**Task 1:** Choose some of the point pattern data above and use `summary` to print a summary of the point pattern. Plot the data by using `plot` or `plot.ppp`.

Choose a few point patterns which you would like to investigate further. Pick, for example, at least one pattern that looks regular and one that looks clustered, and one multitype pattern and one marked pattern (with size information).

**Task 2:** Estimate and plot the summary statistics F, G, J and K by using `Fest`, `Gest`, `Jest`, and `Kest` or `allstats`. (`allstats` works only for unmarked data, the marks can be ignored by using `unmark`.) Try also the functions `Lest` and `pcf`.

Use `help` to see a description of these function.

**Task 3:** To test complete spatial randomness: function `envelope`. Take some of the data sets and try this function. You can try different summary functions (default is the K function).
**Task 4:** Fit a Matern cluster model for one of the clustered point patterns by using the function `kppm(X, clusters="MatClust")` \((X\) is the point pattern).

You can save the result e.g. by writing e.g.
```
modell<-kppm(X, clusters="MatClust")
```

and use
```
plot.kppm(modell)
```
to plot the estimated K function for the data and for the fitted model, and
```
plot(envelope(modell))
```
to check the goodness-of-fit of the model.

**Task 5:** To fit a Strauss model for one of the regular point patterns, one can use the function `ppm(X, ~1, Strauss(r1))` \((r1\) is the interaction radius you have chosen).

You can save the result e.g. by writing e.g.
```
model2<-ppm(X, ~1, Strauss(r1))
```

and use
```
plot(envelope(model2))
```
to check the goodness-of-fit of the model.

**Task 6:** Residuals for a fitted point process model can be plotted e.g. by using `diagnose.ppm` which works for objects of class "ppm" (Strauss process).

**Task 7:** For multitype data, you can estimate and plot the summary functions separately for each type.

Use `help` to see description of `Gcross`, `Kcross`, and `Jcross` (if only two types of points) or `Gmulti`, `Kmulti` and `Jmulti` (if more than two types of points, specify the types you want to study). Apply these functions to some of the data sets to see whether one would suggest any dependence between points of two types.

**Task 8:** For marked data, you can estimate and plot the mark correlation function by using `markcorr`. First, use `help` to see what the function does.