**Problem**

Given a region R, subdivided into two parts (R1 and R2), determine whether the distribution of points that fall into R1 is significantly different than the distribution of points that fall into R2. Parts R1 and R2 may each be comprised of several non-contiguous polygons within R. The areas of R1 and R2 are denoted as A1 and A2, respectively.

**Hypothesis Testing**

Intuitively, if the distribution of points is the same in R1 and R2, then the ratio of the expected numbers of points in R1 and R2 should be equal to the ratio of their respective areas, A1 and A2. This is our null hypothesis and is the same as saying that the number of points per unit area are the same in R1 and R2. The null and alternative hypotheses are formulated below.

**H0:** number of points per unit area in R1 = number of points per unit area in R2

**Ha1:** number of points per unit area in R1 < number of points per unit area in R2

**Ha2:** number of points per unit area in R1 > number of points per unit area in R2

However, because there’s no immediately clear parametric test to assess what constitutes a significant deviation from what we would expect under H0, we can resort to Markov Chain Monte Carlo (MCMC) simulations for hypothesis testing. We use the MCMC approach to simulate 9, 99, 999 or 9999 random point patterns in R, and calculate the number of points in R1 and R2, as well as the ratio , for our original point pattern and for each simulated pattern (i.e., for all 10, 100, 1000, or 10000 point patterns).

Then, we can arrange all values of the ratio in *ascending* order, identify the *rank* of this ratio for our original point pattern (e.g., 5th highest, 278th highest, etc.), and divide this rank by the total number of point patterns (10, 100, 1000, 10000, etc.) to obtain a one-sided pseudo p-value for Ha1. For example, if the rank of the ratio in our original point pattern is 5 and we have 10000 total point patterns, then the pseudo p-value would be 5/1000 = 0.005, which means that it would be very unlikely for us to see a ratio as low as the one that we observe in our data simply by chance. To obtain the pseudo p-value for Ha2, we would repeat the same process, except we would sort the values of ratio in *descending* order.