Multivariate Nonparametric Tests

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Overview

► So far, we have seen only univariate nonparametric tests

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- Today, we'll cover multivariate generalizations
- Two-sample tests
 - Data depth-based: Tukey depth function
 - Graph-based: Friedman and Rafsky test

- In univariate nonparametric analysis, we relied heavily on ranks
- Ranks are straightforward in the univariate case
- We just use the natural ordering of observations along the real line
- Moving from univariate to multivariate setting, we need to make some more considerations
- In \mathbb{R}^d there is no natural ordering
- Just a straightforward extension of the median to define a center can fail
- ► A ℝ^d coordinate-wise median can lie outside the convex hull of the data

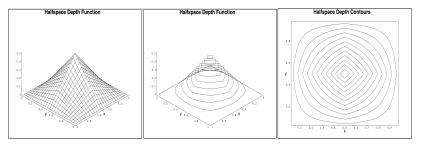
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- The usual ranks:
 - We ranked n observations in ascending order
 - From that we constructed test statistics
 - For instance, the median is defined as the order statistics of rank (n + 1)/2 (when n is odd)
 - The median can be computed in O(n) time
 - The problem is that generalizing this to higher dimension is straightforward
- So we consider a different ranking system
- We rank observations as assigning
 - the most extreme observation depth 1
 - the second smallest and second largest observations depth 2
 - Until we end up with the deepest observation, the median
- This can be extended to higher dimensions more easily

- Tukey propsed the depth function to address this issue
- Take a distribution F on \mathbb{R}^d
- A depth function D(x, F)
- ► Then, the Half space depth function proposed by Tukey, for x ∈ ℝ² is:

 $D_H(x,F) = \inf\{F(H) : x \in H \text{ closed halfspace}\}$

• Example: Uniform distribution on the unit square in \mathbb{R}^2



Source: Serfling (2011). (Slides)

 In contrast, density function is constant with no contours of equal density

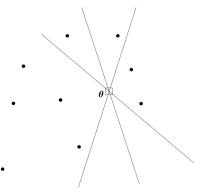
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The sample halfspace depth of θ is the minimum fraction of data points in any closed halfspace containing θ

$$D_H(\theta, X_1, \dots, X_n) = \min_{\|u\|=1} \min_{i=1} \sum_{i=1}^n I(u^T X_i \ge u^T \theta)$$

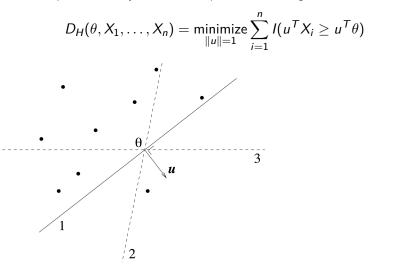
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Source: Rousseeuw and Struyf (1998)

The sample halfspace depth of x is the minimum fraction of data points in any closed halfspace containing θ



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Source: Rousseeuw and Hubert (2015)

- Let $X_1, \ldots, X_{n_1} \sim F$ and $Y_1, \ldots, Y_{n_2} \sim G$
- Null hypothesis $H_0: F = G$
- Alternative: different location shift and/or a scale
- Liu and Singh (1993) test statistic :

$$Q = \sum_{j=1}^{n_2} \sum_{i=1}^{n_1} I(D(X_i, \{X_1, \ldots, X_{n_1}\}) \le D(Y_j, \{X_1, \ldots, X_{n_1}\}))$$

- The statistic Q gauges the overall "outlyingness" of the G population with respect to the given F population
- It can detect whether G has a different location and/or has additional dispersion as compared to F

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 Special case: Depth function for the univariate Mann-Whitney test

$$T = \sum_{j=1}^{n_2} \sum_{i=1}^{n_1} I(X_i < Y_j)$$

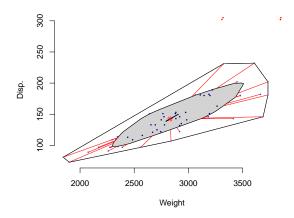
by taking

$$D(x,F)=F(x)$$

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Zuo and He (2006) proved asymptotic normality of this statistic

Car Data Chambers/Hastie 1992



- The star is the Tukey median
- Bag: The dark area contains 50%
- ▶ Fence: Inflating the "bag" by factor 3 relative to Tukey median
- Loop: Convex hull containing all points inside the fence

- Gets increasingly difficult to compute in high dimensions
- Computation time is polynomial in n but exponential in d
- ► Rousseeuw and Struyf (1998) proposed an approximation
- They compute *m* random directions out of all ⁽ⁿ⁾_d directions perpendicular to hyperplanes through *d* data points

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- Set current depth to n
- Repeat *m* times:
 - Draw a random sample of size d
 - Determine a direction u perpendicular to the d-subset
 - Project all data points on the line L through θ with direction u

- Compute the univariate depth k of θ on L
- Set depth to min(current depth, k)
- This algorithm has time complexity $O(md^3 + mdn)$

- Alternative multivariate nonparametric tests are based on graphs
- We consider one test based on minimal spanning trees
- A set of *n* points in \mathbb{R}^d can be computed in $O(dn^2)$ time

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- The Wald-Wolfowitz runs test can be used to evaluate sequences of runs
- ► For instance to test whether the following sequence is random HHHTTTHHHTHHHTTTT

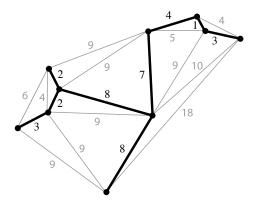
- This sequence of coin tosses has 6 runs HHH TTT HHH T HHH TTTT
- The test statistics is the total number of runs
- Reject H_0 for small and large number of runs
- This has been used to study the hot hand in basketball

- For univariate continuous observations:
 - Pool the observations
 - Rank the observations
 - Count the number of runs
- Run: sequences of observations that are from the same sample and follow each other

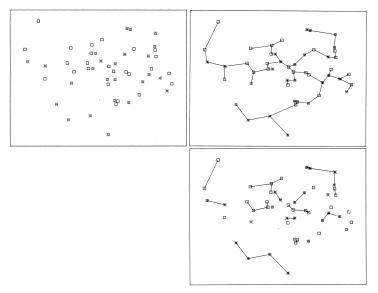
Test statistics is the total number of runs

- The Friedman and Rafsky test is a generalization of Wald-Wolfowitz runs test to higher dimensions
- The difficulty is that we need to sort observations
- Friedman and Rafsky purpose to use minimal spanning trees as a multivariate generalization of the univariate sorted list

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- For univariate sample, the edges of the MST are defined by adjacent observations in the sorted list
- The Wald-Wolfowitz runs test can be described in this alternative way:
 - 1. Construct minimal spanning trees of pooled univariate observations
 - 2. Remove all edges for which the defining nodes originate from different samples
 - 3. Define the test statistics as the number of disjoint subtrees that result
- For multivariate samples, just construct minimal spanning tree in step 1 from multivariate observations



Source: Friedman and Rafsky (1979)

- Reject H_0 for small and large number of subtrees (runs)
- The null distribution of the test statistics can be computed using permutation tests
 - fix tree
 - permute labels
- Good power in finite samples for multivariate data (against general alternatives: location, spread, and shape)

 Has been applied to mapping cell populations in flow cytometry data (Hsiao et al. 2016)

- two cell populations
- d measurements on each cell
- determine whether the expression of a cellular marker is statistically different
- suggesting candidates for new cellular phenotypes
- indicate splitting or merging of cell populations
- Recent development for very high-dimensional data sets (Chen and Friedman 2015)

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