Advanced Permutation Techniques

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Computational Methods in Statistics and Data Science (Stats 406)

Conditioning and Permuting

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- Goal: **estimation**
- **Condition on the sample values**
- Draw **bootstrap replications** with replacement

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For **permutation tests**:

- Goal: **hypothesis testing**
- Select a **test statistic** that is **permutation invariant** in its arguments
- **Condition on feature of the sample** and **permute what remains**
- **Two sample problems** are particularly convenient: **condition on the data** and **permute the labels**.

Models and Parameters

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where $h(x; \theta)$ is a function that may depend on a **parameter** θ.

If H_0 is true, then X and $h(Y)$ have the **same distribution** and we can **permute the labels** for X and $h(Y)$.

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We'll work with the **systolic pressure readings** now, and return to the sys/dia ratio later.

Systolic BP measurements
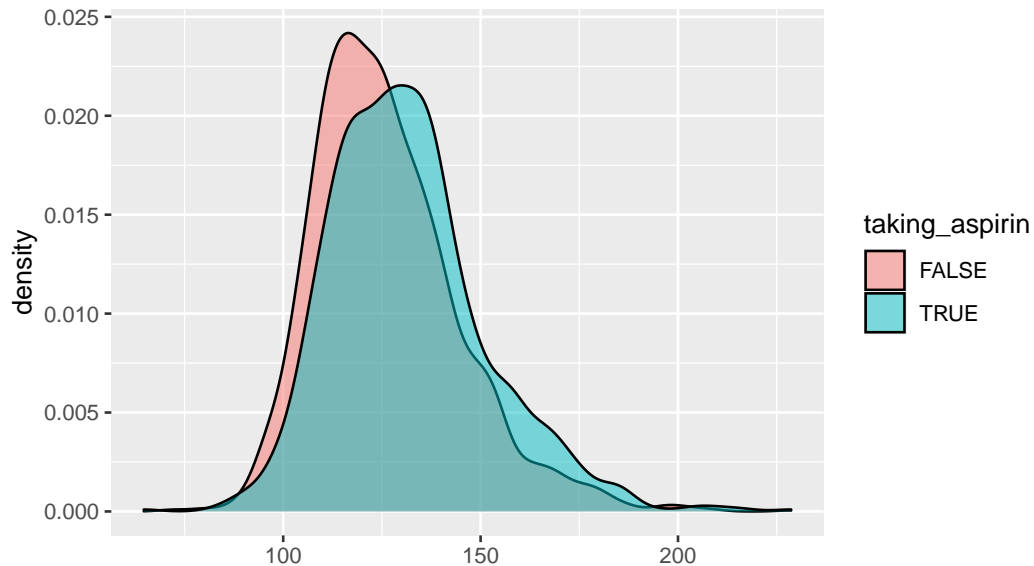
Let's create a confidence interval for $h(x; \theta) = x - \theta$ using a KS test.

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> thetas <- seq(-8, 0, length.out = 100)

> ps <- sapply(thetas, function(theta) {
+    with(nhanes, ## creates variables sys_mean, taking_apsirin
+        ks.test(x = sys_mean[taking_aspirin],
+                y = sys_mean[!taking_aspirin] - theta)$p.value)
+ })
```

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+                y = sys_mean[!taking_aspirin] - theta)$p.value)
+ })

> (ci90 <- range(thetas[ps >= 0.1])) ## 90% CI

[1] -5.979798 -4.686869

> (thetahat <- thetas[which.max(ps)])

[1] -5.333333
```
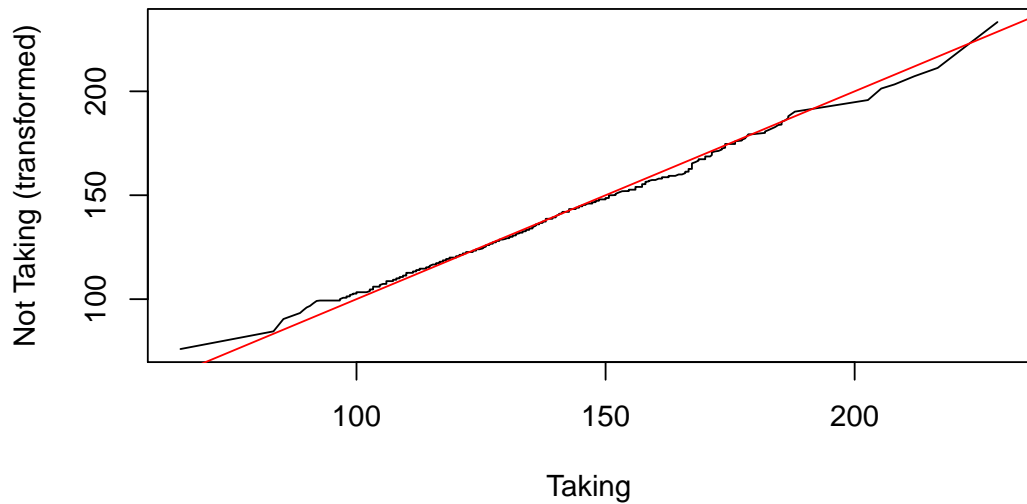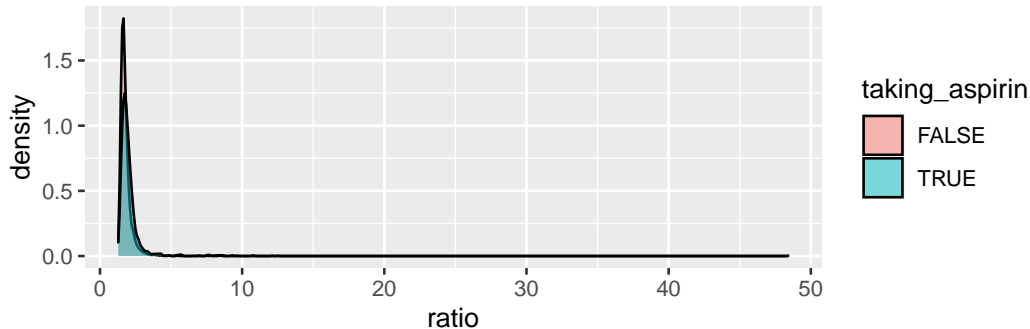
Ratio of Systolic to Diastolic

The **shift model** worked fairly well when looking the systolic BP. Will it work with the **ratio of systolic to diastolic**?

Some models can be rejected everywhere

Now trying with the ratios of systolic to diastolic:

```
> thetas <- seq(-1, 1, length.out = 100)
> ps <- map_dbl(thetas, function(theta) {
+     with(nhanes,
+          ks.test(x = ratio[taking_aspirin],
+                  y = ratio[!taking_aspirin] - theta)$p.value)
+ })
> any(ps >= 0.01)

[1] FALSE
```

Another model

Shift models are common, but we have lots of flexibility to craft others.

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$$h(x) = \begin{cases} x : x \leq 1.2 \\ x^{1+\delta} : x > 1.2 \end{cases}$$
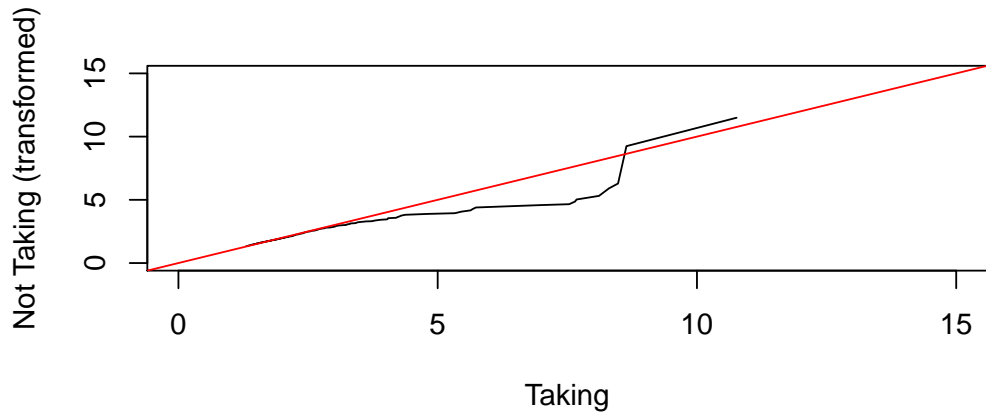
Implementing in R

```
> deltas <- seq(0.1, 0.2,length.out = 100)
> h <- function(x, delta) { x^(1 + delta * (x > 1.2) )}
> ps <- map_dbl(deltas, function(delta) {
+ with(nhanes, ## creates variables sys_mean, taking_apsirin
+      ks.test(x = ratio[taking_aspirin],
+              y = h(ratio[!taking_aspirin], delta))$p.value)
+ })
> any(ps >= 0.01)

[1] TRUE
```
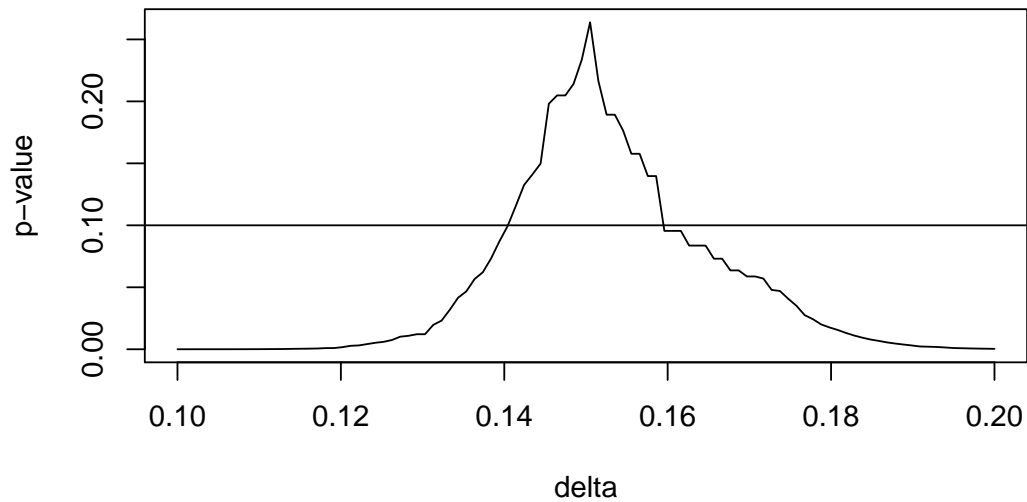
Aligning ECDFs at $\hat{\delta}$

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- When using ranks (KS, WMW) we can tabulate T's distribution without seeing the data ("distribution free")
- For $H_0 : F(x) = G(h(x))$, transform $h(Y)$ and shuffle the labels. Many options for h.

Discrete Data

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If W is also discrete with levels $1, 2, \ldots$, we can **cross classify** with Z into a table. For simplicity, assume $W_i \in \{0, 1\}$.

	$Z = 0$	$Z = 1$	
$W = 0$	A_{00}	A_{01}	$\sum I(W_i == 0)$
$W = 1$	A_{10}	A_{11}	$\sum I(W_i == 1)$
	m	n	$n + m$

where

$$A_{ab} = \sum_{i=1}^{n} I(W_i = a)I(Z_i = b)$$

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Hypothesis test: is the observed table "extreme" if $F = G$?

Creating a discrete variable

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```
> nhanes$healthy <- nhanes$sys_mean <= 120
> library(xtable)
> print(xtable(table(nhanes$healthy, nhanes$taking_aspirin)))
```

	FALSE	TRUE
FALSE	1460	703
TRUE	1094	310

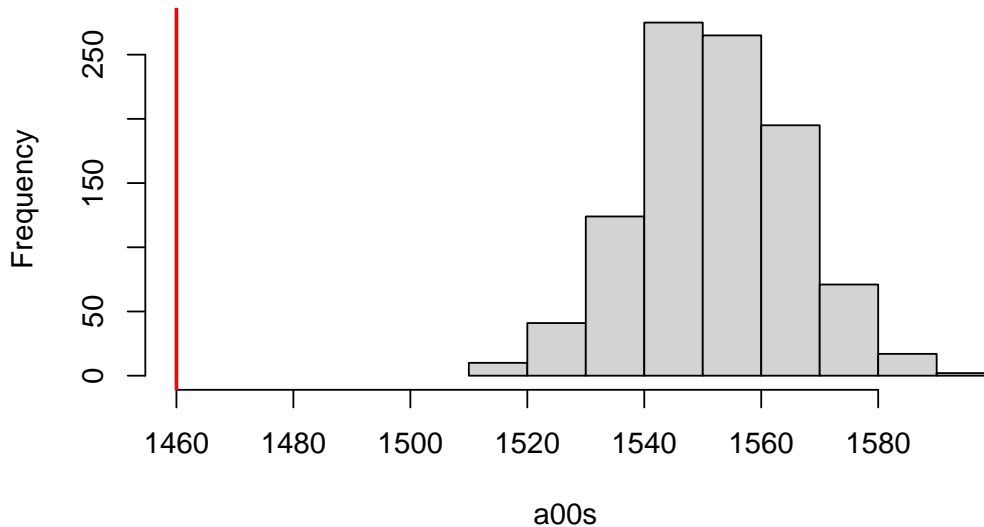**Implementing in R**

```
> observed_a00 <- with(nhanes, table(healthy, taking_aspirin))[1,1]
> a00s <- replicate(1000, {
+     newz <- sample(nhanes$taking_aspirin) # permutes labels
+     table(nhanes$healthy, newz)[1, 1]
+ })
> 2 * min(mean(a00s >= observed_a00), mean(a00s <= observed_a00))

[1] 0
```

Histogram of a00s

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Fisher's Exact Test

This procedure is known as **Fisher's exact test**. It is a **distribution free** test (additionally, the PDF is **hypergeometric**, but we can always permute to get the right answer).

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```
> fisher.test(nhanes$healthy, nhanes$taking_aspirin)$p.value

[1] 1.207e-11
```

Two sample for ordered data

While Fisher's test easily generalizes for **unordered data** with more than two categories, how can we use **ordering of categories** in our data?

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While Fisher's test easily generalizes for **unordered data** with more than two categories, how can we use **ordering of categories** in our data?

Example: recall the study of students located in San Antonio and Phoenix. Teachers were asked about each student if students had "good attention span, completes chores or homework." and could answer one of:

- Not true
- Somewhat true
- Certainly true

Responses by city

	(1) Not true	(2) Somewhat true	(3) Certainly true
Phoenix, AZ	135	290	426
San Antonio, TX	233	492	545

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Our strategy will be to replace "Not true", "Somewhat true", and "Certainly true" with numerical scores, and then compare across the cities (Cochran-Armitage test).

Filling in numeric values

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Suppose there a **latent variable Y** such that if

- $Y \leq \theta_1$, the student does not complete homework;
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If we could observe Y, we could use it's numerical score, or better yet, **its rank**.

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```
> col_totals <- colSums(hwtab)
> (midranks <-  col_totals / 2  + cumsum(c(0, col_totals))[1:3])
     (1) Not true  (2) Somewhat true (3) Certainly true
            184                759                 1636
```

Difference of means on midranks

Now that we have a numerical score to use for each observation, we one of our existing permutation tests, such as the **difference of means** test.

```
> w <- midranks[gamoran$B4Y]
> (obs_stat <- mean(w[gamoran$PH.AZ], na.rm = TRUE)
+      - mean(w[!gamoran$PH.AZ], na.rm = TRUE))

[1] -76.91
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> null_distribution <- replicate(1000, {
+     newZ <- sample(gamoran$PH.AZ)
+     mean(w[newZ], na.rm = TRUE) - mean(w[!newZ], na.rm = TRUE)
+ })
```
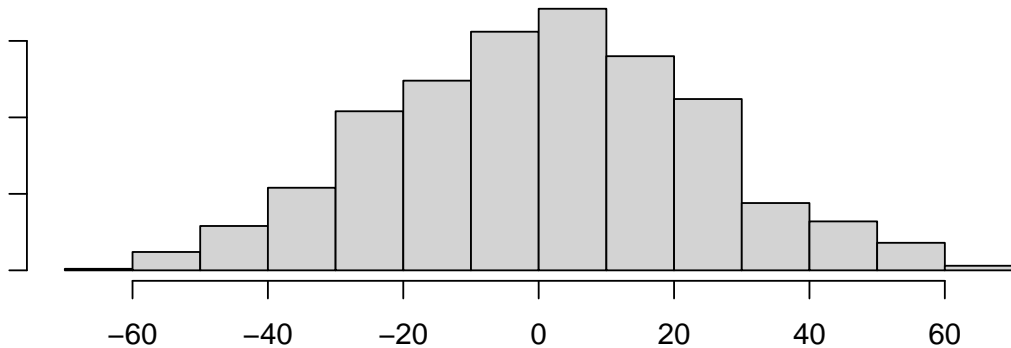
```
> 2 * min(mean(obs_stat <= null_distribution),
+         mean(obs_stat >= null_distribution))

[1] 0
```

Models for discrete data

Note that after replacing the category labels with a numeric score W (e.g. the midrank, quantiles from a Normal distribution), we are testing

$$H_0 : F_0(x) = F_1(x) \text{ vs. } F_0(x) \neq F_1(x)$$

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Previously, saw that we could test **models based on functions h** such that

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For discrete data, we come up with h functions that operate on cells of the table. (e.g., move 10 "somewhat true" students from San Antonio to the "Not true" column).

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Under the hypothesis that $F_{WZ} = F_W F_Z$ (independent), we could arbitrarily permute all the Z values and any statistic $T(W, Z)$ would have the same distribution.
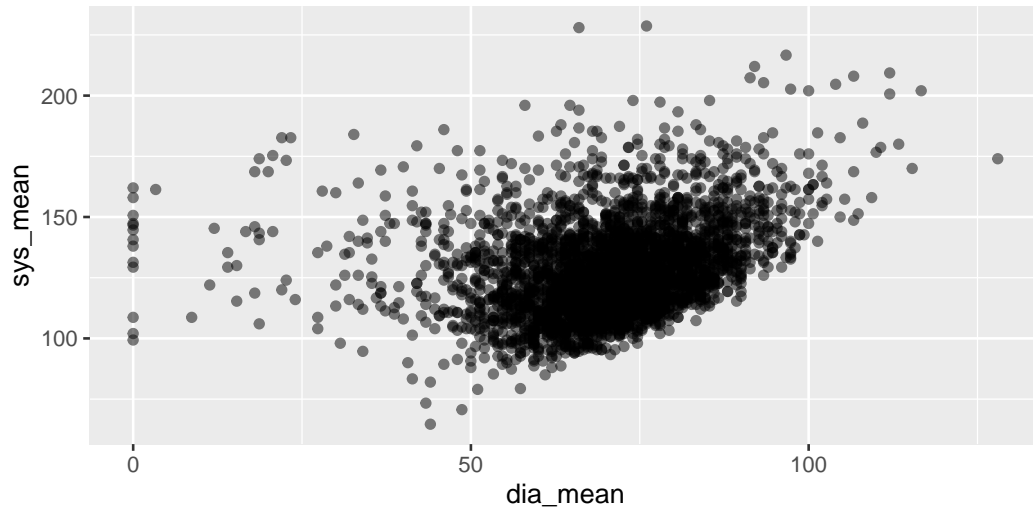
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We can test this hypothesis with a **test statistic for pairs**.

Systolic and Diastolic BP

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```
> observed_cor <- with(nhanes, cor(sys_mean, dia_mean))
> cors <- replicate(1000, {
+    shuffled_dia <- sample(nhanes$dia_mean)
+    cor(nhanes$sys_mean, shuffled_dia)
+ })
> 2 * min(mean(cors >= observed_cor), mean(cors <= observed_cor))

[1] 0
```
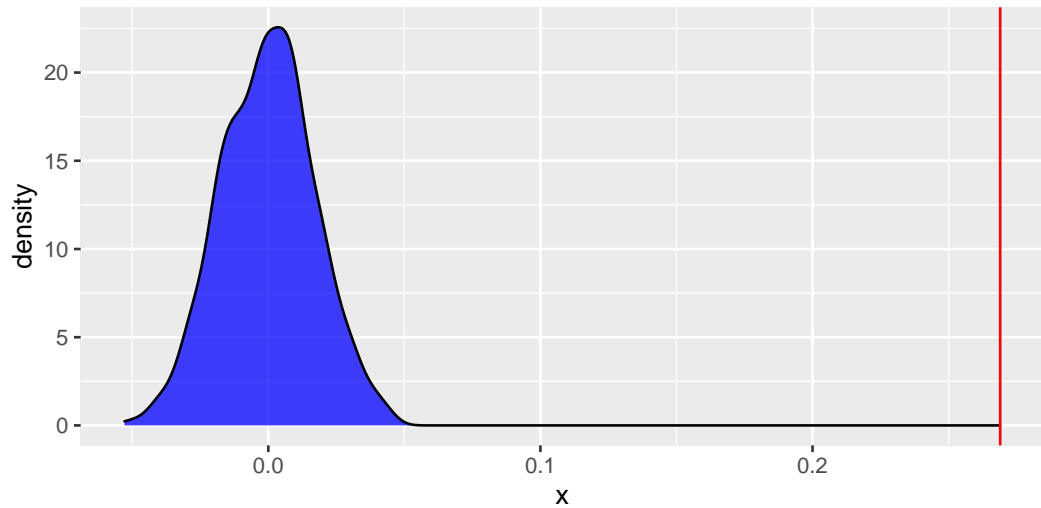
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More on independence tests

Many other options for test statistics:

- Generalizations of correlation to non-linear dependence (see Rizzo, ch 8)
- Distribution free methods based on ranks
- Chi-squared and G^2 type statistics for categorical data (see Agresti's *Categorical Data Analysis* book)

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Note: `cor.test` in R does not implement a permutation test – it uses an assumption that the variables are jointly Normal.

Connections to randomized trials

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For example, the students in Phoenix and San Antonio where assigned to either participate in a social capital building program (**treatment**) or not (**control**).

From a causal perspective, we want to ask "what could have been different if students had been assigned to a different condition?" One answer is that we would see the same response for all subjects:

$$[Y_i \mid Z_i = 1] = [Y_i \mid Z_i = 0]$$

(note: this is stronger than just saying the treatment and control subjects have the same distribution)

We call this the **"sharp null hypothesis of no effect"**.

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For other kinds of randomization mechanisms, we need to **respect the distribution of** Z.

Clustered assignment

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So far, we have been treating the students in the Gamoran et al. study as if they are samples from Phoenix and San Antonio.

More importantly, they are **clustered** in schools and **schools were assigned** to either participate in a social capital building program or not.

```
> school_assignments <- group_by(gamoran, Y1SCHOOLID) %>%
+     summarize(z = first(z))
> table(school_assignments$z)

FALSE  TRUE
   26    26
```

Permuting by school

We've already computed midranks for all subjects for whether the student completed homework. Let's get the null distribution based on the clustered assignment:

```
> (w_clus <- mean(w[gamoran$z], na.rm = TRUE) - mean(w[!gamoran$z], na.rm =

[1] -20.89

> null_distribution_cluster <- replicate(1000, {
+     newZ <- sample(school_assignments$z)
+     names(newZ) <- school_assignments$Y1SCHOOLID
+     studentZ <- newZ[as.character(gamoran$Y1SCHOOLID)]
+     mean(w[studentZ], na.rm = TRUE) - mean(w[!studentZ], na.rm = TRUE)
+ })
```
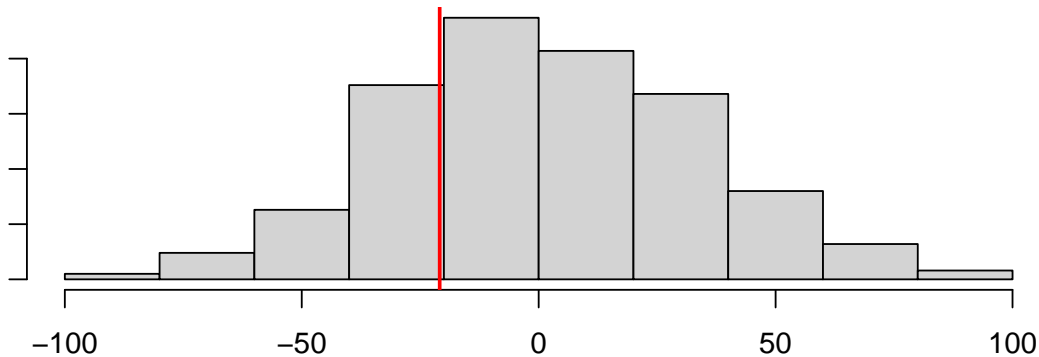
```
> 2 * min(mean(w_clus <= null_distribution_cluster),
+         mean(w_clus >= null_distribution_cluster))

[1] 0.512
```

Re-randomizing the wrong way

How much would we hurt ourselves if we thought that **students had been individually assigned** to the social capital program?

```
> null_distribution_wrong <- replicate(1000, {
+     newZ <- sample(gamoran$z)
+     mean(w[newZ], na.rm = TRUE) - mean(w[!newZ], na.rm = TRUE)
+ })
> 2 * min(mean(w_clus <= null_distribution_wrong),
+         mean(w_clus >= null_distribution_wrong))

[1] 0.414
```

Independence and Randomization Tests Summary

- Setting: IID pairs of (W, Z) or randomly assigned Z and outcome W.
- Hypothesis test: $H_0 : F(w, z) = F(w)F(z)$ or sharp null of no effect
- Procedure:
  - IID Pairs: shuffle either W and Z and compute test statistic
  - Random assignment: follow assignment procedure for Z and compute test statistic
- The usual technique of using a model function h also applies such that $H_0 : h(W)$ and Z are independent
- Be careful to reflect the true randomization procedure.

Multivariate Tests

Multivariate Tests

Suppose now that we have **two samples** of **random vectors** (with p components):

$$X_i = (X_{i1}, X_{i2}, \ldots, X_{ip})', \quad i = 1, \ldots, n$$
$$Y_j = (Y_{j1}, Y_{j2}, \ldots, Y_{jp})', \quad j = 1, \ldots, m$$

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Again, we want to test same distributions:

$$H_0 : F(x_1, x_2, \ldots, x_p) = G(y_1, y_2, \ldots, y_p), \quad \forall x, y \in \mathbb{R}^p$$

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Option 2: Think about observations as **points in space**.

Joint Distribution of Systolic and Diastolic
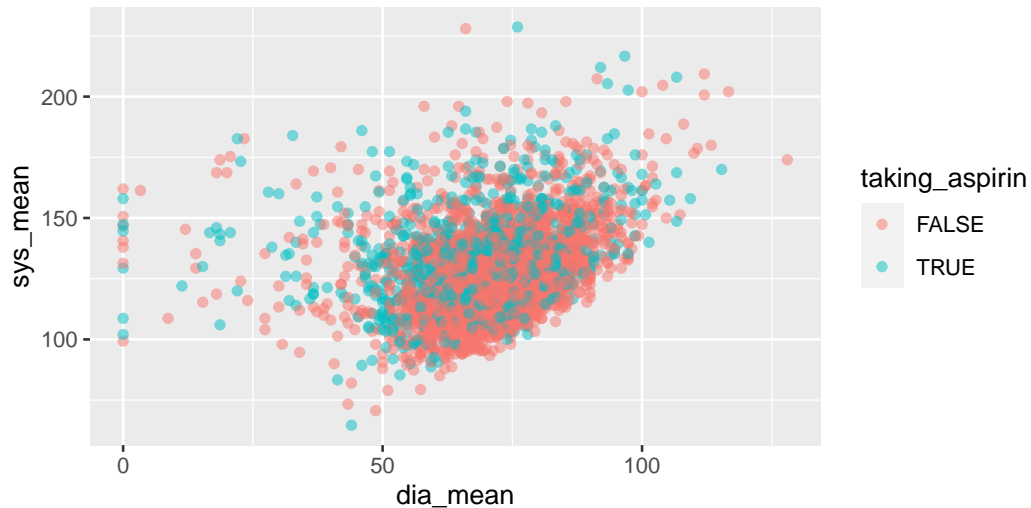
Nearest Neighbor Test

Let's use the "joint sample" notation:

$$(Z_i, W_{i1}, W_{i2}, \ldots, W_{ip})$$

Idea: For each point (in both samples), find the **point that is closet** in distance:

$$N(i) = \text{argmin}_j \sqrt{(X_{i1} - X_{j1})^2 + (X_{i2} - X_{j2})^2 + \cdots + (X_{ip} - X_{jp})^2}$$

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Write the group label of the neighbor as $Z_{N(i)}$.

Our test statistic counts the number of neighbors **in the same sample**:

$$T(Z, W) = \sum_{i=1}^{n} I(Z_i = Z_{N(i)})$$

Computing Distances and Neighbors

```
> sys_dia_dist <- as.matrix(dist(nhanes[, c("sys_mean", "dia_mean")]))
> sys_dia_dist[1:5, 1:5]

      1     2     3     4     5
1  0.00 46.43 30.40 27.73 45.38
2 46.43  0.00 25.73 32.28 20.67
3 30.40 25.73  0.00  6.60 15.33
4 27.73 32.28  6.60  0.00 20.54
5 45.38 20.67 15.33 20.54  0.00
```

```
> diag(sys_dia_dist) <- Inf # can't be closest to ourselves
> nearest_neighbors <- apply(sys_dia_dist, 1, which.min)
> nearest_neighbors[1:5]

   1    2    3    4    5
 849 1974  424  969   72
```
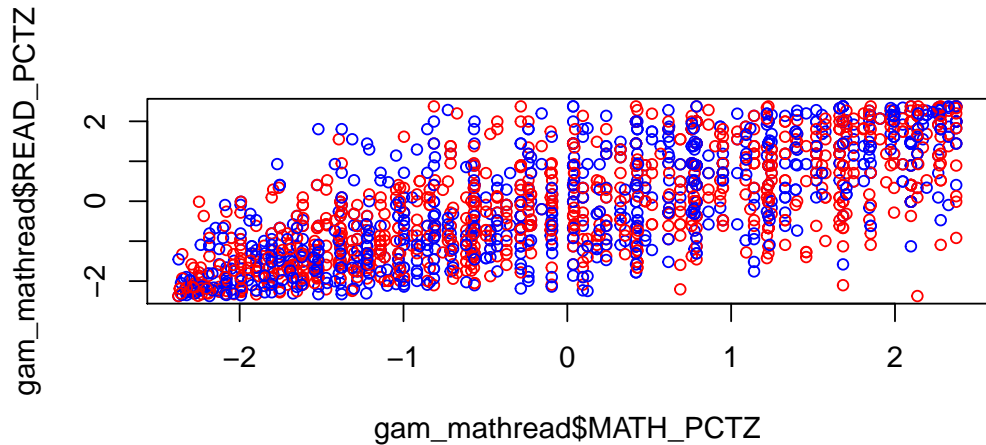
```
> teststat <- function(z, nn) {
+     sum(z == z[nn])
+ }
> observed_t <- teststat(nhanes$taking_aspirin, nearest_neighbors)
> ts <- replicate(1000, {
+     z <- sample(nhanes$taking_aspirin)
+     teststat(z, nearest_neighbors)
+ })
> 2 * min(mean(observed_t <= ts), mean(observed_t >= ts))

[1] 0.068
```

Visualizing Statistic
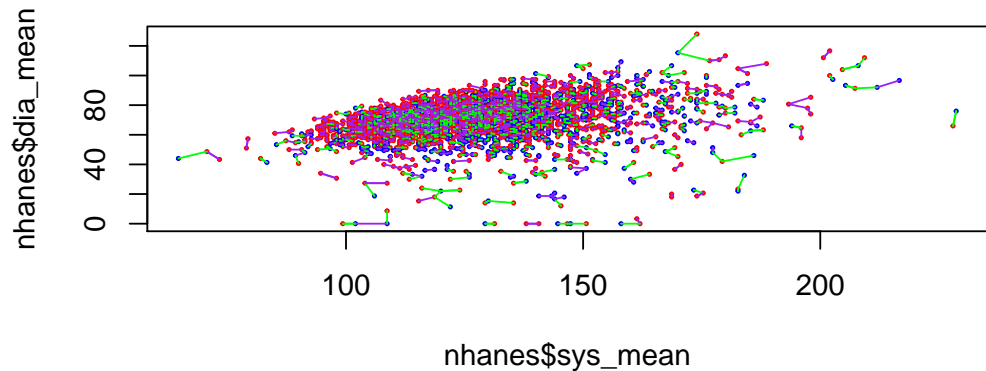
Nearest neighbor for math and reading outcomes

```
> math_read_dist <- as.matrix(
+     dist(gam_mathread[, c("READ_PCTZ", "MATH_PCTZ")]))
> diag(math_read_dist) <- Inf # can't be closest to ourselves
> mrnn <- apply(math_read_dist, 1, which.min) # row wise apply
> mrnn_obs_t <- teststat(gam_mathread$z, mrnn)
```

```
> nn_cluster <- replicate(1000, {
+     newZ <- sample(school_assignments$z)
+     names(newZ) <- school_assignments$Y1SCHOOLID
+     studentZ <- newZ[as.character(gam_mathread$Y1SCHOOLID)]
+     teststat(studentZ, mrnn)
+ })
> 2 * min(mean(mrnn_obs_t <= nn_cluster),
+         mean(mrnn_obs_t >= nn_cluster))

[1] 0.78
```

Advanced Permutation Techniques Conclusion

We saw several more advanced **permutation methods**

- Using **models** to make conditioning possible.
- Permuting **tables** or other **discrete data**, replacing discrete values with numbers
- Testing **independence** between two variables by permuting one
- Connection between **permutation and randomization**
- **Multivariate tests** using distances or graphs

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Common aspect is that we can use Monte Carlo to draw from the possible permutations/randomizations to evaluate a statistic under the null hypothesis. Many of these methods can be combined.