Suppose we have two dependent samples and we’d like to carry out a hypothesis test to detect a difference. After we check assumptions, we could conduct a $t$ test and make inference on the difference between the population means, $\mu_1 - \mu_2$.

**Question:** What can we do if the assumption of normality is violated?

**Answer:** In practice, we would typically try a transformation first. If the transformed data allows for the normality of the sample mean assumption to be met, then we can conduct a $t$ test on the transformed data.

If a transformation doesn’t work (i.e. there is still a violation of the normality assumption even on the transformed data), then we could apply a non-parametric (a.k.a. distribution free) test. We’ll learn the sign test.

*Note: We try a transformation first since the $t$-test has more ______________ than the sign test.*

**Forming Hypotheses**
Since the sign test is non-parametric (no parameters), the hypothesis is written in words. Our $H_0$ will be that the distributions are the same (there is no difference) and $H_A$ will be that the distributions are shifted in some way.

**Test Statistic**
The sign test uses the *sign* of the differences, unlike the paired $t$ test which uses the sign and magnitude of the differences. In the case of the sign test we’ll throw out differences that are 0, and for the remainder of the data set, we have

$$B_s = \begin{cases} 
N_+ & \text{if } H_A: Y_1 > Y_2 \\
N_- & \text{if } H_A: Y_1 < Y_2 \\
\max\{N_+, N_-\} & \text{if } H_A: Y_1 \neq Y_2
\end{cases}$$

**P-value**
To find the P-value for the sign test, we first need to find the distribution of the test statistic, $B_s$. Remember, we find P-values under the assumption the null hypothesis is true. So, if the null hypothesis were true, then we’d expect each difference to be ______________.

Notice, each difference can be positive or negative (we threw out the “0” differences).

What is $P\{\text{difference being positive}\}$ under the null hypothesis of no difference?

What is $P\{\text{difference being negative}\}$ under the null hypothesis of no difference?

Then $B_s \sim$ and $P =$

$$\begin{cases} 
N_+ & \text{if } H_A: Y_1 > Y_2 \\
N_- & \text{if } H_A: Y_1 < Y_2 \\
\max\{N_+, N_-\} & \text{if } H_A: Y_1 \neq Y_2
\end{cases}$$
In R, binom.test($N_1,n_d$) performs the sign test for us. We’ll calculate the P-value in 2 ways.

**Example 9.12**

Y = skin graft survival in days

- **Group 1**: HL-Antigen compatibility “close”
- **Group 2**: HL-Antigen compatibility “poor”

<table>
<thead>
<tr>
<th>Patient</th>
<th>Close $Y_1$</th>
<th>Poor $Y_2$</th>
<th>$d = Y_1 - Y_2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>37</td>
<td>29</td>
<td>+</td>
</tr>
<tr>
<td>2</td>
<td>19</td>
<td>13</td>
<td>+</td>
</tr>
<tr>
<td>3</td>
<td>57</td>
<td>15</td>
<td>+</td>
</tr>
<tr>
<td>4</td>
<td>93</td>
<td>26</td>
<td>+</td>
</tr>
<tr>
<td>5</td>
<td>16</td>
<td>11</td>
<td>+</td>
</tr>
<tr>
<td>6</td>
<td>23</td>
<td>18</td>
<td>+</td>
</tr>
<tr>
<td>7</td>
<td>20</td>
<td>26</td>
<td>-</td>
</tr>
<tr>
<td>8</td>
<td>63</td>
<td>43</td>
<td>+</td>
</tr>
<tr>
<td>9</td>
<td>29</td>
<td>18</td>
<td>+</td>
</tr>
<tr>
<td>10</td>
<td>60+</td>
<td>42</td>
<td>+</td>
</tr>
<tr>
<td>11</td>
<td>18</td>
<td>19</td>
<td>−</td>
</tr>
</tbody>
</table>

**TABLE 9.7 Skin Graft Survival Times**

Patients 3 and 10 died before completing the observation of skin graft survival time. This data set has the “censored” feature, since the patients’ death prevents us from observing past a certain time point.

A QQplot of the non-censored data shows a clear violation of the normality assumption and we cannot invoke the CLT. Why?

Conduct a sign test at the $\alpha = 0.05$ significance level to determine whether skin grafts with close HL-Antigen compatibility tend to survive longer.