# **Resampling Techniques and their Application**

#### -Class 9-

#### Frank Konietschke

Institut für Biometrie und Klinische Epidemiologie Charité - Universitätsmedizin Berlin, Berlin frank.konietschke@charite.de



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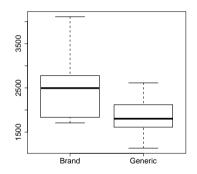
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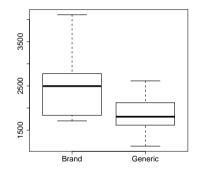
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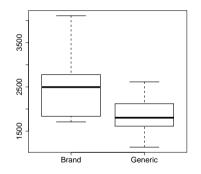


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• Aim:  $H_0$ :  $\mu_1 = \mu_2$  and confidence interval

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- On average,  $(\underbrace{(X_k \mu_1)}_{\leq 0} \underbrace{(Y_k \mu_2)}_{\leq 0}) \leq 0$

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- Reject  $H_0$ , if  $|T| \ge t_{1-\alpha/2}(n-1)$

### **Example Evaluation**

```
brand=c(4108,2526,2779,3852,1833, 2463,2059,1709,1829,2594)
generic=c(1755,1138,1613,2254,1310,2120,1851,1878,1682,2613)
plot(brand, generic, pch=19, cex=1.3)
n=length(brand)
x=cbind(brand,generic)
var(x)
diff=brand-generic
mD=mean(diff)
vd=var(diff)
T=sqrt(n)*mD/sqrt(vd)
pvalue=2*min(pt(T,n-1), 1-pt(T,n-1))
t.test(brand,generic,paired=TRUE)
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- But how? Differences?

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    - Resampling from all data and thus ignoring dependencies

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- Note that centering is not necessary (why?)

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- This method is equivalent to....

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- Ignoring the dependency

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- Ignoring the dependency

• Permuting (or drawing with replacement) all data is not intuitive

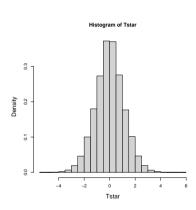
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- Reference: Konietschke and Pauly (2015)

#### Illustration

```
x=brand
y=generic
plot(x,y,pch=19,cex=1.3)
n = 10
d=x-y
T=sqrt(n)*mean(d)/sd(d)
pvalue=2*min(pt(T,n-1),1-pt(T,n-1))
pvalue
Tstar=c()
xy=c(x,y)
for(i in 1:100000){
xstar=sample(xy) #permutation overall
dstar=xstar[1:n]-xstar[(n+1):(2*n)]
Tstar[i] = sqrt(n)*mean(dstar)/sd(dstar)
pstar= 2*min(mean(Tstar<=T),mean(Tstar>=T))
pstar
```



• Data generation

- Data generation
- Different methods are possible

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- $\Phi(x)$ : CDF of N(0, 1)

# **Project**

• In a paired data setting, permuting data overall and thus ignoring the dependency is somewhat counter intuitive. Verify the validity of the method for the paired t-test in a simulation study at 5% level of significance. Use  $n_{sim} = 10,000$  and  $n_{perm} = 10,000$  permutation runs. Generate bivariate normal data with variance  $\sigma_i^2 = 1$  and different covariances  $\sigma \in \{-0.95, -0.5, 0, 0.5, 0.95\}$  and sample sizes  $n \in 10,20$ .