



### ANOVA: Model & Assumptions

**Data**:  $Y_{ij}$  for  $j=1,\cdots,n_i; i=1,\cdots,k$ 

**Model**:  $Y_{ij} = \mu_i + \varepsilon_{ij}$  where  $\varepsilon_{ij}$  = error term

#### **Assumptions**:

- Constant Variance Assumption:  $Var(\varepsilon_{ij}) = \sigma^2$
- Independence Assumption:  $\{\varepsilon_{1j}, \cdots, \varepsilon_{kj}\}$  are independent random variables
- **Normality Assumption:**  $\varepsilon_{ij}$  ~ Normal(0,  $\sigma^2$ )

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#### Residual Analysis

$$Y_{ij} = \mu_i + \varepsilon_{ij}$$

• In the model,  $\varepsilon_{ij}$  is the *error term*. We want  $\varepsilon_{ij} \sim N(0, \sigma^2)$ . To check to see if this is true, we examine the residual errors:

$$\widehat{\varepsilon}_{ij} = Y_{ij} - \widehat{\mu}_i$$

 If the model fit is a good fit, then the residuals should be scattered around zero (randomly).



## Residual Analysis

#### **Residual plots:**

- plot  $\hat{\epsilon}_{ij}$  for each treatment group
- plot the quantile-quantile normal plot of  $\hat{\epsilon}_{ij}$
- plot the histogram of ε̂<sub>ii</sub>

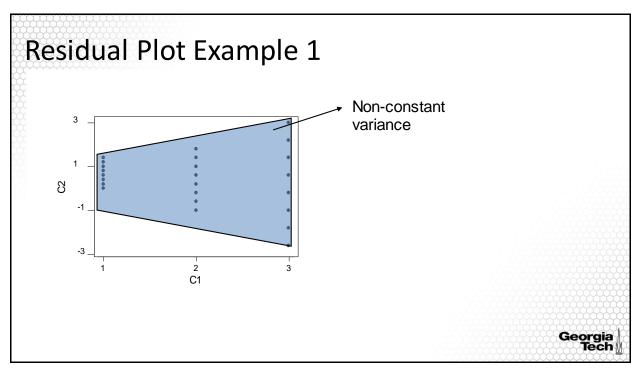
#### If the scatter of $\hat{\epsilon}_{ij}$ is <u>not random</u>, it could be that:

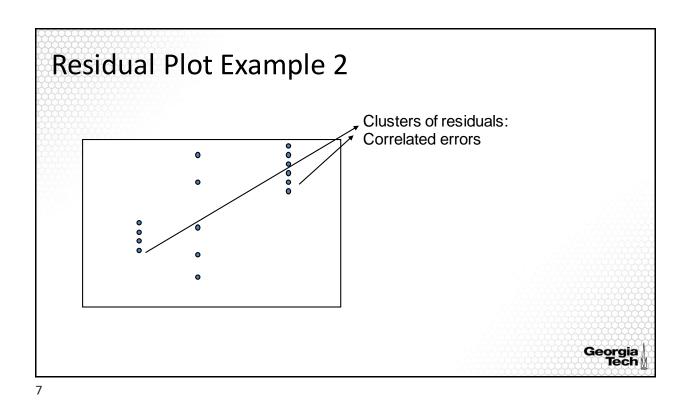
- · sample responses are not independent
- · variances of responses are not equal

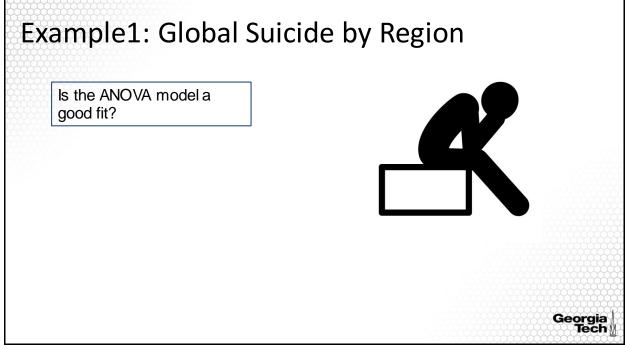
If the quantile-quantile normal plot and the histogram show departure from normality, you may consider a transformation.

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# Residual Analysis

```
## Discard groups with 1 observation

region = suicide_data$region

groups.1 = c(which(region=="NORTHERN AMERICA"), which(region=="WESTERN ASIA"))

suicide_data = suicide_data[-groups.1,]

model.1 = aov(suicidesper100k ~ region, data=suicide_data)

## Diagnostic plots
```

plot(model.1)
resid.model.1=residuals(model.1)

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