Paired Comparison Design (Sewage Experiment)

- **Objective :** To compare two methods MSI and SIB for determining chlorine content in sewage effluents; y = residual chlorine reading.

★response : reading
★treatment factor : method (qualitative), 2 levels – MSI, SIB
★block factor : sample (qualitative), 8 levels – 1, 2, ⋯, 8, block size = 2
★Exp'tal unit = ? 16 EUs
★Design matrix

Table 1: Residual Chlorine Readings, Sewage Experiment

$\tau_2-\tau_1 = (\alpha_i+\tau_2)-(\alpha_i+\tau_1)$

$y_{SIB,i}-y_{MSI,i}$ (within block comparison)

α_i's also removed in $\bar{y}_{SIB,\cdot}-\bar{y}_{MSI,\cdot}$ $(=\bar{d})$ but α_i's still influence $\hat{\sigma}^2$

Sample	Method: MSI	Method: SIB	d_i
1	0.39	0.36	−0.03
2	0.84	1.35	0.51
3	1.76	2.56	0.80
4	3.35	3.92	0.57
5	4.69	5.35	0.66
6	7.70	8.33	0.63
7	10.52	10.70	0.18
8	10.92	10.91	−0.01

blocks

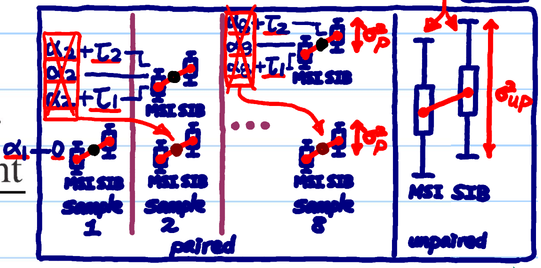
$y_{ij}-\bar{y}_{i\cdot}$ cf. $d_i-\bar{d}$

Successful blocking
btwn-block variation : large
within-block variation : small

method	sample	y
MSI	1	0.39
SIB	1	0.36
MSI	2	0.84
SIB	2	1.35
⋮	⋮	⋮
MSI	8	10.92
SIB	8	10.91

Data matrix — α_i's still in them

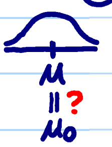
- **Experimental Design :** Eight samples were collected at different doses and contact times. Two methods were applied to each of the eight samples. It is a *paired comparison* design because the pair of treatments are applied to the same samples (or units).



Paired Comparison Design vs. Unpaired Design

one-sample problem : $z_1, \cdots, z_n$ iid $\sim N(\mu, \sigma^2)$, $H_0: \mu = \mu_0$ ← a known constant

- *Paired Comparison Design* : Two treatments are randomly assigned to each *block* of *two* units. Can eliminate block-to-block variation and is effective if such variation is large. Examples: pairs of twins, eyes, kidneys, left and right feet. (Subject-to-subject variation much larger than within-subject variation). ← within-block variation



btwn block variation →

For block effects, we are not interested in their estimation or testing. But, if we ignore block effects (either before or after exp't), the analysis of treatment effects suffer.

$Y = X_1B_1 + X_2B_2 + E$ → $X_1B_1 + \cancel{H_1X_2B_2} + \underbrace{(I-H_1)X_2B_2 + E}_{E^*}$

- *Unpaired Design* : Each treatment is applied to a *separate* set of units, or called the *two-sample* problem. Useful if pairing is unnecessary; also it has more degrees of freedom for error estimation (see LNp. 4-4).

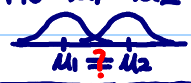
btwn block variation ≈ 0 ⇒ homogeneous EUs

★ Exp'tal units : water samples

unpaired — one factor exp't
EU1 • • • EU16 ← 16 EUs : homogeneous
r → MSI, SIB ← r ← completely randomized → $\frac{16!}{8!8!}$

paired — 2 factor exp't
sample1: EU11, EU12 (MSI, SIB) • • • sample8: EU81, EU82 (MSI, SIB) ← 16 EUs : hetrogeneous btwn samples, homogeneous within samples
2^8 ← restrictedly randomized

2-sample problem : 1-way layout of a 2-level factor
y_{1j}'s iid $\sim N(\mu_1, \sigma^2)$
y_{2j}'s iid $\sim N(\mu_2, \sigma^2)$
$H_0: \mu_1 = \mu_2$



Paired t tests ← conceptual model: $y \sim B_0 + \text{sample} + \text{method} + \varepsilon$ ··· (*)

7 parameter (sample) 1 parameter (method)

(main-effect model, no interaction btwn block & treatment factors, why?)

- **Paired t test :** Let y_{i1}, y_{i2} be the responses of treatments 1 and 2 for unit i, $i = 1, \dots, N$. Let $d_i = y_{i2} - y_{i1}$, $\bar{d}$ and s_d^2 the sample mean and variance of d_i.

FYI. alternative viewpoint: ① block effects α_i's: nuisance parameters ② $\hat{\alpha}_i$'s: suff. stat. of α_i's ③ y_{ij}'s $|$ α_i's ⇒ d_i's appear

$$t_{paired} = \frac{\bar{d} - 0}{s_d/\sqrt{N}}$$

$\bar{y}_{\cdot 2} - \bar{y}_{\cdot 1} \to \bar{d}$

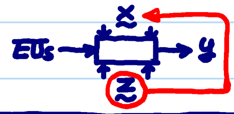
$s_d^2 = \sum (d_i - \bar{d})^2 / N-1$

one-sample problem: $d_1, \dots, d_N$ iid $\sim N(\mu, \sigma^2)$

$H_0: \mu = 0$ ← effect of method

$0 \quad \bar{d}$

$Var(\bar{d}) = \sigma^2/N$



Always put block factors before treatment factors in sequential ANOVA (why?)

F-test for "method"

Ω: (*)

ω: $B_0 + \text{sample} + \varepsilon$

both models contain "sample"! The variation caused by "sample" is removed from ε.

The two treatments are declared significantly different at level α if

$$|t_{paired}| > t_{N-1,\alpha/2}. \qquad (1)$$

(exercise, use *) $(t_{paired})^2 = F = \frac{\|P_{\Omega\ominus\omega}(y)\|^2/1}{RSS_\Omega/df_\Omega}$, where $\|P_{\Omega\ominus\omega}(y)\|^2/1 = N\bar{d}^2/2$ and $RSS_\Omega/df_\Omega = s_d^2/2$

$\Omega \ominus \omega = span\{v\}$, $v = \begin{bmatrix} -1 \\ \vdots \\ -1 \\ 1 \\ \vdots \\ 1 \end{bmatrix}$ (-1's: y_{i1}'s; 1's: y_{i2}'s)

*: $y_{ij} = \hat{\mu} + \hat{\alpha}_i + \hat{\tau}_j + \hat{\varepsilon}_{ij}$

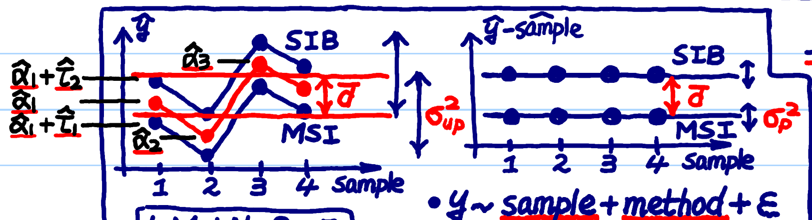
$\hat{\varepsilon}_{i1} = -\hat{\varepsilon}_{i2}$

$d_i = \hat{\tau}_2 - \hat{\tau}_1 + (\hat{\varepsilon}_{i2} - \hat{\varepsilon}_{i1})$

$\bar{d} = \hat{\tau}_2 - \hat{\tau}_1$

$d_i - \bar{d} = \hat{\varepsilon}_{i2} - \hat{\varepsilon}_{i1} = 2\hat{\varepsilon}_{i2}$

total df : 2N
df for intercept : 1
df for treatment factor : 1
df for block factor : N−1
df for residuals : 2N−1−1−(N−1) = N−1



LM, LNp.8-17

- $y \sim \text{sample} + \text{method} + \varepsilon$
- $y \sim \text{method} + \varepsilon^*$

Unpaired t tests ← (one-way layout, 2-sample problem)

conceptual model: $y \sim B_0 + \text{method} + \varepsilon'$ ··· (Δ)

1 parameter (method)

- **Unpaired t test :** The unpaired t test is appropriate if we randomly choose N of the $2N$ units to receive one treatment and assign the remaining N units to the second treatment. Let $\bar{y}_i$ and s_i^2 be the sample mean and sample variance for the ith treatment, $i = 1$ and 2. Define

2-sample model in LNp.2

$\mu_1 \quad \mu_2$; $\bar{y}_1 \quad \bar{y}_2$

F-test for method

Ω: (Δ)

ω: $y = B_0 + \varepsilon'$

$F = \frac{\|P_{\Omega\ominus\omega}(y)\|^2/1}{RSS_\Omega/df_\Omega}$, where $RSS_\Omega/df_\Omega = s^2/2$

(exercise) $(t_{unpaired})^2 = F$

$Var(\bar{y}_2 - \bar{y}_1) = \sigma_2^2/N + \sigma_1^2/N$

$$t_{unpaired} = (\bar{y}_2 - \bar{y}_1)/\sqrt{(s_2^2/N) + (s_1^2/N)}.$$

$\bar{y}_2 - \bar{y}_1 = \bar{d}$; $(s_2^2/N) + (s_1^2/N) \equiv s^2/N$

$\Omega \ominus \omega = span\{v\}$ given in LNp.4-3

The two treatments are declared significantly different at level α if

$$|t_{unpaired}| > t_{2N-2,\alpha/2}. \qquad (2)$$

total df : 2N
df for intercept : 1
df for treatment factor : 1
df for residuals : 2N−1−1 = 2N−2

- Note that the degrees of freedom in (1) and (2) are $N-1$ and $2N-2$ respectively. Unpaired t-test has more df's, but make sure that the unit-to-unit variation is under control (if this method is to be used).

$t_{2N-2,\alpha/2} < t_{N-1,\alpha/2}$

- If block effects significant (large btwn block variation) model (*) is better ⇒ $\hat{\sigma}^2_{(\Delta)} >> \hat{\sigma}^2_{(*)}$
- If block effects insignificant (btwn block variation ≈ 0) model (Δ) is better (⇒ $\hat{\sigma}^2_{(\Delta)} \approx \hat{\sigma}^2_{(*)}$) ⇒ $t_{unpaired}$ has high power, and we can get better (accurate) estimate of σ^2 under (Δ)