

Statistical modelling in ISTA



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*... all models are approximations.
Essentially, all models are wrong, but some are useful.
However, the approximate nature of the model must
always be borne in mind....*

George Box, 1987

Outcomes from a statistical model: estimates



Point estimate: e.g. mean

Variance of the estimate

$\sqrt{\text{Variance of the estimate}}$



standard **uncertainty**



Main statistical model used in ISTA: linear $\left\{ \begin{array}{l} \text{fixed} \\ \text{random} \\ \text{mixed} \end{array} \right\}$ effects model

(Example: **AN**alysis **O**f **VA**riance model: linear fixed effects model)

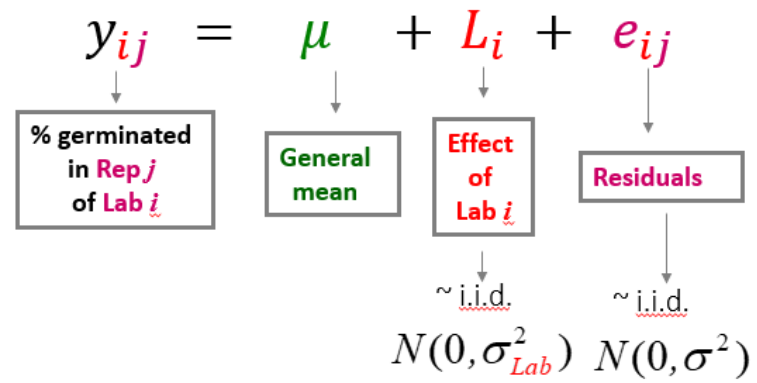
Examples of use of the linear fixed
random
mixed effects model in ISTA

1. Germination Proficiency Tests:

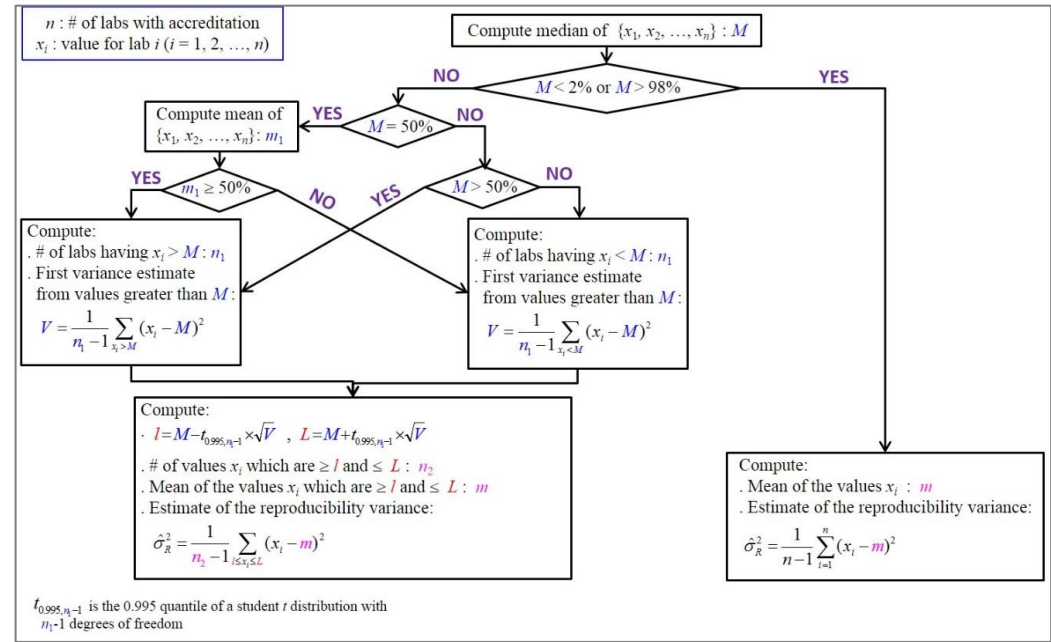
Ratings are based on z-scores:

$$Z_i = \frac{x_i - m}{\hat{\sigma}_R}$$

The denominator of the z-scores can be viewed as the **reproducibility** standard deviation estimated from a linear random effects model:



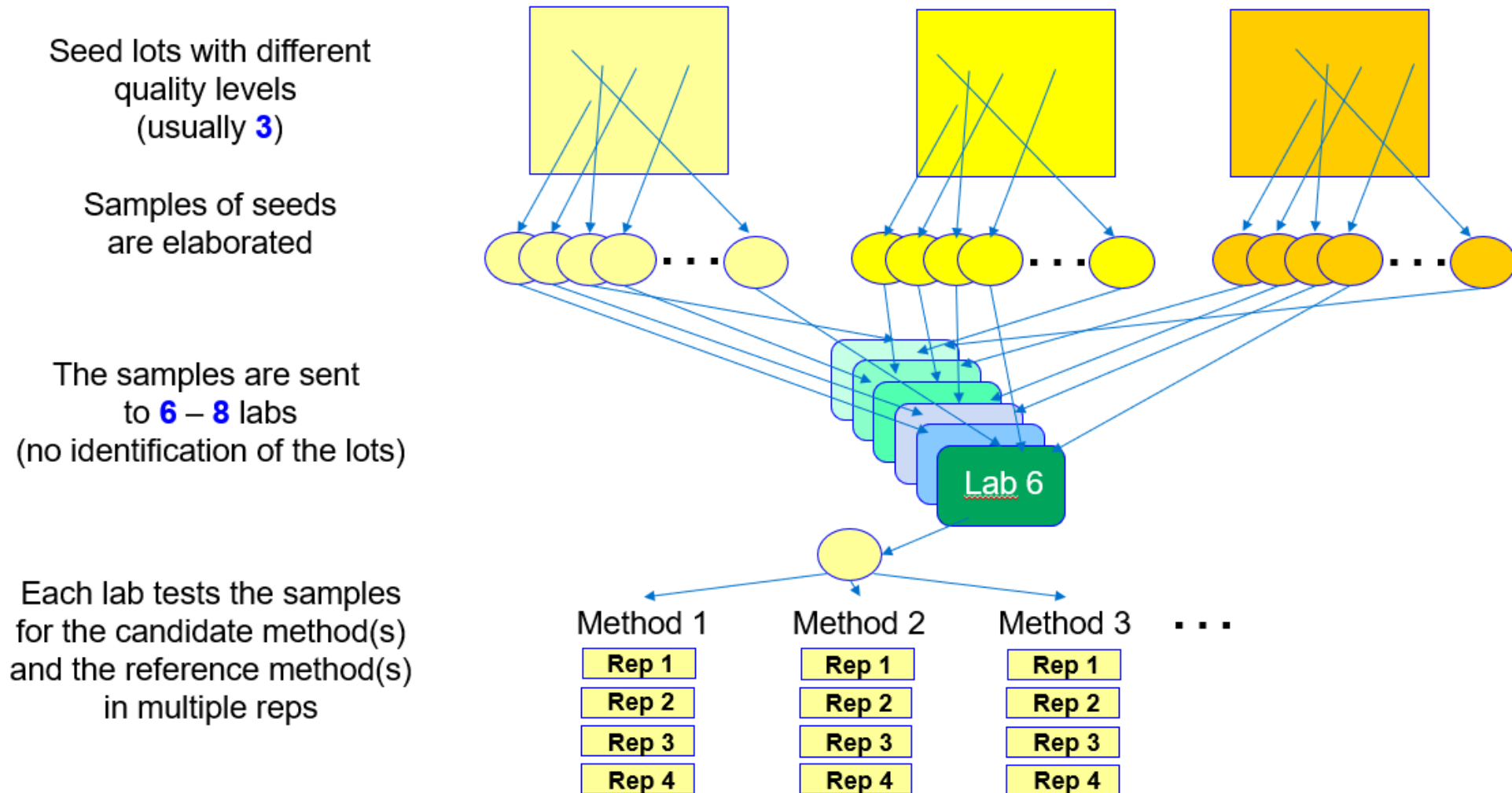
→ **Reproducibility** std-dev: $\hat{\sigma}_R = \sqrt{\hat{\sigma}_{Lab}^2 + \hat{\sigma}^2 / \#_of_reps}$



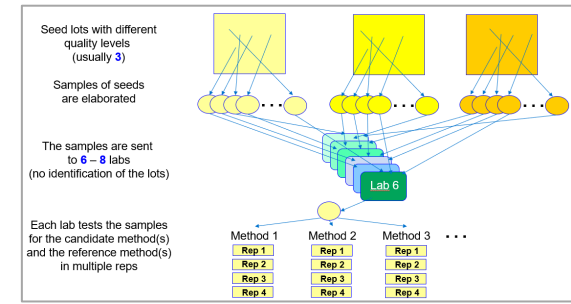
Consistent with ISO 5725-2, 1994

Examples of use of the linear $\left\{ \begin{array}{l} \text{fixed} \\ \text{random} \\ \text{mixed} \end{array} \right\}$ effects model in ISTA

2. Analysis of germination Method Validation studies:



Examples of use of the linear fixed
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2. Analysis of germination Method Validation studies:

Assessing **repeatability/reproducibility** for each method:



For each method, fit the following linear mixed effects model:

$$y_{ijk} = \pi + \alpha_i + L_j + (\alpha L)_{ij} + e_{ijk}$$

↓

% germinated
in Rep *k*
of Lot *i*
and Lab *j*

↓

General
mean

↓

Effect
of
Lot *i*

↓

Effect
of
Lab *j*

~ i.i.d.
 $N(0, \sigma_{Lab}^2)$

↓

Interaction
effect
between
Lot *i*
and Lab *j*

~ i.i.d.
 $N(0, \sigma_{Lot \times Lab}^2)$

↓

Residuals

~ i.i.d.
 $N(0, \sigma^2)$

→ **Repeatability** std-dev: $\sqrt{\widehat{\sigma^2}}$

Model for 1 lab: $y_{ik} = \pi + \alpha_i + e_{ik}$

then: $\text{Var}[y_{ik}] = \text{Var}[\pi + \alpha_i + e_{ik}] = \text{Var}[e_{ik}] \approx \widehat{\sigma^2}$

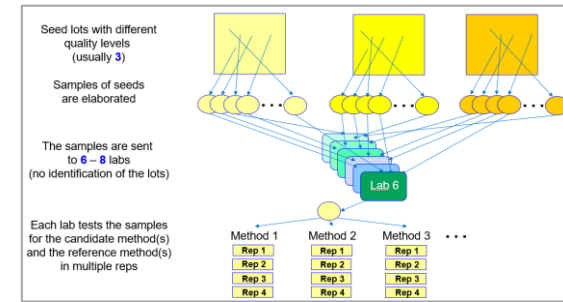
→ **Reproducibility** std-dev:

of the mean
over K reps:

$$\sqrt{\widehat{\sigma_{Lab}^2} + \widehat{\sigma_{Lot \times Lab}^2} + \widehat{\sigma^2}/K}$$

$$\begin{aligned} \text{Var}[\bar{y}_{i.}] &= \text{Var} \left[\pi + \alpha_i + L_j + (\alpha L)_{ij} + \frac{1}{K} \sum_{k=1}^K e_{ijk} \right] \\ &= \text{Var}[L_j] + \text{Var}[(\alpha L)_{ij}] + \frac{1}{K^2} \sum_{k=1}^K \text{Var}[e_{ijk}] \\ &\approx \widehat{\sigma_{Lab}^2} + \widehat{\sigma_{Lot \times Lab}^2} + \widehat{\sigma^2}/K \end{aligned}$$

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2. Analysis of germination Method Validation studies:

Comparing Method, Lot, and Method x Lot means:



Fit the linear mixed effects model:

$$y_{ijk} = \mu + \alpha_i + \beta_j + L_k + (\alpha\beta)_{ij} + (\alpha L)_{ik} + (\beta L)_{jk} + (\alpha\beta L)_{ijk}$$

in which:

- . y_{ijk} is the observed trait analyzed (%) for Method i in Rep l of Lot j and Lab k .
- . μ is the intercept.
- . α_i is the fixed effect of Method i .
- . β_j is the fixed effect of Lot j .
- . L_k is the random effect of Lab k . $L_k \sim \text{i.i.d. } N(0, \sigma_{Lab}^2)$.
- . $(\alpha\beta)_{ij}$ is the interaction effect between Method i and Lot j .
- . $(\alpha L)_{ik}$ is the random interaction effect between Method i and Lab k .
 $(\alpha L)_{ik} \sim \text{i.i.d. } N(0, \sigma_{Method \times Lab}^2)$.
- . $(\beta L)_{jk}$ is the random interaction effect between Lot j and Lab k .
 $(\beta L)_{jk} \sim \text{i.i.d. } N(0, \sigma_{Lot \times Lab}^2)$.
- . $(\alpha\beta L)_{ijk}$ is the random interaction effect between Method i , Lot j and Lab k .
 $(\alpha\beta L)_{ijk} \sim \text{i.i.d. } N(0, \sigma_{Method \times Lot \times Lab}^2)$.
- . e_{ijk} are the residuals. $e_{ijk} \sim \text{i.i.d. } N(0, \sigma^2)$.

→ ANOVA table for the fixed effects (Method, Lot and Method x Lot)

→ Least Squares (LS) Means comparisons

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2. Analysis of germination Method Validation studies:

Given that germination percentages have a binomial distribution, one could ask why are we not using **G**eneralized **L**inear **M**ixed effects **M**odel (**GLMM**) for the analysis?

- Output from different GLMM algorithms (e.g. the ones implemented in SAS GLIMMIX procedure, in glmmPQL() from MASS R package, glmer() from lme4 R package, ...) have been compared: **they provide estimates that can be very different**
- When fitting a GLMMM, it is assumed that the random effects on the linear predictor scale are normally distributed: **interpretation is not obvious as well as the transformation back to the data scale**
- Literature review : **ISO organization has no specific recommendation, few approaches found are not convincing**

 Best approach is to use a **L**inear **M**ixed effects **M**odel (**LMM**)

Other statistical models based on probability distributions



1. Modeling over-dispersion for non-commercial seed lots (e.g. wild species)

True proportion of germinated seeds in the lot: π

$X_i = 1$ if seed i germinates, 0 otherwise

Bernoulli variable

Sample of n seeds



$Y = \sum_{i=1}^n X_i$: number of germinated seeds

Miles's dispersion factor : $f = \frac{\sigma}{\sigma_B}$

where $\sigma_B^2 = n\pi(1 - \pi)$ and σ^2 is the variance among the reps of a germination test

Commercial seed lot

π is a constant



$Y \sim \text{Binomial}(n, \pi)$ with π being the true germination proportion in the seed lot

Laffont, J-L., Hong, B., Kuo, B-J. and K.M. Remund (2019). Exact theoretical distributions around the replicate results of a germination test. *Seed Science Research* **29**, 64-72.



Mean(f) = 1
Median(f) \leq 0.9

Non-commercial seed lot

$\pi \sim \text{Beta}(a, b)$

(the probability for an individual seed to germinate is unknown or random)



$Y \sim \text{Beta-Binomial}(n, \alpha, \beta)$ with
 $\alpha = \pi \left(\frac{n-1}{f^2-1} - 1 \right)$ and $\beta = \alpha \left(\frac{1}{\pi} - 1 \right)$

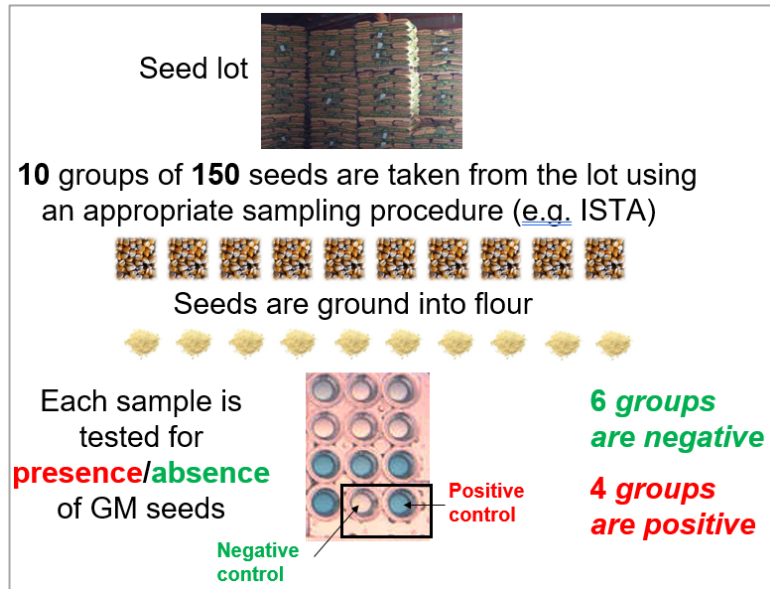


Over dispersed rep results:

$$\sigma^2 = n\pi(1 - \pi) \left(1 + \frac{n-1}{\alpha + \beta + 1} \right) = n\pi(1 - \pi)f^2$$

Mean(f) \gg 1

2. Group testing estimator



6 groups of 150 seeds are negative

4 groups of 150 seeds are positive

Point estimate of p , the true proportion of GM seeds in the lot

$$\hat{p} = 1 - \left(1 - \frac{4}{10}\right)^{\frac{1}{150}}$$

= 0.34%

Derived from the distribution of the number of positive groups:

binomial distribution $B(n, 1 - (1 - p)^m)$

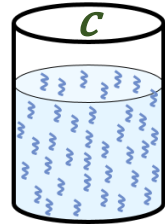
n : number of groups

m : number of individuals per group



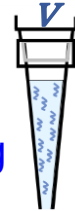
3. Volume subsampling

Concentration

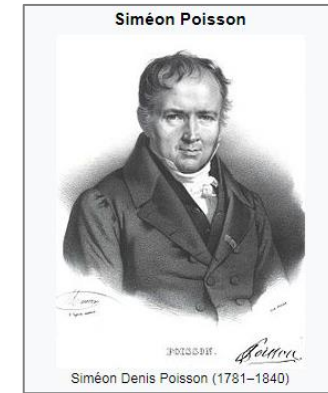


subsampling

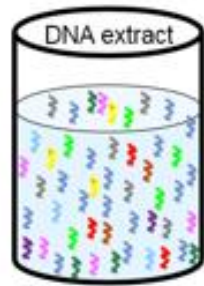
Volume



number of λ
in the
subsample is
Poisson(cV)



Max
group
size



DNA copy
from:
seed # 1
seed # 2
...
seed # n



Total # of copies
 $T \sim \text{Poisson}(\lambda)$

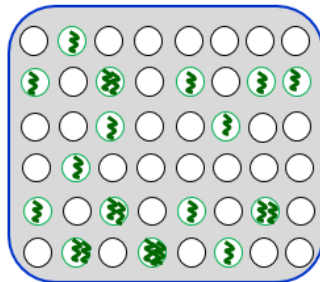
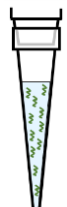
number of copies from
each seed given a total
 $T = t$ of copies is
Multinomial($t, 1/n, \dots, 1/n$)

*Poissonization theorem
for multinomials:*
unconditionally, number
of copies X_i for seed i
is **Poisson**(λ/n)
and X_i are independent

**Simpler
distributions!**

dPCR

of copies
 $M \sim \text{Poisson}(\theta)$



number X of empty partitions
given $M = m$ has a
distribution with pmf:

$$P(X = x | M = m) = \binom{k}{x} \sum_{i=0}^{k-x} (-1)^i \binom{k-x}{i} \left(1 - \frac{x+i}{k}\right)^m$$

Unconditionally,
 X is
Binomial($k, e^{-\theta/k}$)





Thank you!



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