Rating systems overview for quantification

Bangkok
Ordinary meeting
2005

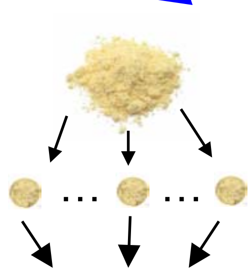
Quantification can be done through

Quantitative methods such as real-time PCR

Testing sub-samples for presence/absence

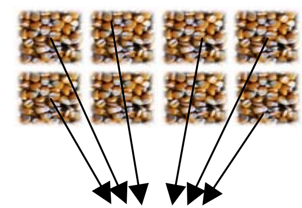
One sample

Multiple flour sub-samples



Multiple measures

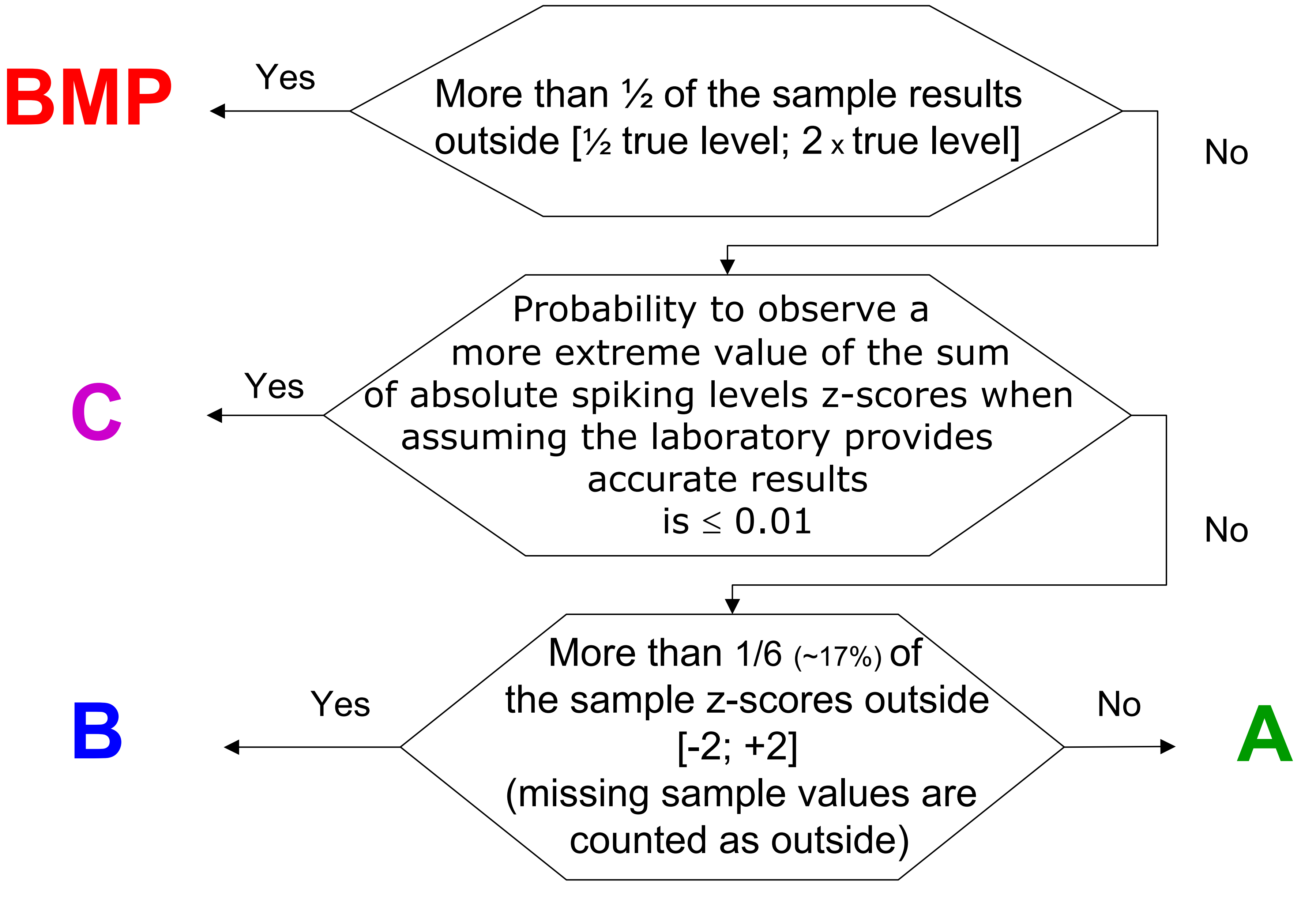
Sub-samples of seeds



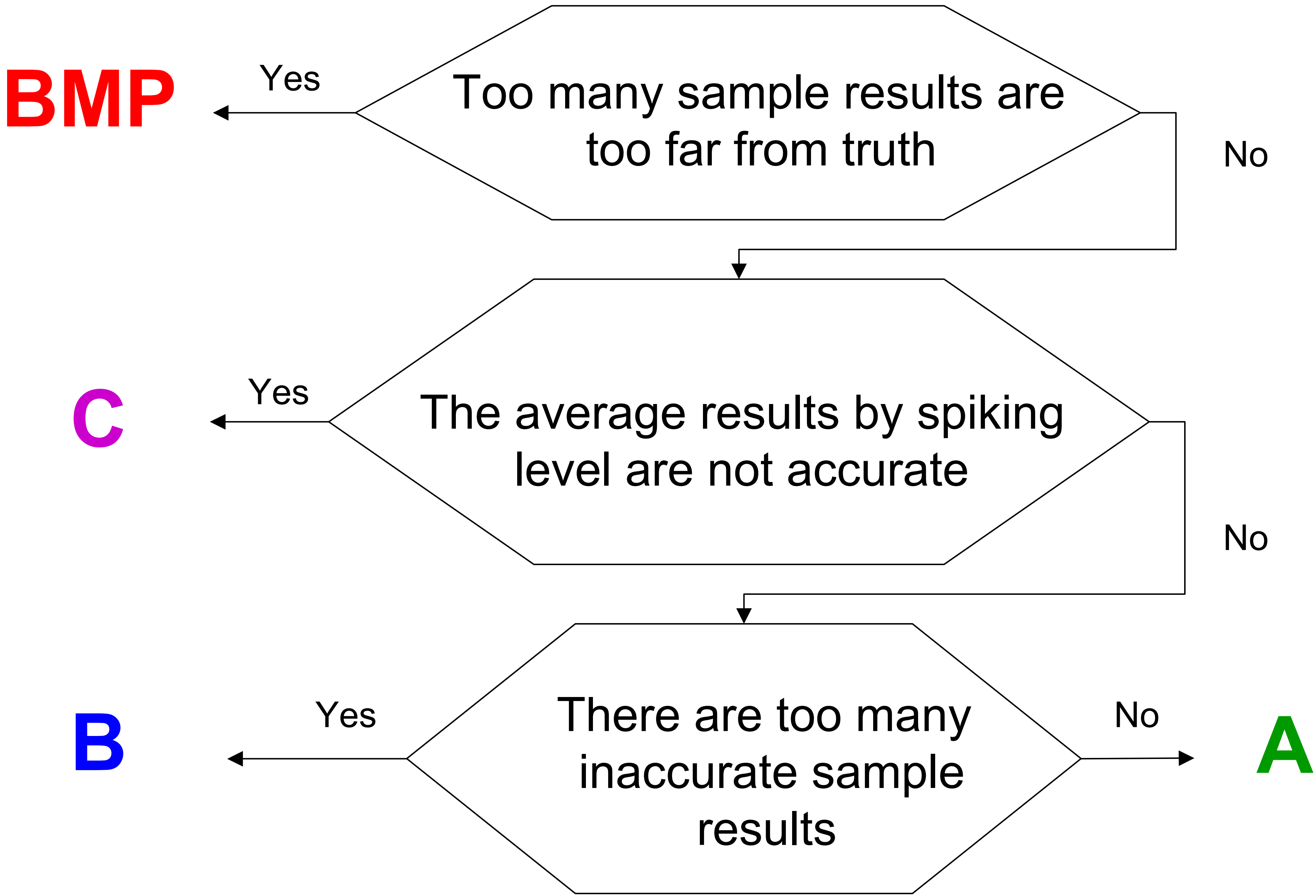
Test for presence/absence on each sub-sample

One sample result reported by the participating laboratories

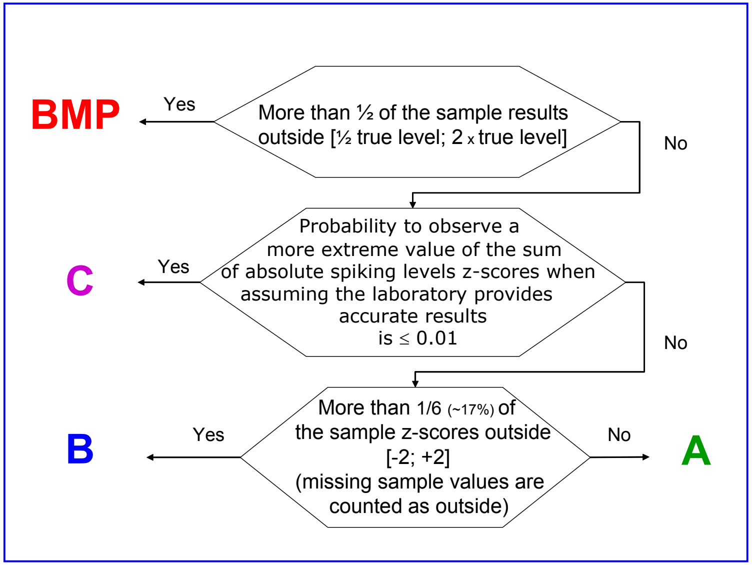
Rating system for quantification: decision tree



Rating system for quantification: decision tree



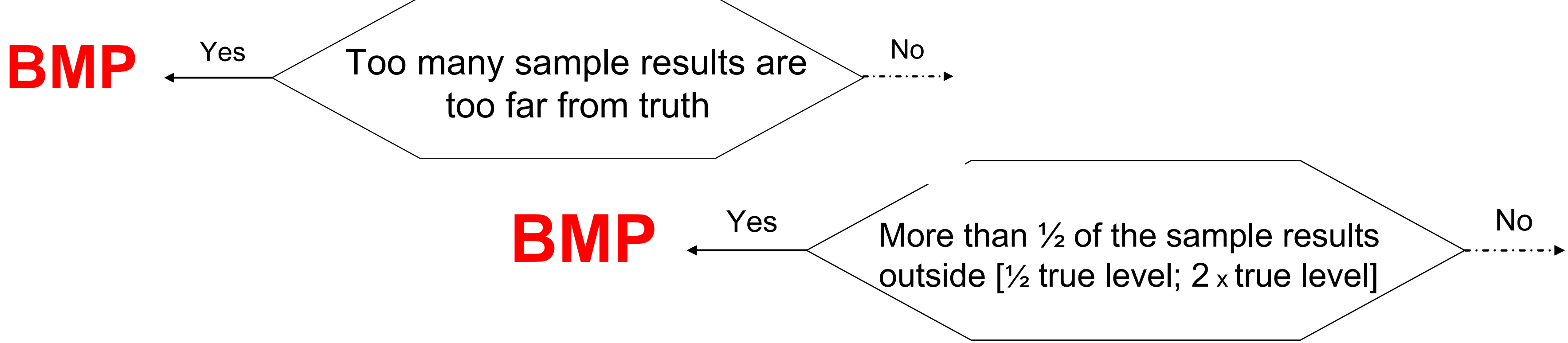
Three suggested rating systems for quantification



Rating System 1:
True level = number of GM seeds / total number of seeds in each sample

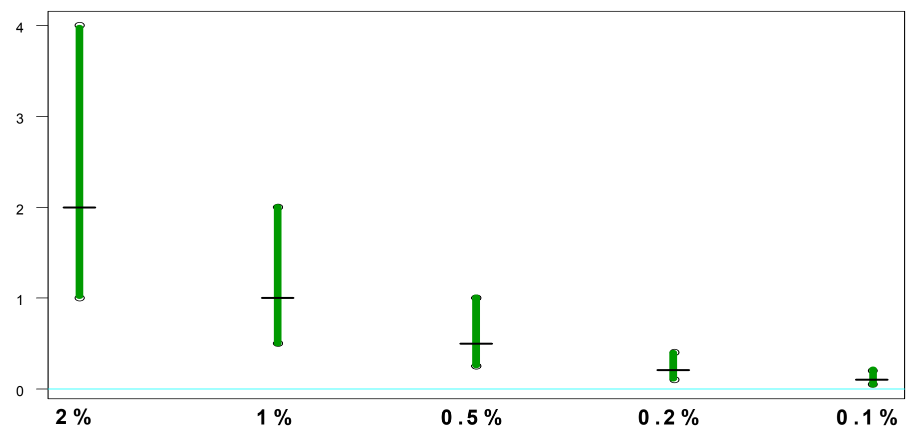
Rating System 2:
True level = weight of GM seeds / total weight of seeds in each sample

Rating System 3:
True level = for a given spiking level, median of the sample results reported by the participating laboratories

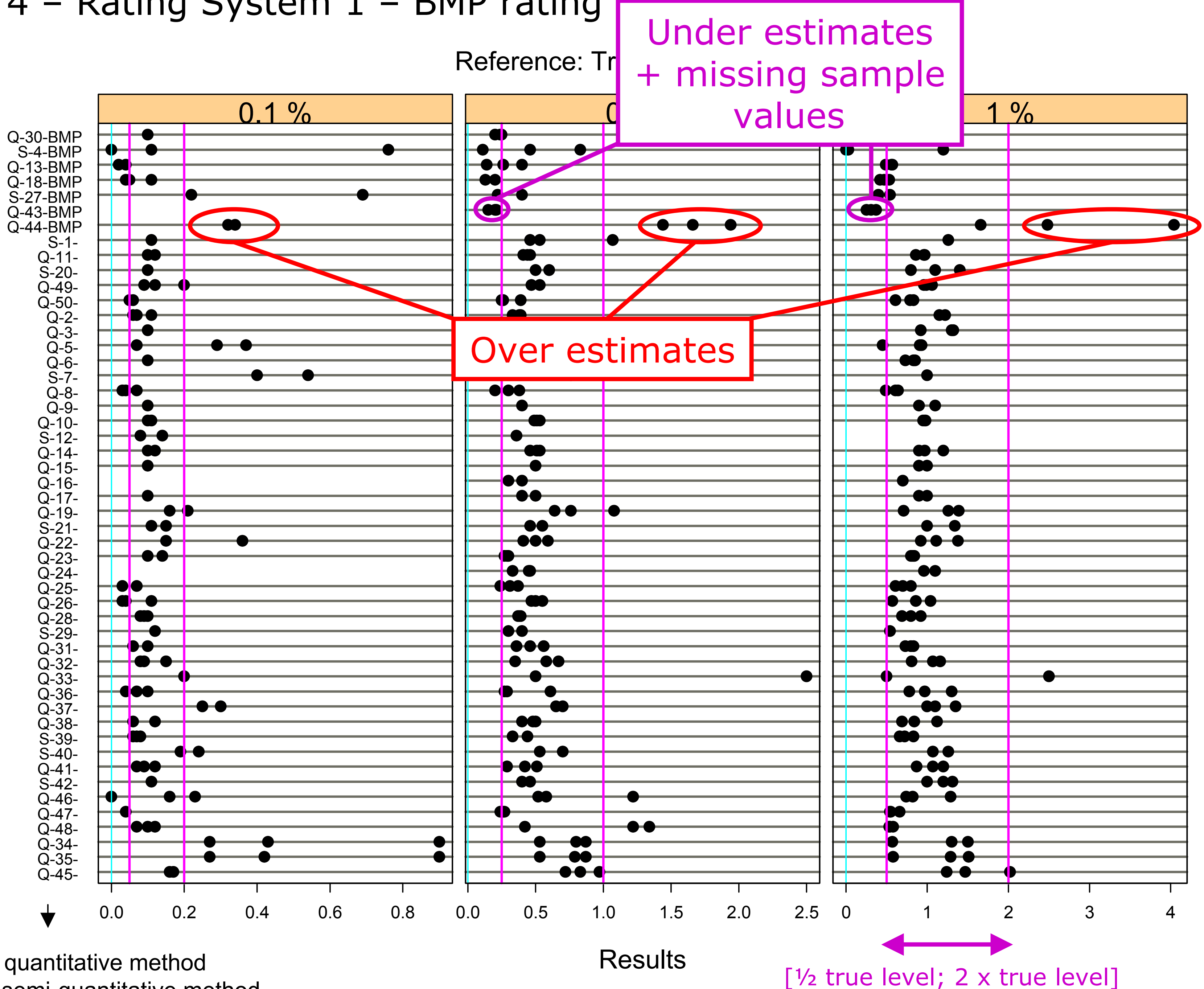


- Selected criteria is based on sample results reported by the participating laboratories and on a simple rule

- The size of the “acceptance” interval decreases with the true level



PT4 – Rating System 1 – BMP rating

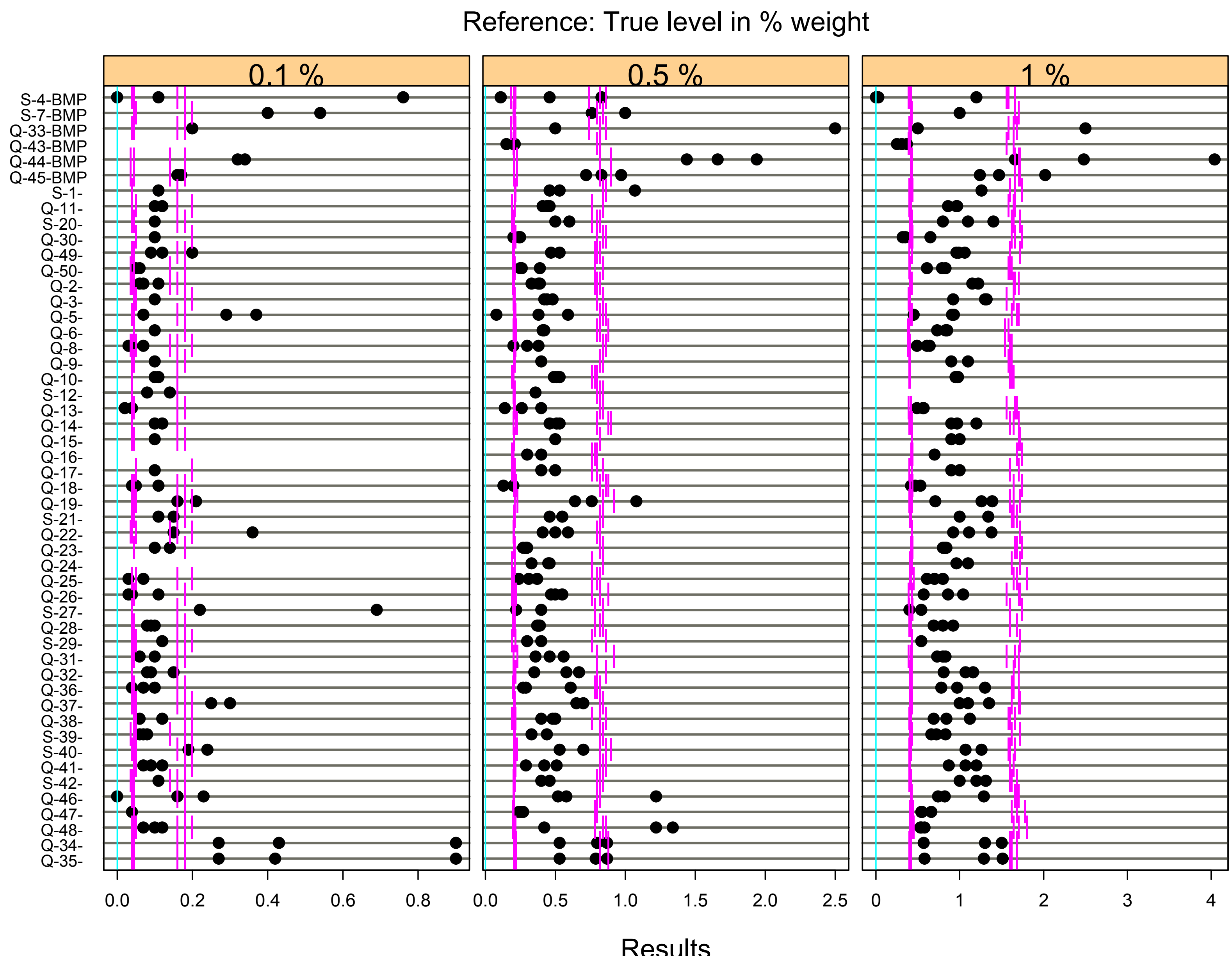


Q: quantitative method

S: semi-quantitative method

PT4 – Rating System 2 – BMP rating

Different "acceptance" limits for each sample when true level is %Weight



For **C**, **B** and **A** ratings, we will use the **z-scores tool**

(used in Germination rating)

z-scores

Consider a value x from a distribution with mean μ and standard-deviation σ. The formula for converting x into its corresponding **z-score** is:

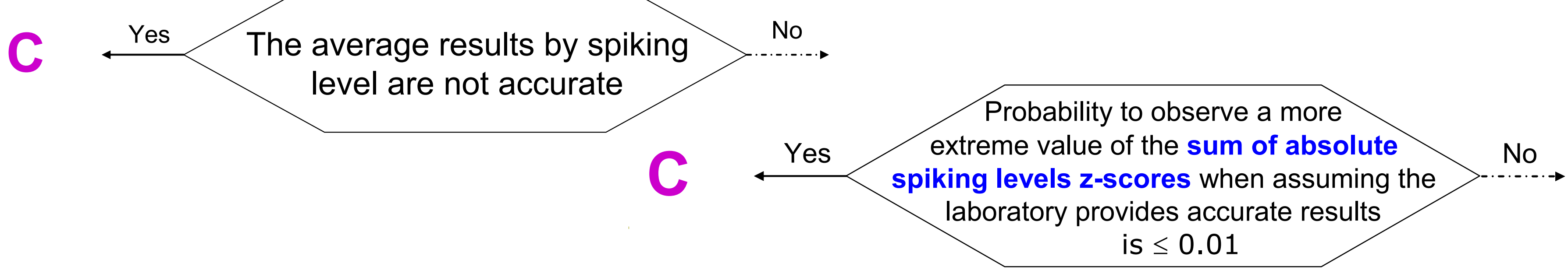
$$z = \frac{x - \mu}{\sigma}$$

→ Indicates how far and in what direction x deviates from μ , in units of σ

→ z-scores distribution's mean = **0**
z-scores distribution's std-deviation = **1**

→ When the distribution of reference is normal, the z-scores distribution is also normal and the probability to have a z-score in the interval [-2 ; +2] is ~ **0.95**

→ Useful to establish rules from distributions with different means and/or different standard-deviations



Consider the following z-scores computed for each Lab and each spiking-level:

$$z\_score = \frac{(mean\ of\ the\ sample\ results) - (true\ \ level)}{(Intra\_Lab\ std\_deviation\ \ estimate)/\sqrt{\#\ of\ samples\ \ provided\ \ by\ spiking\ \ leve}}$$

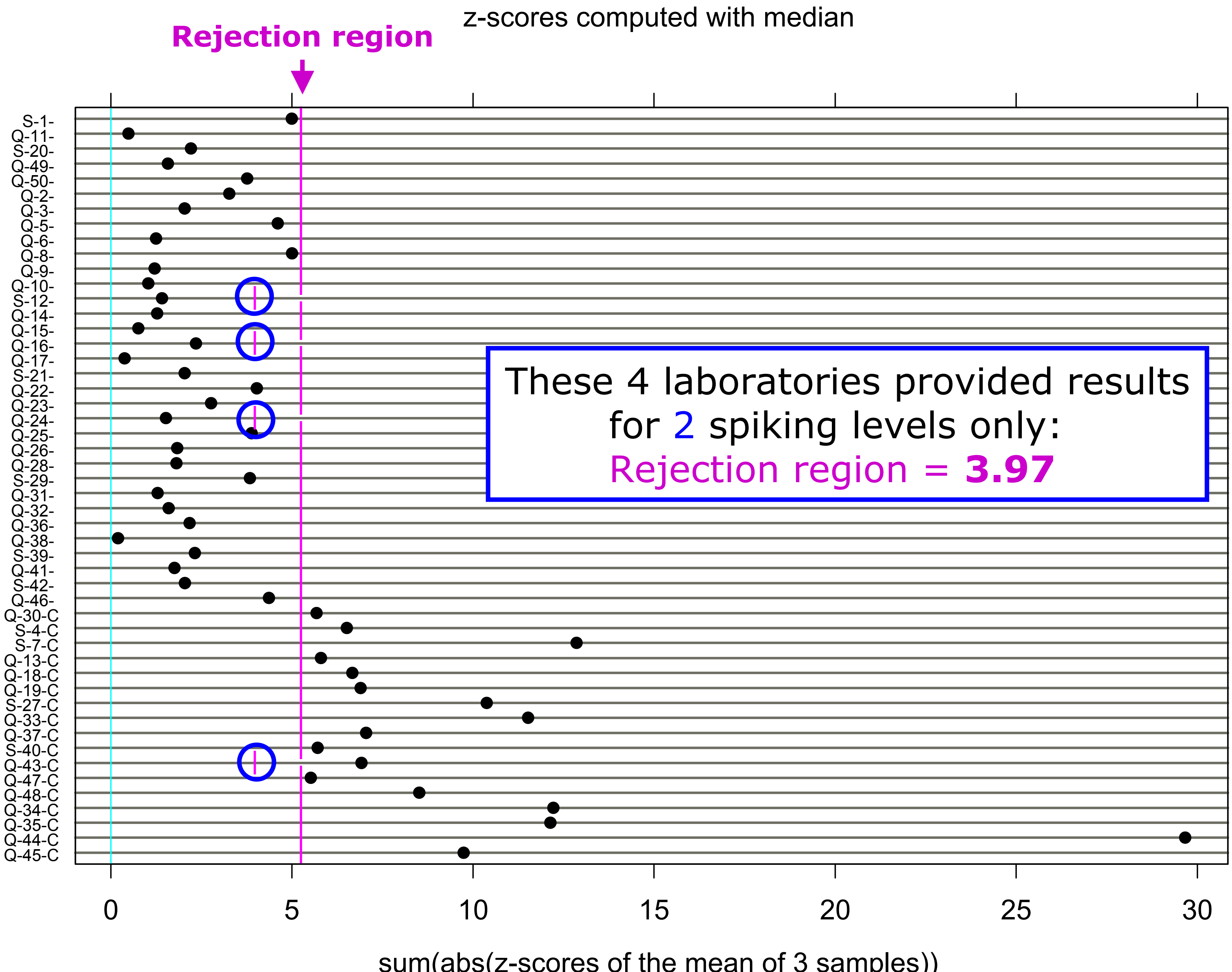
The theoretical distribution of the sum of these absolute independent z-scores for a given Lab can be defined using simulations.

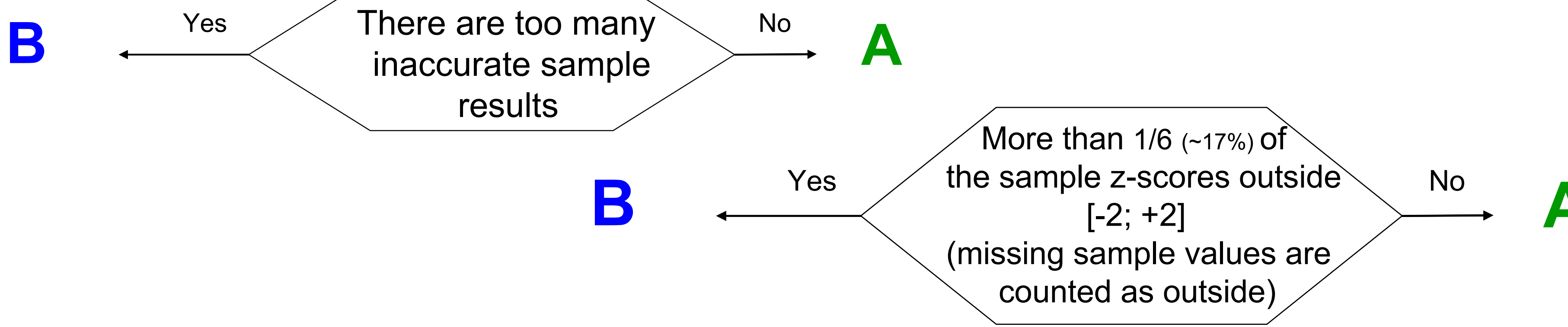
We can then define the rejection region at the 0.01 level:

# of spiking levels in the proficiency test	Rejection region at 0.01 level
1	2.55
2	3.97
3	5.25
4	6.43
5	7.55
…	

3 spiking levels: if sum of absolute z-scores > 5.25 → C rating

PT4 – Rating System 3 – C rating





Consider the following z-scores computed for each (Lab x spiking-level x sample) combination:

$$z\_score = \frac{(sample\ result) - (true\ \ level)}{Intra\_Lab\ std\_deviation\ estimate}$$

A z-score outside [-2 ; +2] has low probability (~ 0.05) to occur for a laboratory providing accurate sample results.

How to estimate the intra-laboratory standard-deviation for a “normal” / “average” / “reference” laboratory?

Estimate of the intra-Lab standard deviation

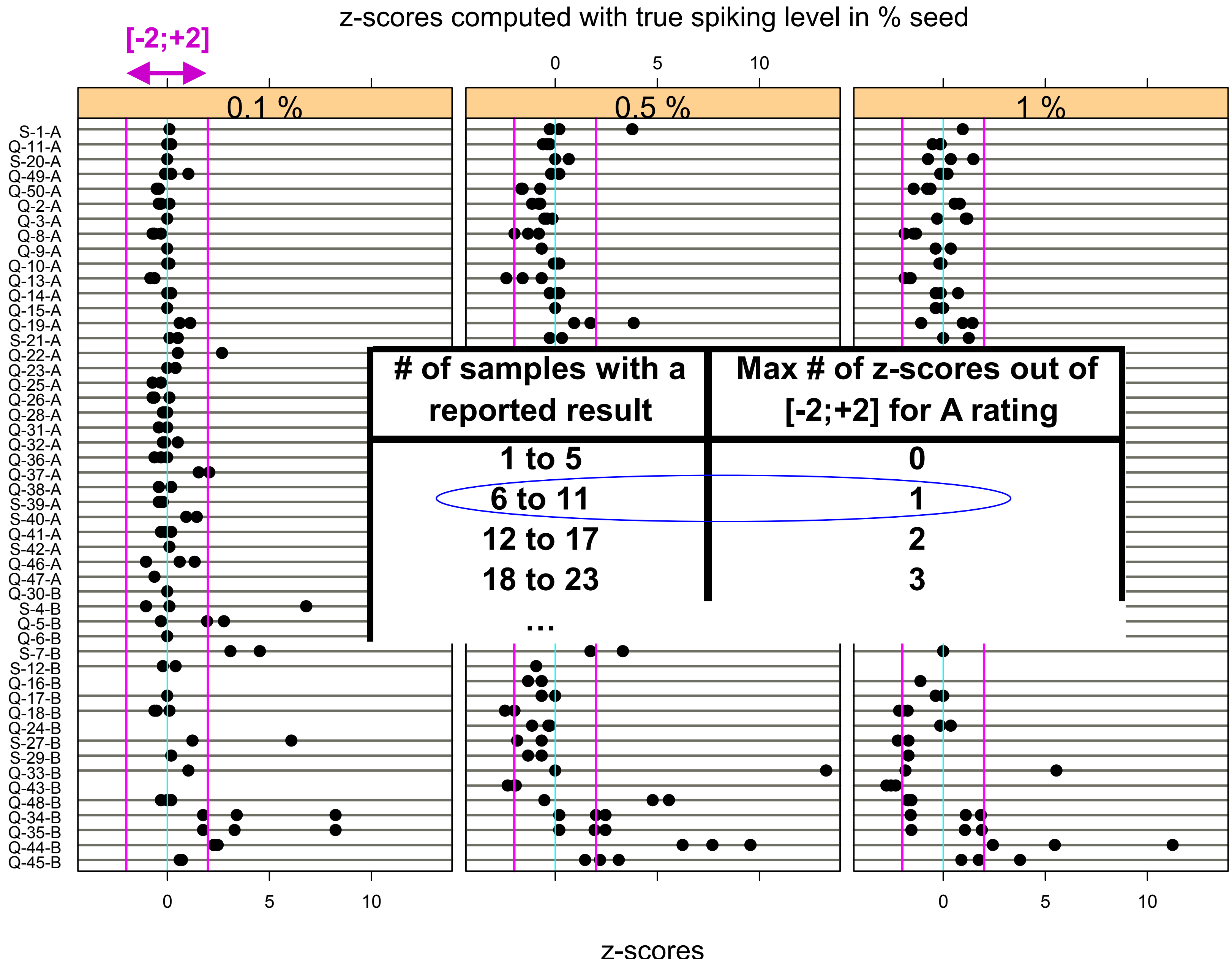
. For each Lab k and each spiking level i, compute the variance of the sample results: $\hat{\sigma}_{ik}^2$

. Carry out the Cochran's test at the 95% level to see if the Lab with the highest variance has an outlying spread of replicates.

. Compute the mean of the variances for a given spiking level i (except the one identified with the Cochran's test): $\hat{\sigma}_i^2$

. The intra-Lab standard-deviation estimate is then: $\sqrt{\hat{\sigma}_i^2}$

PT4 – Rating System 1 – A/B rating



# of samples with a reported result	Max # of z-scores out of [-2;+2] for A rating
1 to 5	0
6 to 11	1
12 to 17	2
18 to 23	3
...	

PT4 rating summary for quantification