



# Mechanistic and Statistic Partitioning the Technical Variability of Ligand Binding Assays in Distinct Formats

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ICH M10 LBA Guideline

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Distinct LBA assays

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LBA (PK, Biomarker, ADA)

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Partitioning technical variabilities

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Deterministic effect

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4PL model

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Linear Mixed Models

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LLOQ

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Gyros-Lab

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SIMOA

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Zero-inflated models

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# ICH M10 LBA Guideline

- $\pm 20\%$  for RE & CV, except for the LLOQ and ULOQ, where it should not exceed 25%.
- For non-accuracy and precision validation runs, at least 2/3 of the total QCs and at least 50% at each concentration level should be within  $\pm 20\%$  of the nominal values.
- TE should not exceed 30% (40% at LLOQ and ULOQ).
- Detailed regression models including weighing factors for LBA assays, which are deterministic factors for technical variability for LBAs, are not available in ICH M10.
- Stochastic factors, including batch effects, are not detailed in ICH M10.
- Both distinct formats of LBAs and inherent Ab-Ag affinity and avidity are crucial for technical variability.

**25 July 2022 EMA/CHMP/ICH/172948/2019**

**Committee for Medicinal Products for Human Use**

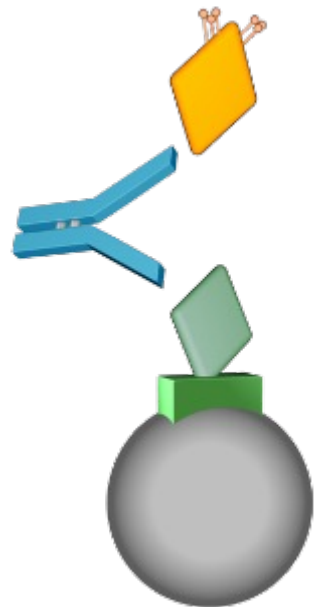
**ICH Guideline M10 on Bioanalytical Method Validation and Study Sample Analysis**

**Step 5**





Sandwich  
Immunoassay



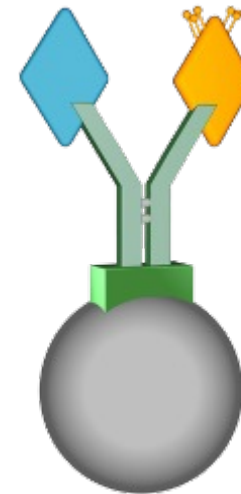
Bridging  
Immunoassay



Indirect  
Antibody  
Assay

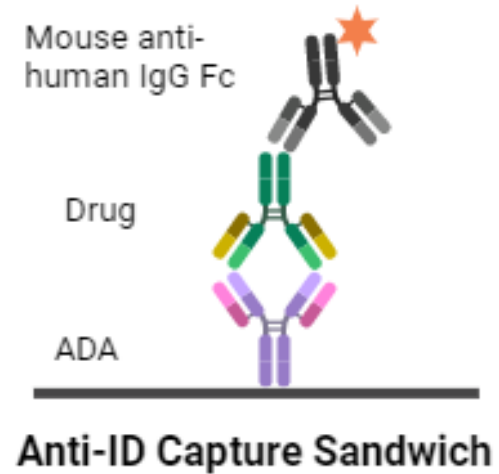
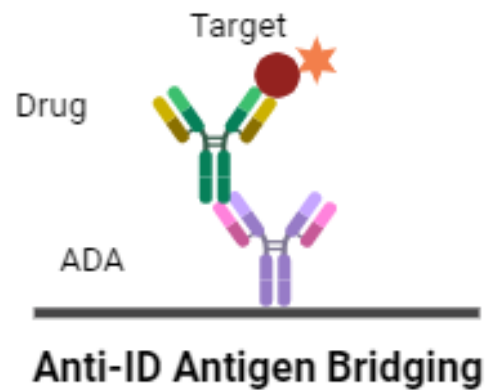
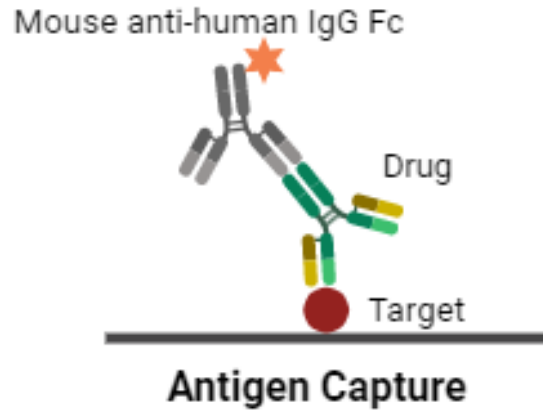


Reversed  
Antibody  
Assay



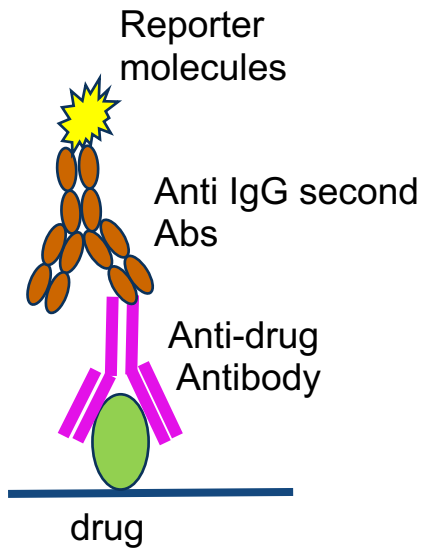
Sequential  
Assay  
Procedure

# Classical PK Assay Formats

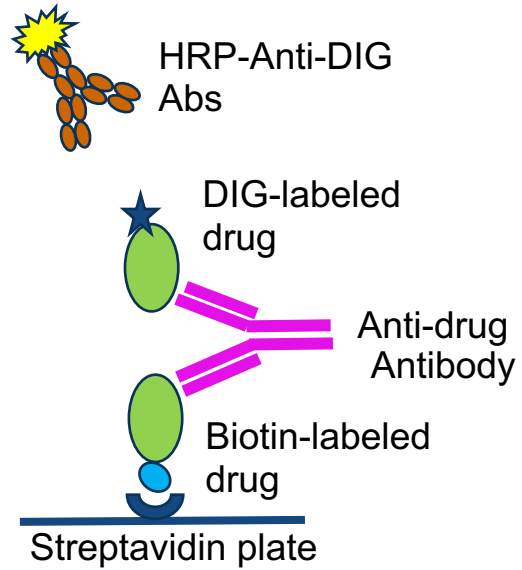


# Distinct Formats for Anti-Drug Antibodies Assays

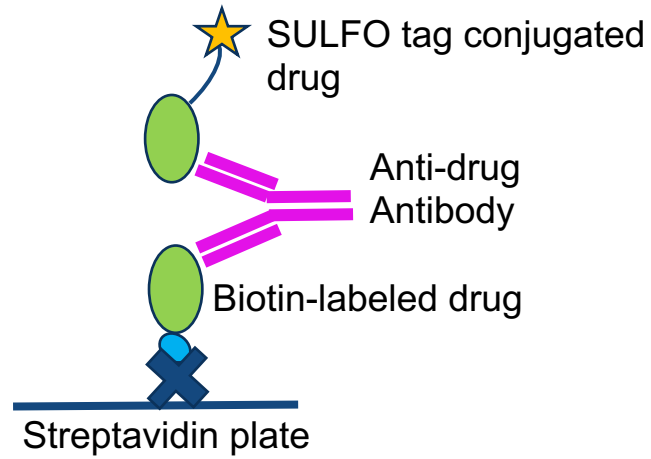
**ELISA  
Absorbance**



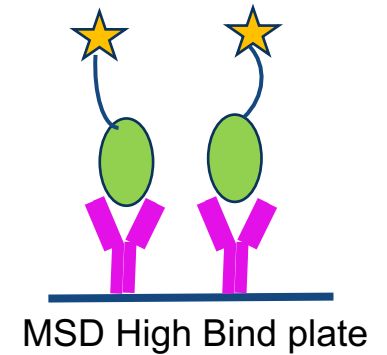
**ELISA  
Absorbance**



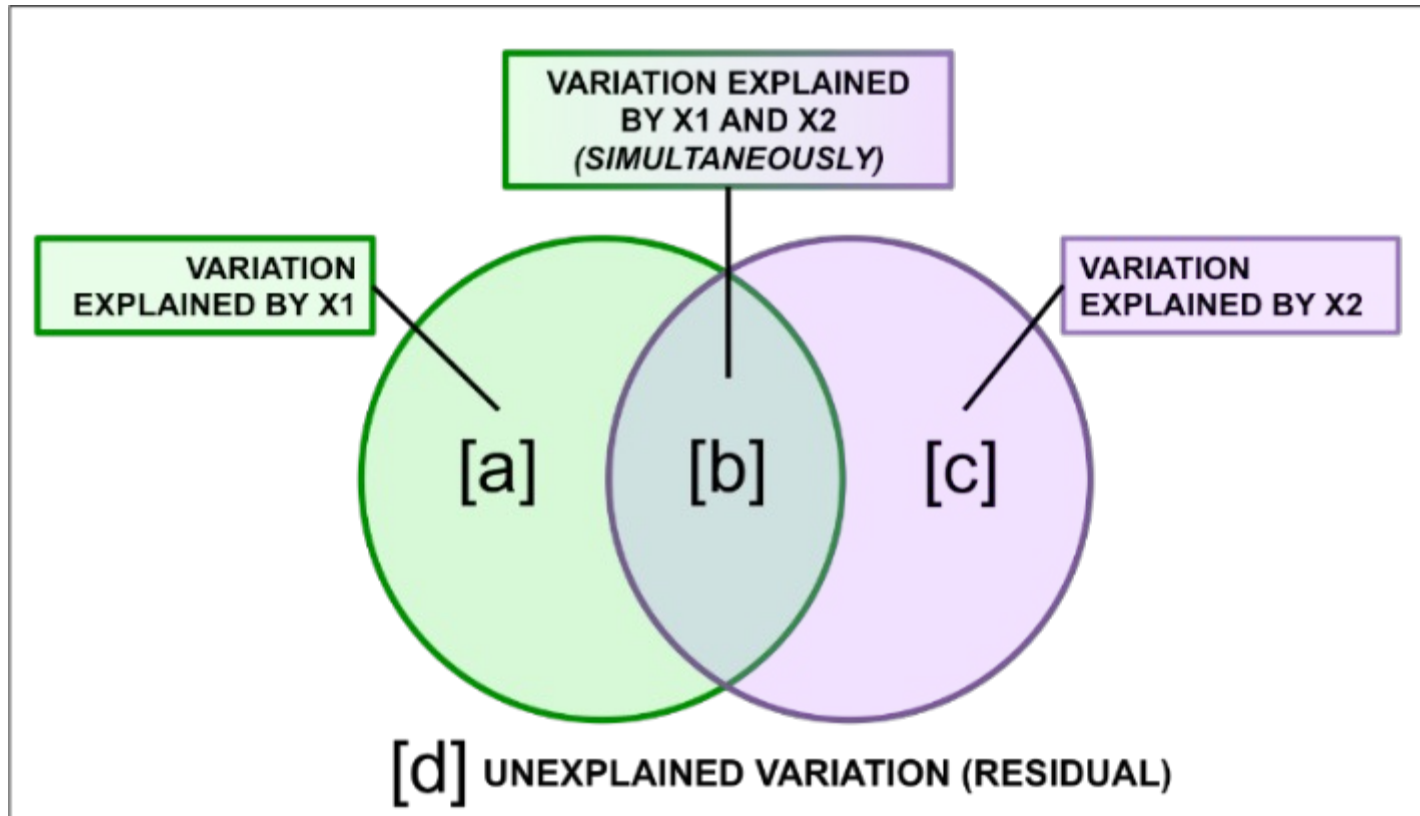
**MSD  
Bridge Assay**



**MSD  
Direct format**



# Partitioning Technical Variabilities (Stochastic)



$$Y \sim X1 + X2$$

$$R^2 = \frac{\text{variance of fitted model values}}{\text{variance of response values}}$$

(Coefficient of determination)

# Variability and LLOQ are Not Independent

In-Well (Without X  
Dilution Factor)

Deterministic  
Factors

Stochastic  
Factors

Platform	LLOQ	CV%
ELISA	~1 ng/mL	<15%
MSD	~2 pg/mL	<15%
ELLA	~1 pg/mL	<20%
Gyros-Lab	~1 pg/mL	<25%
SIMOA	~0.2pg/MI	<30%

In general, LLOQ and variability are negative correlated.



## Deterministic Effect

$$\frac{[RL]}{[R][L]} = \frac{k_{\text{on}}}{k_{\text{off}}} = K$$

$K$ , the equilibrium affinity constant, has dimensions of  $M^{-1}$ . As  $K$  (analogous to the thirst of the delegates) increases, so the concentration of the receptor–ligand complexes increases at the expense of the free species. Alternatively,

$$\frac{[R][L]}{[RL]} = \frac{k_{\text{off}}}{k_{\text{on}}} = K_d$$

$$Y(t) = A + \frac{K - A}{(C + e^{-B(t-M)})^{1/\nu}}$$

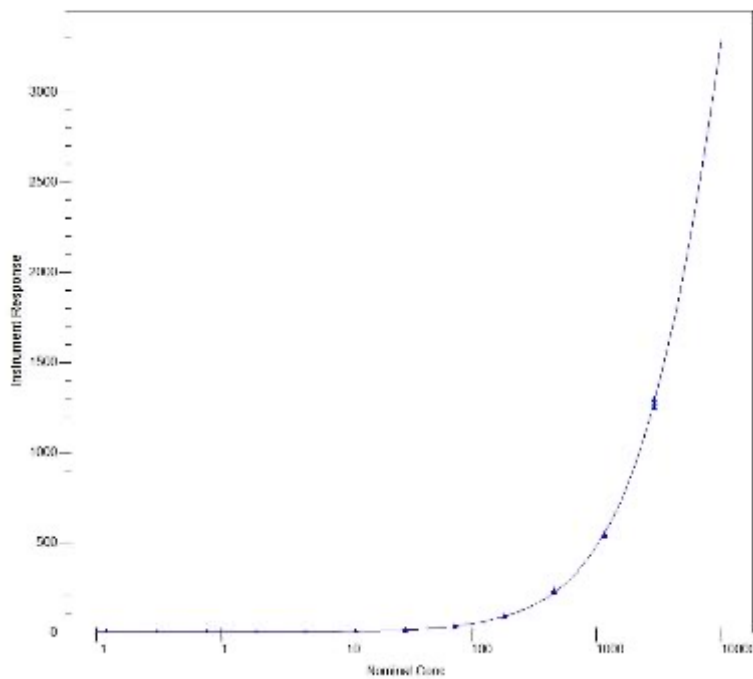
$$y = d + \frac{a - d}{1 + \left(\frac{x}{c}\right)^b}$$

$$x = c \left( \frac{a - d}{y - d} - 1 \right)^{\frac{1}{b}}$$

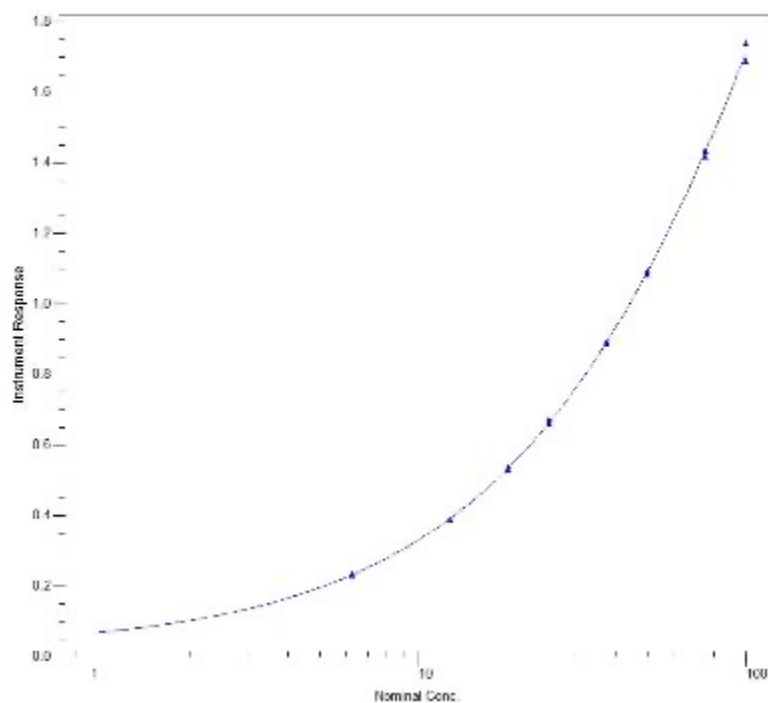
- Simple linear regression can work well for ELISA, especially for IVD kits;
- Weighing factor for 4/5 PL impact result, including CV% and RE%;
- Log-log transformation may be needed;
- For laboratory developed test (LDT), determined by LBA platforms.

# Standard Curves (Data Transformation)

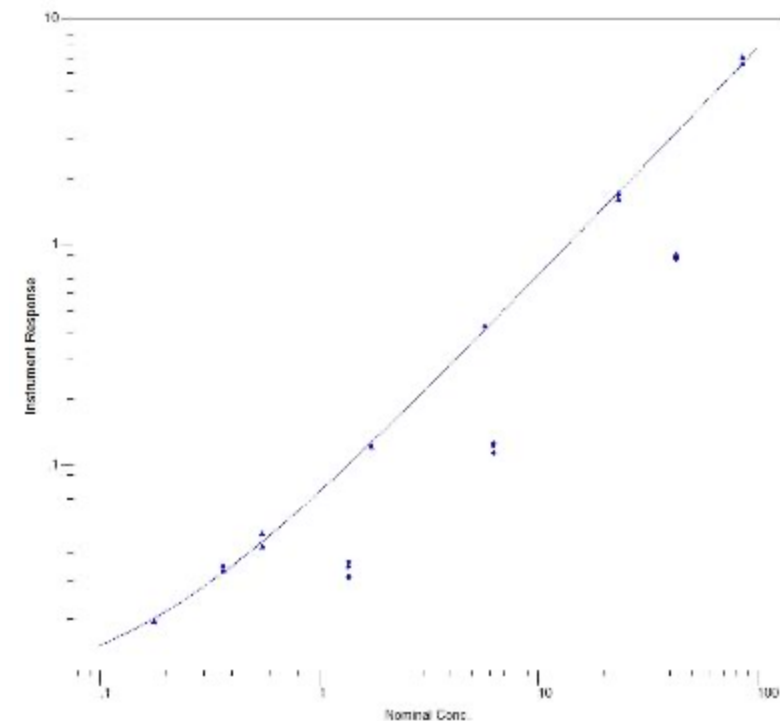
Analytical Run 16 analyzed on 12-May-2021 Calibration Standards for INI (g 2nd gen) (ppm/L)  
 Regression Method - NPL (MARQUARDT) - Weighting Factor - 1/Y\*\*2  
 Response = (Min - Max) / (1 + (Conc / Ed50) \*\* Slope) \*\* MI + Max  
 Min = 0.005840 Max = 8926.195518 Slope = 1.022811 C = 15385.220104 M = 0.925565 R-Squared = 0.9975  
 (Study BTM-3291.MV (CXCL10, II Pre, II-6, INI-g))



Analytical Run 4 analyzed on 23-Apr-2022 Calibration Standards for Lactoferrin (ng/ml)  
 Regression Method - 4PL (MARQUARDT) - Weighting Factor - 1  
 Response = (Min - Max) / (1 + (Conc / Ed50) \*\* Slope) + Max  
 Min = 0.002114 Max = 5.751194 Slope = 0.896806 Ed50 = 273.331422 R-Squared = 0.9695  
 (Study BTM-3720.MV)



Analytical Run 9 analyzed on 27-Apr-2021 Calibration Standards for pTau181 (pg/ml)  
 Regression Method - 4PL (MARQUARDT) - Weighting Factor - 1/Y\*\*2  
 Response = (Min - Max) / (1 + (Conc / Ed50) \*\* Slope) + Max  
 Min = 0.000034 Max = 23726.06363 Slope



# Linear Mixed Model

$$\begin{aligned} \mathbf{y}_i &= \mathbf{X}_i\boldsymbol{\beta} + \mathbf{Z}_i\mathbf{b}_i + \boldsymbol{\varepsilon}_i \\ \mathbf{b}_i &\sim \mathbf{N}_q(\mathbf{0}, \boldsymbol{\Psi}) \\ \boldsymbol{\varepsilon}_i &\sim \mathbf{N}_{n_i}(\mathbf{0}, \sigma^2\boldsymbol{\Lambda}_i) \end{aligned}$$

where

- $\mathbf{y}_i$  is the  $n_i \times 1$  response vector for observations in the  $i$ th group.
- $\mathbf{X}_i$  is the  $n_i \times p$  model matrix for the fixed effects for observations in group  $i$ .
- $\boldsymbol{\beta}$  is the  $p \times 1$  vector of fixed-effect coefficients.
- $\mathbf{Z}_i$  is the  $n_i \times q$  model matrix for the random effects for observations in group  $i$ .
- $\mathbf{b}_i$  is the  $q \times 1$  vector of random-effect coefficients for group  $i$ .
- $\boldsymbol{\varepsilon}_i$  is the  $n_i \times 1$  vector of errors for observations in group  $i$ .
- $\boldsymbol{\Psi}$  is the  $q \times q$  covariance matrix for the random effects.
- $\sigma^2\boldsymbol{\Lambda}_i$  is the  $n_i \times n_i$  covariance matrix for the errors in group  $i$ .

**Scientist  
Lot  
Batch  
Instrument**

## High Analyte Concentration

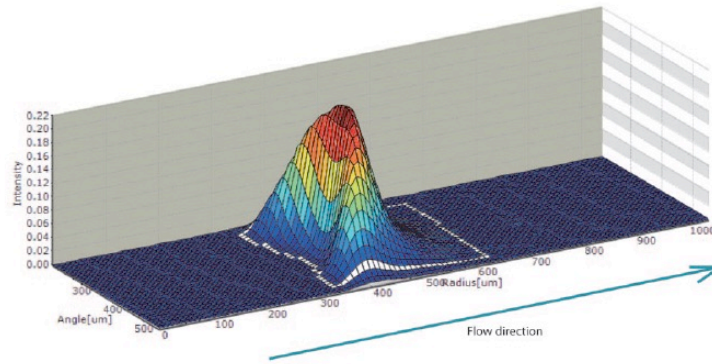


Figure 1: Example of desired binding profile in Gyrolab Viewer

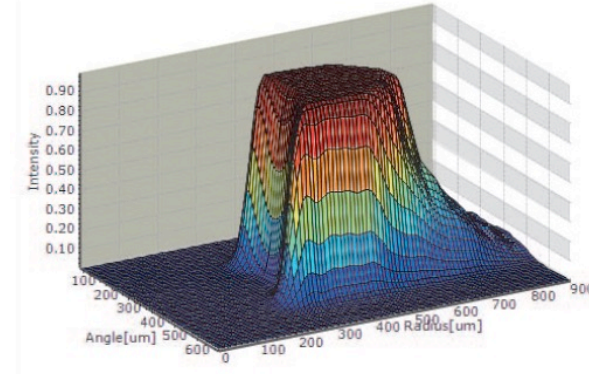


Figure 2: Example of binding profile that indicates saturated detector signal

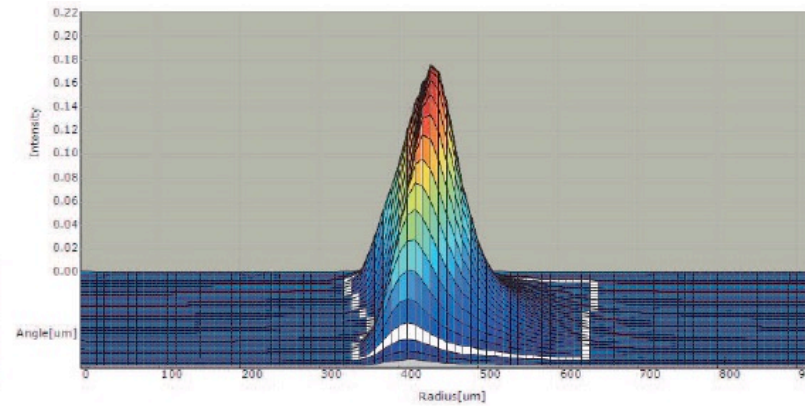
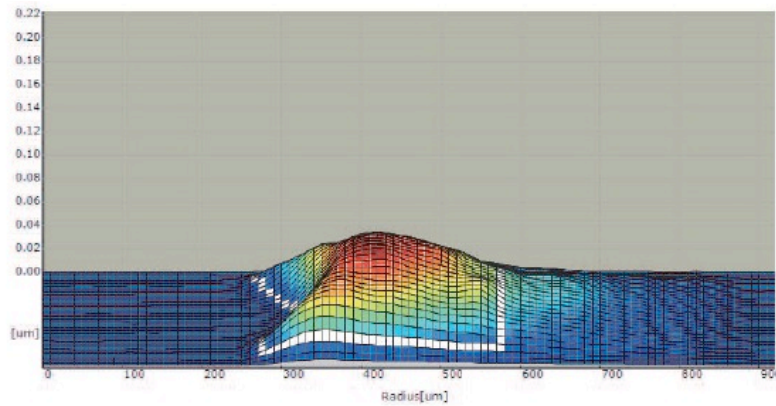
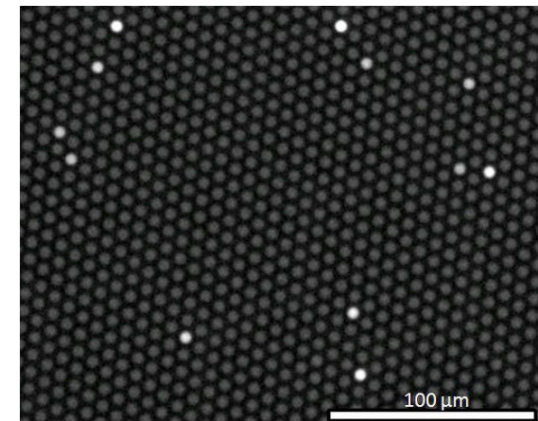
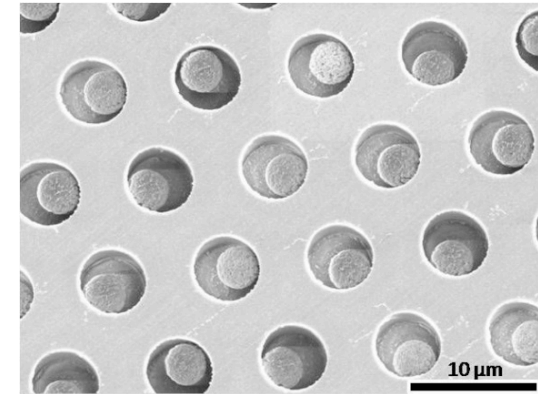
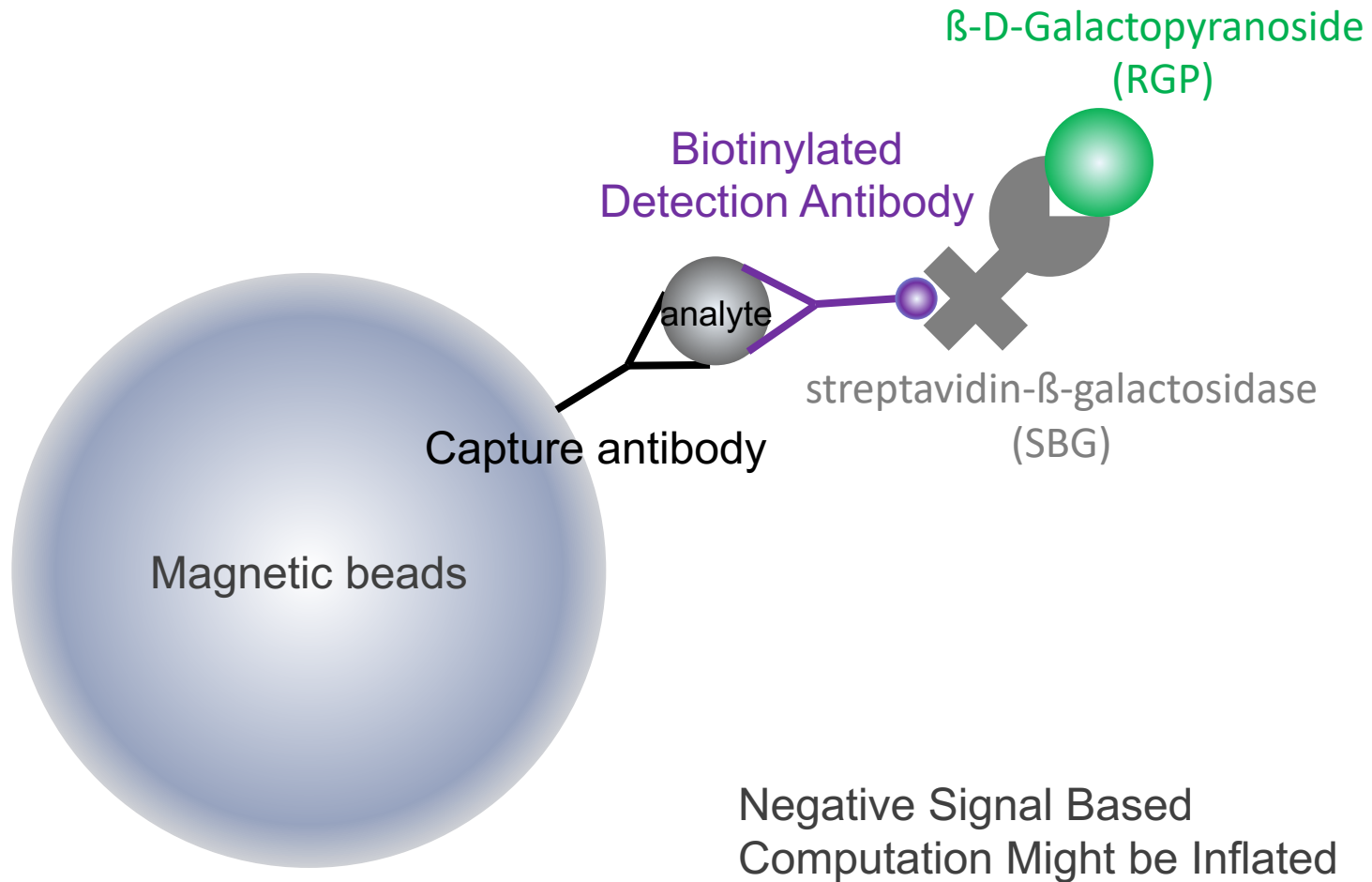


Figure 3: Example of binding profiles that indicate lower affinity (left) and higher affinity (right) between capture reagent and analyte

# SIMOA (Digital-ELISA)





# Zero-Inflated Models (SIMOA)

$$f(k; \lambda) = \Pr(X=k) = \frac{\lambda^k e^{-\lambda}}{k!}$$

$$\lambda = -\ln(N\text{-neg}/N\text{-total})$$

$$\lambda = E(X) = \text{Var}(X).$$

$$\text{CV} = \text{std}/\text{mean} = \sqrt{\lambda}/\lambda$$

$$f_{Y|\mathbf{X}, \mathbf{W}}(y; \mathbf{x}, \mathbf{w}, \boldsymbol{\beta}, \boldsymbol{\vartheta}, \boldsymbol{\alpha}) = \begin{cases} \pi + (1 - \pi)p_{Y|\mathbf{X}}(0; \mathbf{x}, \boldsymbol{\eta}, \boldsymbol{\vartheta}), & \text{for } y = 0; \\ (1 - \pi)p_{Y|\mathbf{X}}(y; \mathbf{x}, \boldsymbol{\eta}, \boldsymbol{\vartheta}), & \text{for } y \in \mathbb{N}^+, \end{cases}$$

For Fit-for-Purpose Design, Relaxed Criteria Might be Needed.



# Summary

- **Technical variability control (TVC) is the prerequisite for assess biological variabilities;**
  - **A better understanding the deterministic and stochastic partitioning LBA holds the promise to foster validation accomplishment;**
  - **Distinct formats my have specific criteria for validation as the sensitivity might be at the cost of technical variabilities;**
  - **LBA platforms should be carefully chosen, given the characteristics of analytes;**
  - **Linear mixed model can be employed to dissect technical variability;**
  - **Zero-inflated model can be applied to SIMOA platform;**
  - **ICH M10 Guideline may require science-based adaptation, namely, fit-for-purpose.**
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 Thank You



 **FRONTAGE**