

Risk assessments using a Bayesian approach:

Evaluation of impact from analytical method performance on process capability

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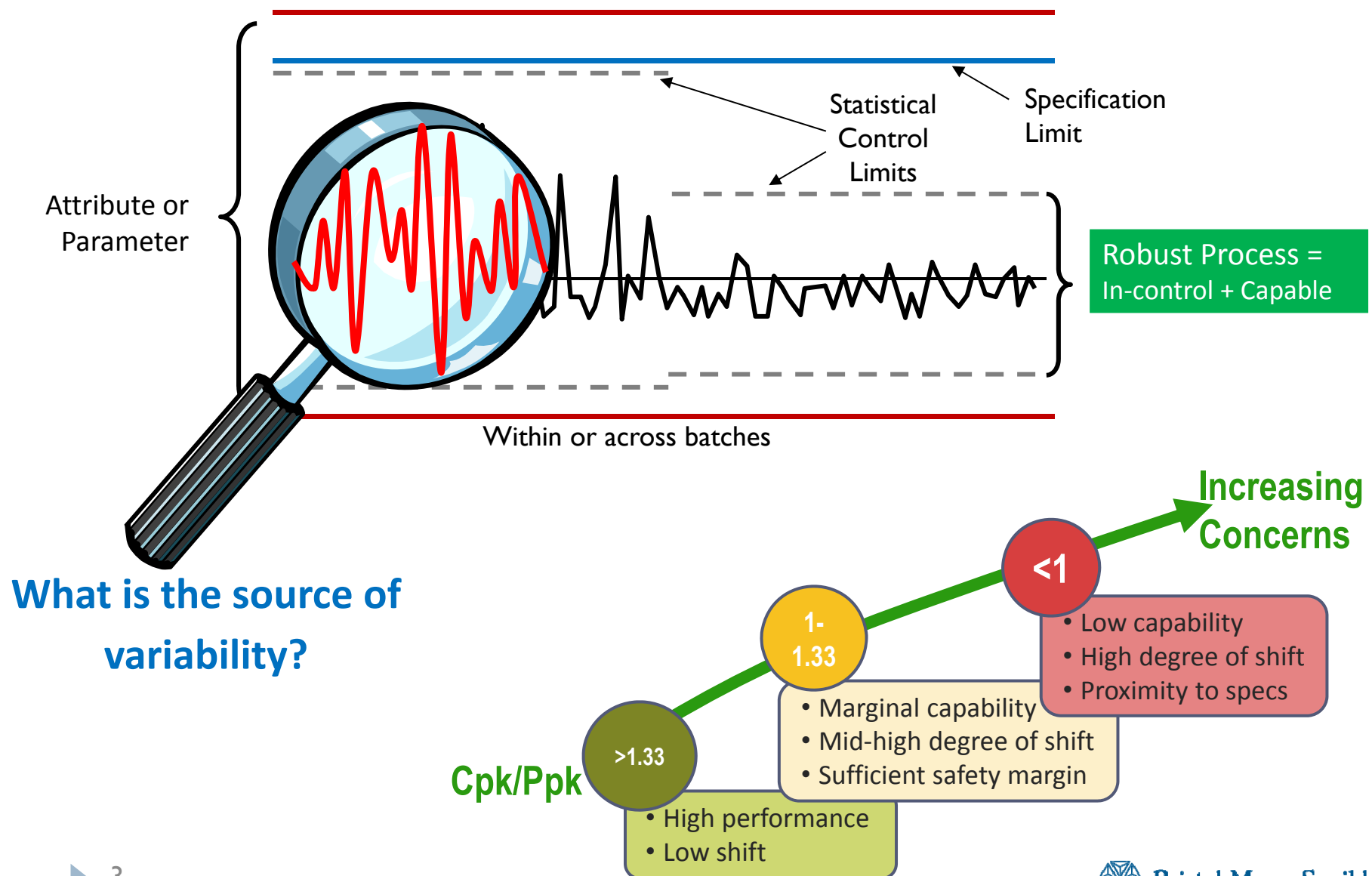
Global Statistics

Bristol-Myers Squibb

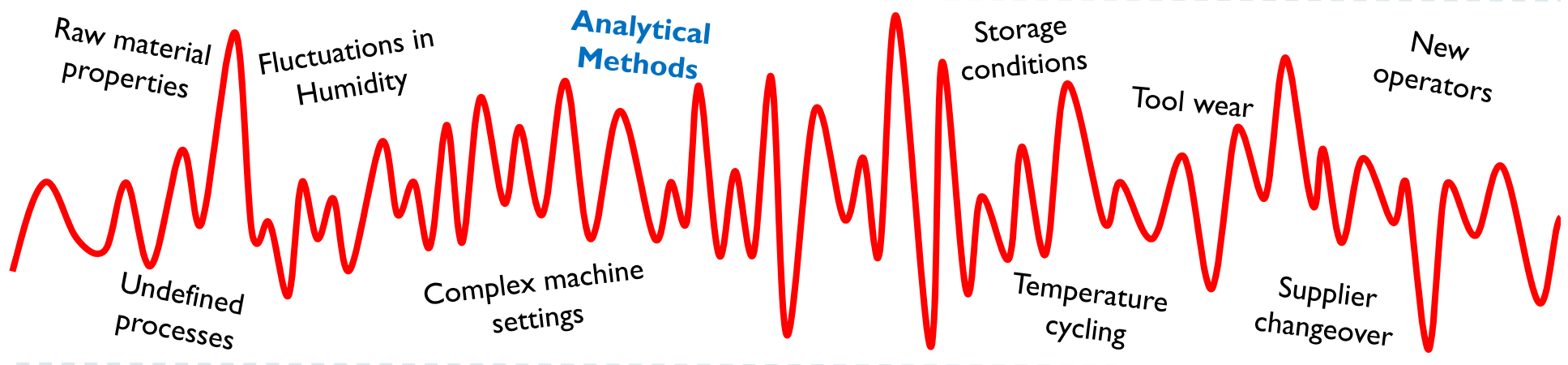
Outline

- ❑ Business needs for using advanced statistical modelling tool to build effective control strategy through life-cycle
 - Achieve robustness goal through continuous process verification
 - Control analytical performance is critical
 - BMS's vision in delivering analytical performance through continuous analytical verification
- ❑ Bayesian's advantages in establishing risk-based control strategy
- ❑ A case study on protein concentration method
- ❑ Summary and next steps

Robustness through Continuous Process Verification



Understand Sources of Variance



Raw materials + Processes + Environment + Analytical Method = Quality Variations

To what degree should **each source of variance** be controlled to meet the robustness goal?

Continuous Analytical Verification

History

No formal / systematic process for assessing and mitigating risks to method performance

Method Performance Expectations not designed to deliver on Robustness Targets

Method development does not consistently address key risks across the breadth of the manufacturing / analytical operating space

Validation / Tech Transfer is primarily a Regulatory exercise, it is not designed to ensure method performance

Variability in how lab unit operations are executed across analysts /sites

Very difficult to monitor method performance

Vision

ID Method and Performance Expectations

Evaluate Risks & Design & Execute studies to develop optimal Method

Validate Method

Execute Method

Evaluate Performance vs Expectations

Establish Analytical Target Profile (ATP) for each method type / technique; aligned across all partners

Leverage Risk Assessment /Modeling tools to optimize method performance at edges of process (process, material, analytical) that pose risk to method performance

Risks to method performance are understood and communicated

Method Validation / Transfer demonstrates ATP is met

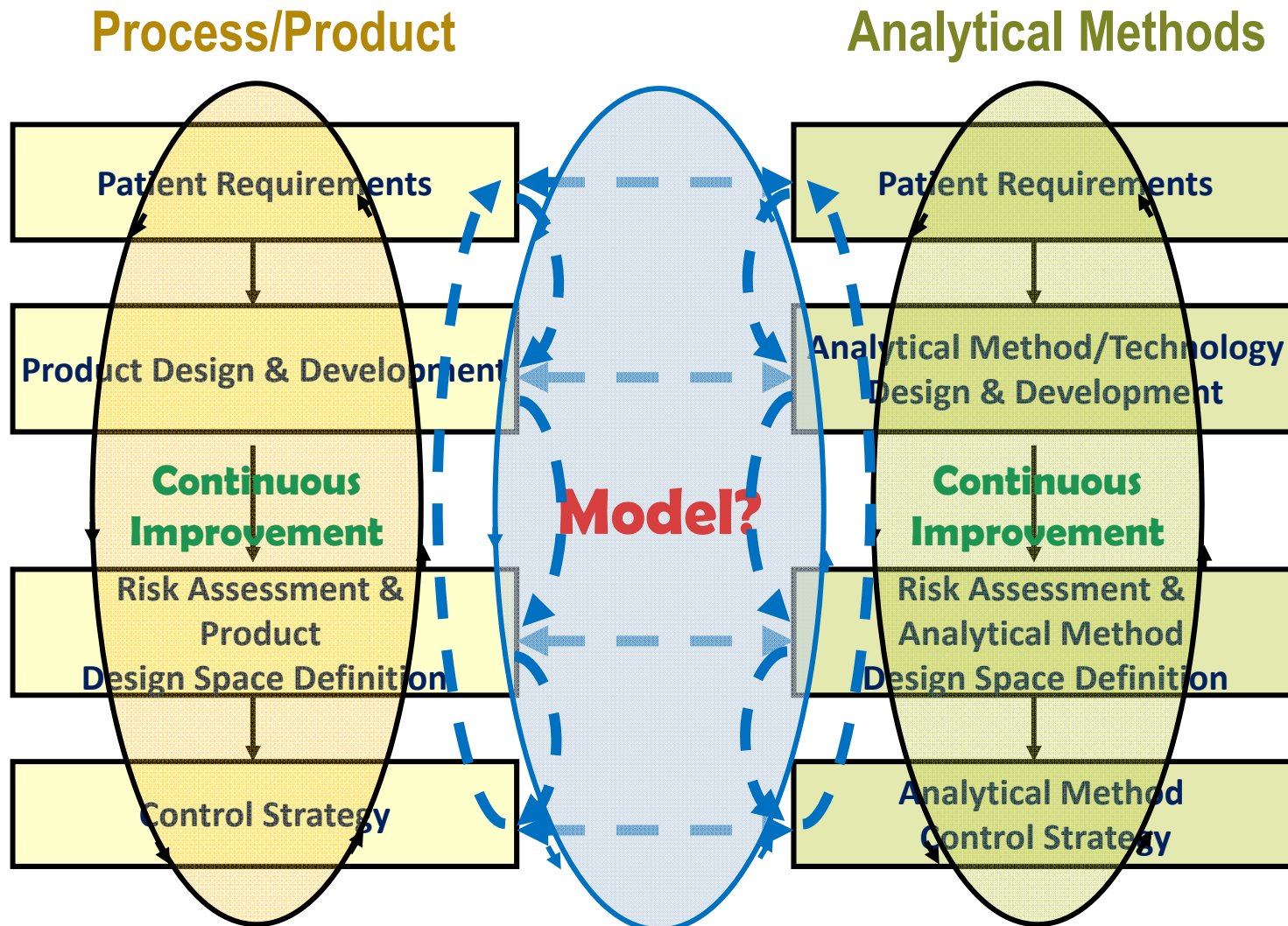
Establish Best Practices for Lab Unit Ops across sites; all sites trained same way

Establish Method Performance Monitoring tools to enable ongoing assessment of method performance

Aligned method review with method monitoring plan



Need for Advanced Statistical Modelling



Bayesian Hierarchical Modeling

Frequentist

$P(\text{data} \mid \text{performance})$

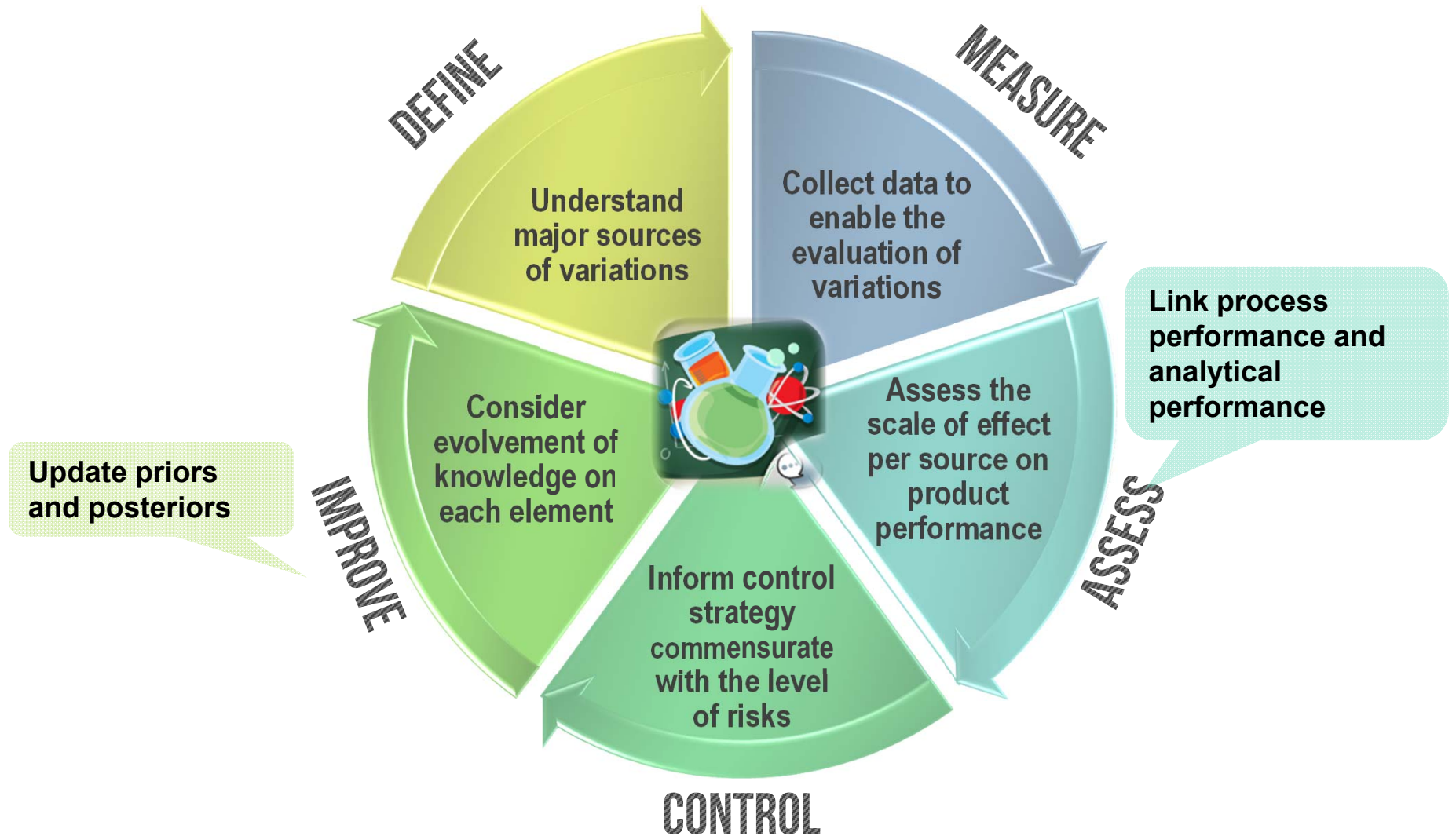
vs.

Bayesian

$P(\text{performance} \mid \text{observed data} + \text{prior information})$

- ❑ Convenient connection of complex analytical and process components
- ❑ Natural and principled way of combining **prior information** (e.g. historical process and analytical data)
- ❑ **Continuous learning** capability based on accumulated knowledge
- ❑ **Predictive inference** (posterior distribution) based on varied hypotheses
- ❑ **Uncertainty** about future performance

Build Risk-based Control Strategy



A Case Study

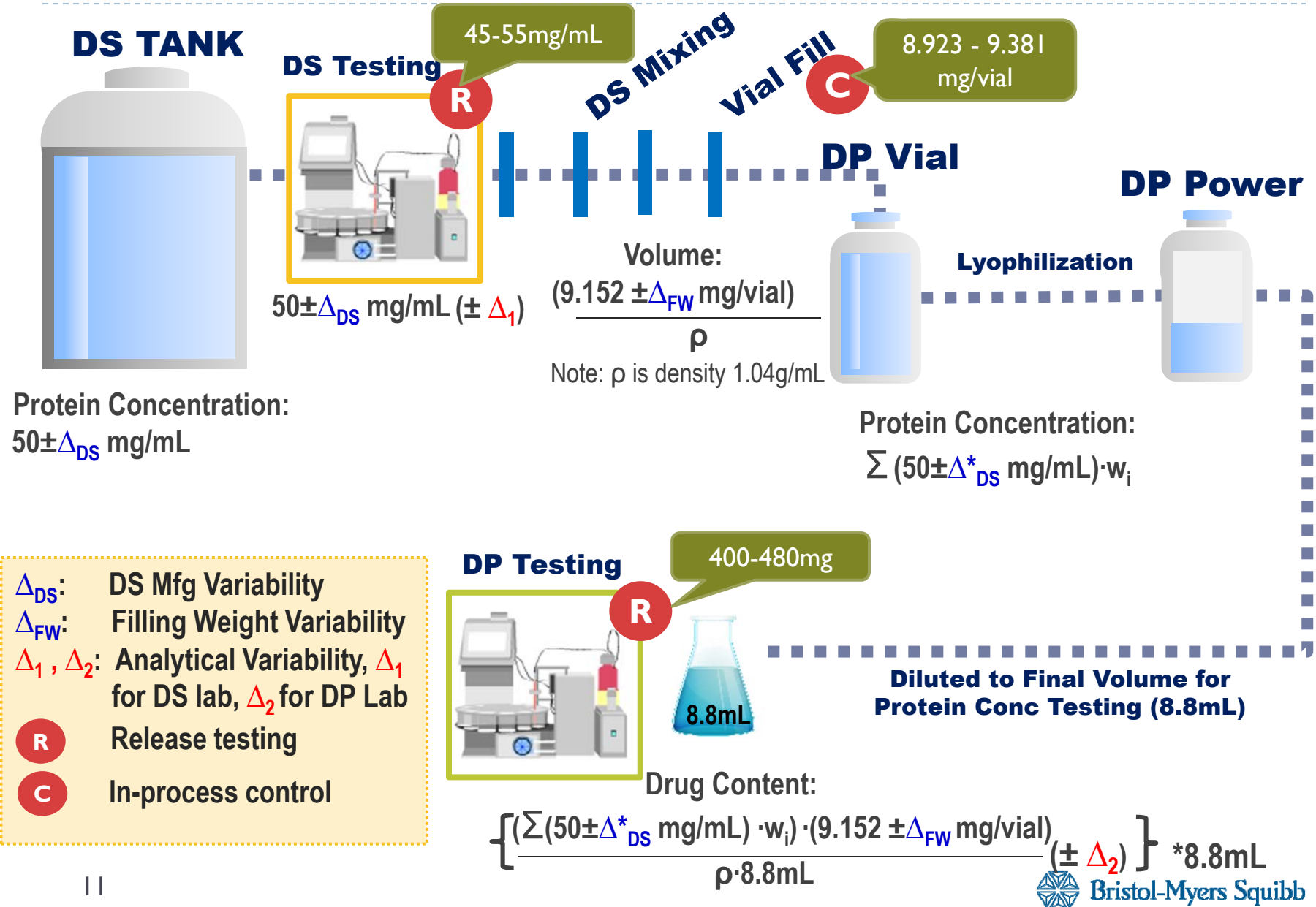
Background

- ❑ **CQA: Drug Content (DP) / Protein Concentration (DS)**
- ❑ **Target of Control**

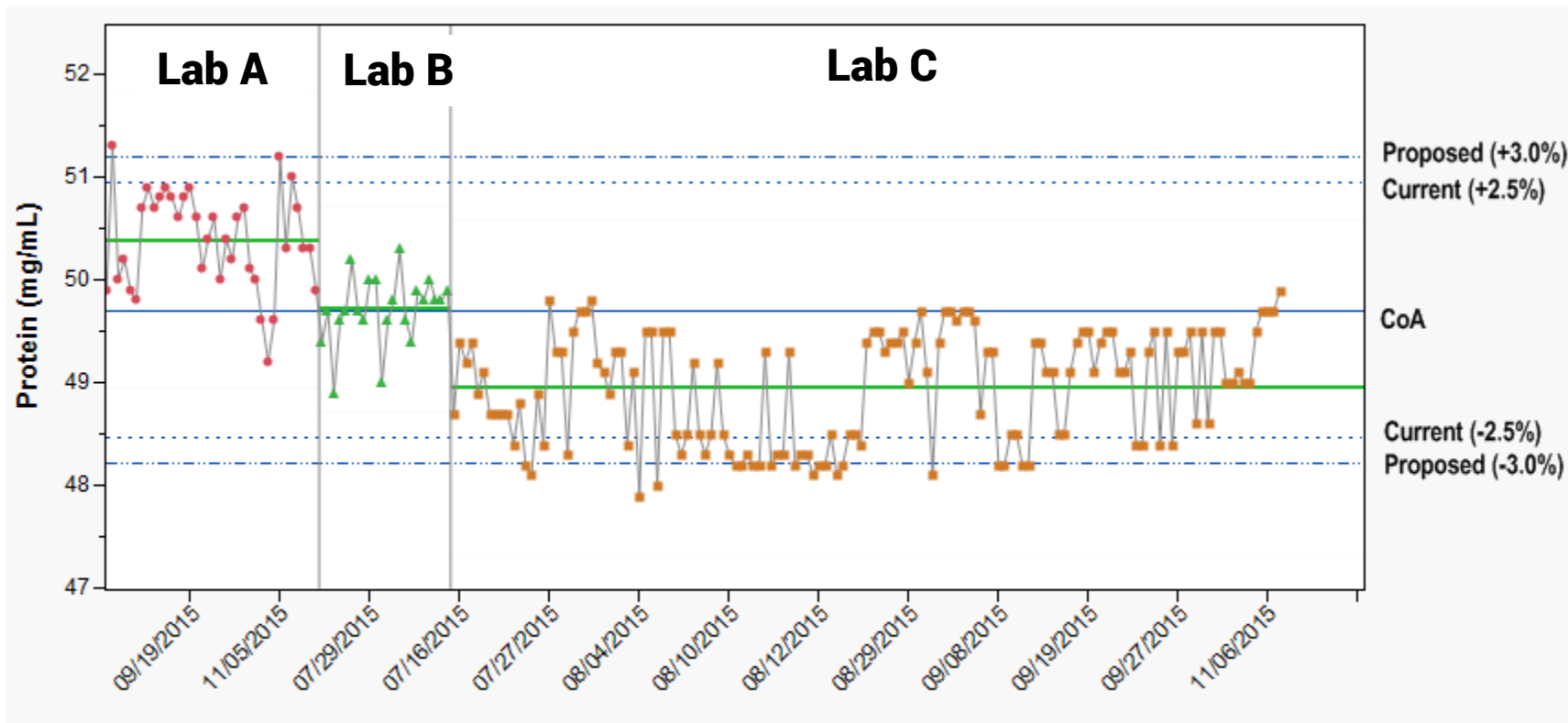
Elements of Control	Acceptance Criteria
DS Protein Concentration	<ul style="list-style-type: none">• 45.0-55.0 mg/mL
DP Drug Content	<ul style="list-style-type: none">• 400-480mg
DP Fill Weight	<ul style="list-style-type: none">• 8.923 - 9.381 mg/vial
Analytical Variability (DS & DP)	<p>System Suitability (SS): 3 tests on Reference Material (RM)</p> <ul style="list-style-type: none">i. RSD of the three $\leq 2.0\%$ii. Average of the three within $\pm 2.5\%$ difference from the RM lot release value (49.7%) <p><i>Note: same method for DS and DP with different execution labs</i></p>

- ❑ **Problem:** To what degree the analytical method should be controlled, such that process performance of DS and DP won't be significantly impacted?

Understanding the Variabilities



Reference Material Trends



Consideration of the lab factor into the risk assessment.

Modeling Flow

Model 1: Predict the analytical variability from DS lab (Δ_1)

Historical Data: Observed DS results and corresponding SS results (N=34)

Output: analytical variability (Δ_1) and true manufacturing variability (Δ_{DS})

Model 2: Predict the individual vial weight

Historical Data : Fill weight batch mean, within batch SD (N=10)

Output: individual vial weight (n= 10,000x200 vials)

Model 3: Predict the analytical variability from DP lab (Δ_2)

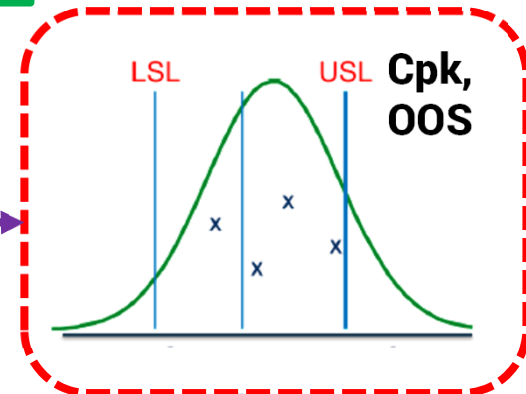
Historical Data: Observed DP results and corresponding SS results

Output: analytical variability (Δ_2)

Model 4: Predict measured DP drug content per vial

Input:

Output: measured DS protein concentration and DP drug content for each simulated vial



Model 1: Analytical Variability of DS Lab

Objective:

- Obtain predictive inference for true DS protein concentration.
- Obtain predictive inference for analytical variability from DS lab.

Data: Measured DS and the matching SS results (average of three RM). N=34

$$PC_i^{DS.Obs} \sim PC_i^{DS} + \Delta_1$$

$$PC_i^{DS} \sim N(\mu_{DS}, \sigma_{DS})$$

$$\Delta_1, SS_1, SS_2, SS_3 \sim N(\mu_i^{DS}, \sigma_i^{DS})$$

$$SS_{report}^{DS} \sim \sum_{k=1,2,3} SS_k / (3 \cdot CoA) \cdot I(LowerCriteria, UpperCriteria) \quad \text{SS criteria on mean}$$

$$\mu_i^{DS} \sim N(\mu_{M\mu}^{DS}, \tau_{M\mu}^{DS})$$

Priors:

$$\mu_{DS} \sim N(50, 100)$$

$$\sigma_{DS} \sim U(0, 100)$$

$$\mu_{M\mu}^{DS} \sim N(0, 100)$$

$$\tau_{M\mu}^{DS} \sim U(0, 10)$$

$$\sigma_i^{DS} \sim U(0, 1)$$

where PC_i^{DS} is the protein concentration for the i^{th} DS lot ($i = 1, 2, \dots, 34$); $\mu_i^{DS}, \sigma_i^{DS}$ is the population mean and standard deviation for analytical error under the same testing circumstance in DS lab (repeatability); $\mu_{M\mu}^{DS}, \tau_{M\mu}^{DS}$ is the population mean and standard deviation for analytical error under varied testing circumstance in DS lab (intermediate precision); μ_{DS}, σ_{DS} DS process mean and process standard deviation



Model 2: DP Fill Weight

Objective: Obtain predictive inference for filling weight of individual vials

Data: Fill weight batch mean, and within batch standard deviation ($N = 10$)

$$FW_{ij} \sim N(FW_i, \sigma_i)$$

$$FW_i \sim N(\mu_g, \sigma_g)$$

$$\tau_i = \frac{1}{\sigma_i^2} \sim \Gamma(\alpha, \beta)$$

Priors:

$$\mu_g \sim N(9.152, 100)$$

$$\sigma_g \sim U(0, 10)$$

$$\alpha \sim \Gamma(0.001, 0.001)$$

$$\beta \sim \Gamma(0.001, 0.001)$$

where FW_{ij} is the fill weight for the j^{th} vial ($j = 1, 2, \dots, 200$) from the i^{th} lot ($i = 1, 2, \dots, 10$).

Model 3: Analytical Variability of DP Lab

Objective: Obtain predictive inference for analytical variability from DP Lab

Data: Measured DP and the matching SS results

$$\Delta_2, SS_1, SS_2, SS_3 \sim N(\mu_k^{DP}, \sigma_k^{DP})$$

$$SS_{report}^{DP} \sim \sum_{k=1,2,3} SS_k / (3 \cdot CoA) \cdot I(LowerCriteria, UpperCriteria) \quad \text{SS criteria on mean}$$

$$\mu_k^{DP} \sim N(\mu_{M\mu}^{DP}, \sigma_{M\mu}^{DP})$$

Priors:

$$\mu_{M\mu}^{DP} \sim N(0, 100) \quad \sigma_{M\mu}^{DP} \sim U(0, 5) \quad \sigma_k^{DP} \sim U(0, 1)$$

where $\mu_k^{DP}, \sigma_k^{DP}$ is the population mean and standard deviation for analytical error under the same testing circumstance in DP lab (repeatability); $\mu_{M\mu}^{DP}, \sigma_{M\mu}^{DP}$ is the population mean and standard deviation for analytical error under varied testing circumstance in DP lab (intermediate precision).

Model 4: Predict DP drug content

Objective:

- Obtain predictive inference on true DP drug content.

Data: predicted true DS protein concentration (Model 1), predicted DP fill weight per vial (Model 2), analytical errors for DS and DP lab (Model 1, 3)

$$PC_{ij}^{DP*} = \frac{FW_{ij}^* * PC_i^{DS*}}{\rho}$$

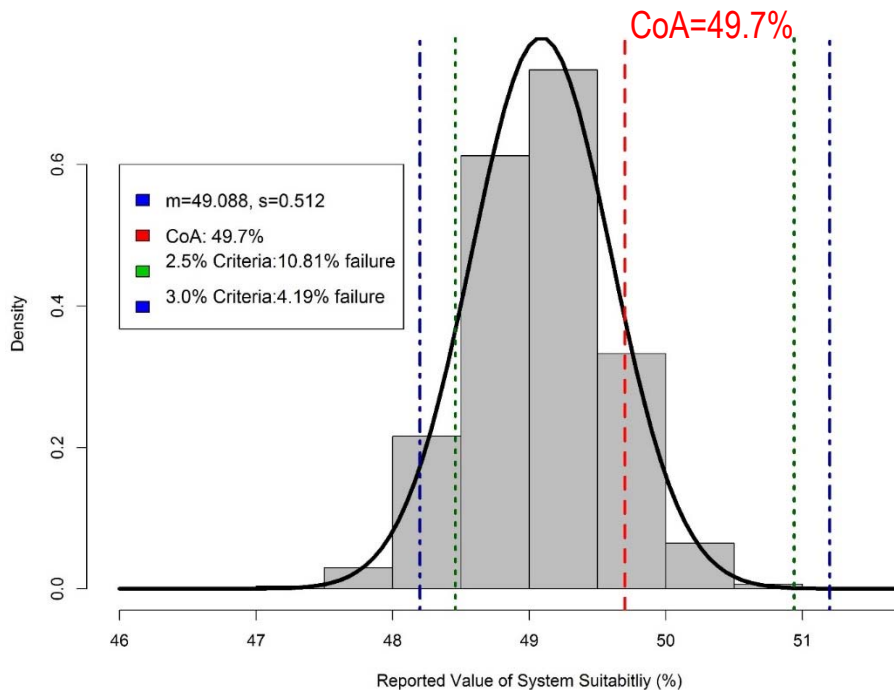
$$PC_{ij}^{DP.Obs*} = PC_{ij}^{DP*} + \Delta_2^*$$

$$|SS_{report}^{DP*}| \leq \text{WRS Criterion}$$

where PC_i^{DS*} is predicted true protein concentration for the i^{th} DS lot from Model 1; PC_{ij}^{DP*} is simulated true protein concentration for the j^{th} vial ($j = 1, 2, \dots, 200$) produced from the i^{th} DS lot ($i = 1, 2, \dots, N$); $PC_{ij}^{DP.Obs*}$ is the estimated tested protein concentration for the j^{th} vial produced from the i^{th} DS lot.

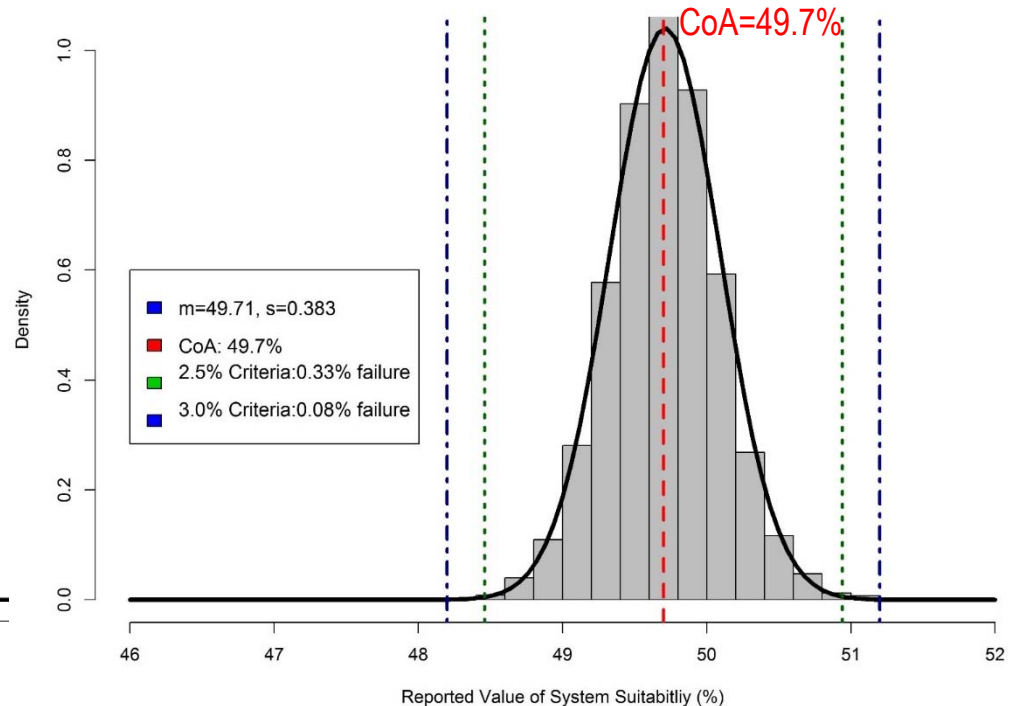
Prediction: Distribution of System Suitability Results

DS Lab



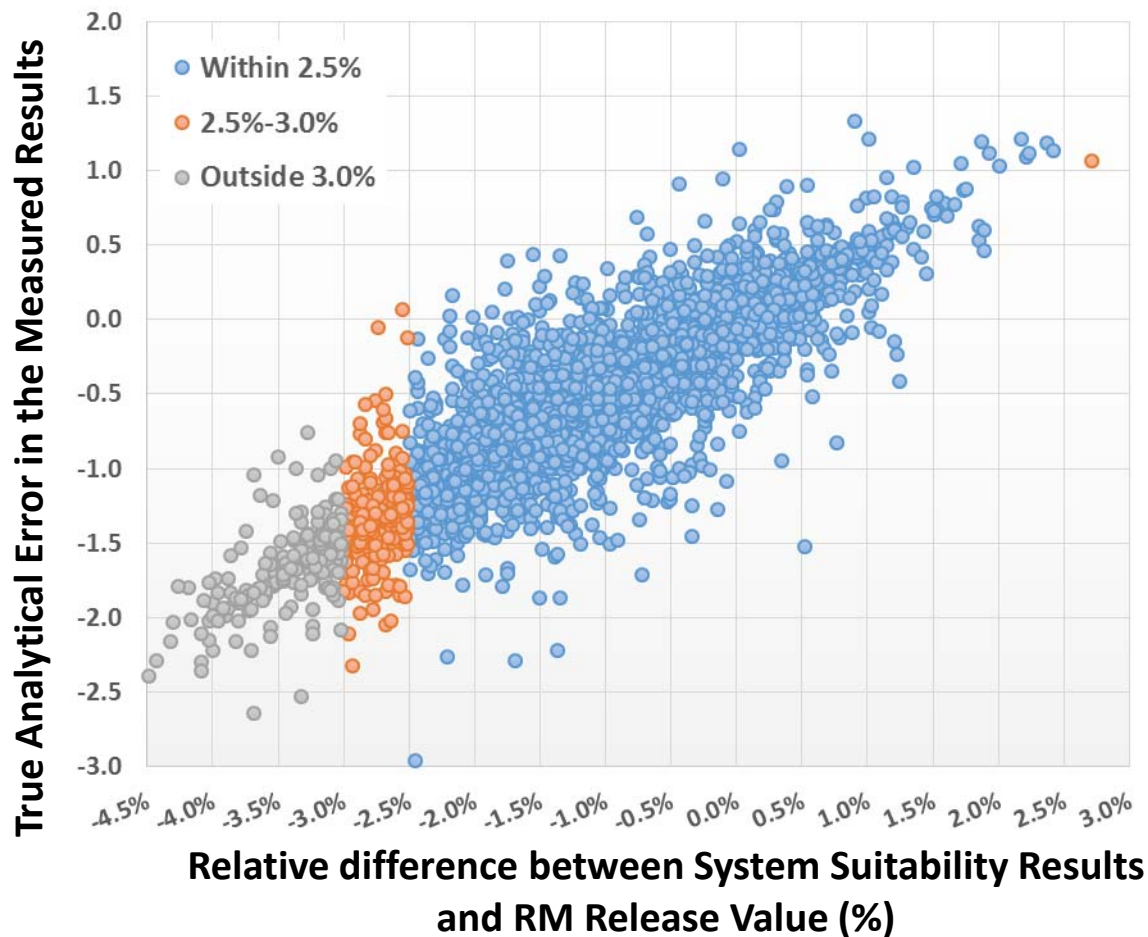
Widening the SS criteria will reduce the failure rate by > 6%

DP Lab



RM has small chance of failing either SS criteria

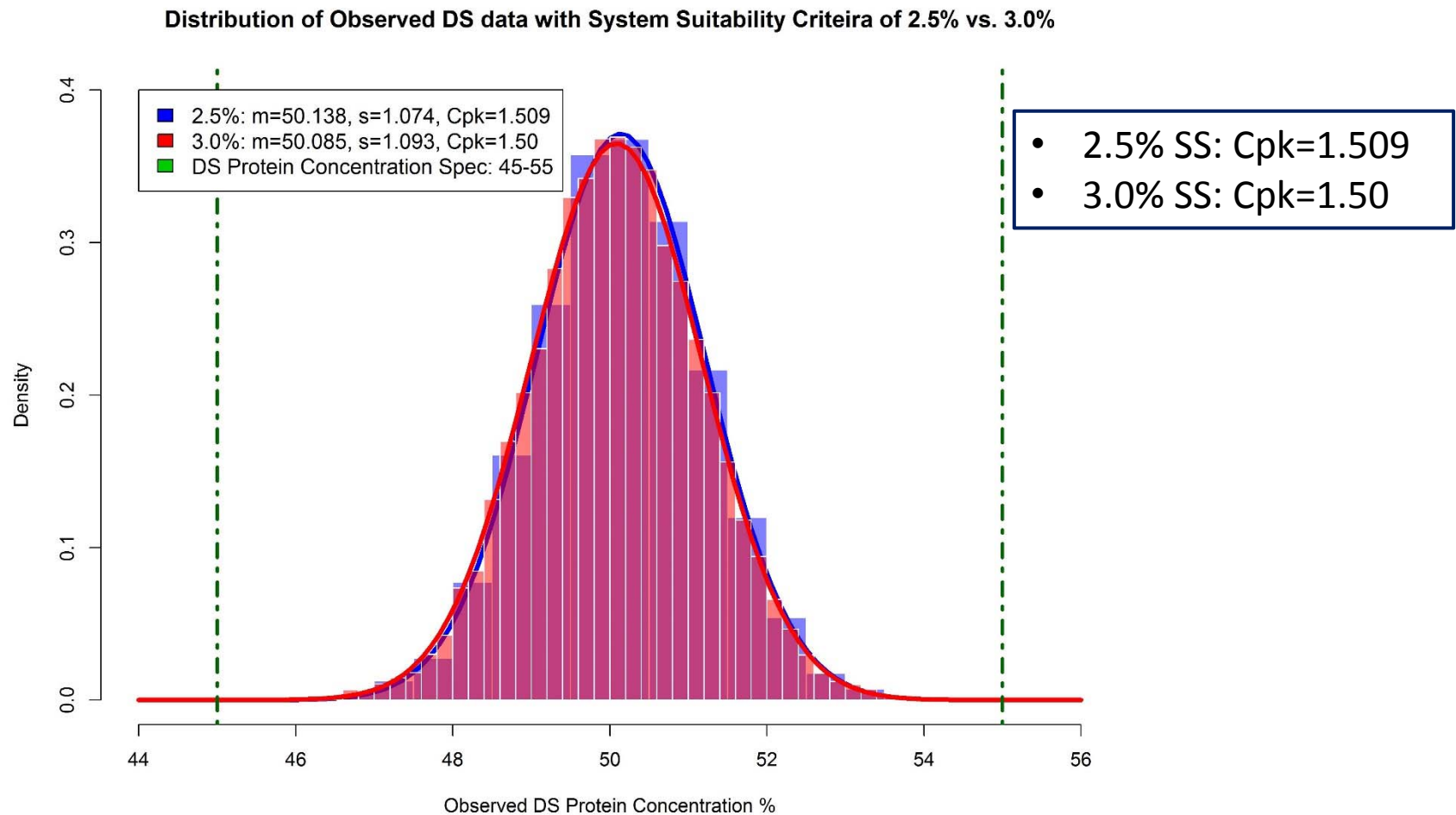
Simulation Result: SS vs. Analytical Error (DS)



Widening the SS criteria from 2.5% to 3.0% will potentially introduce more negative analytical error into the DS results.

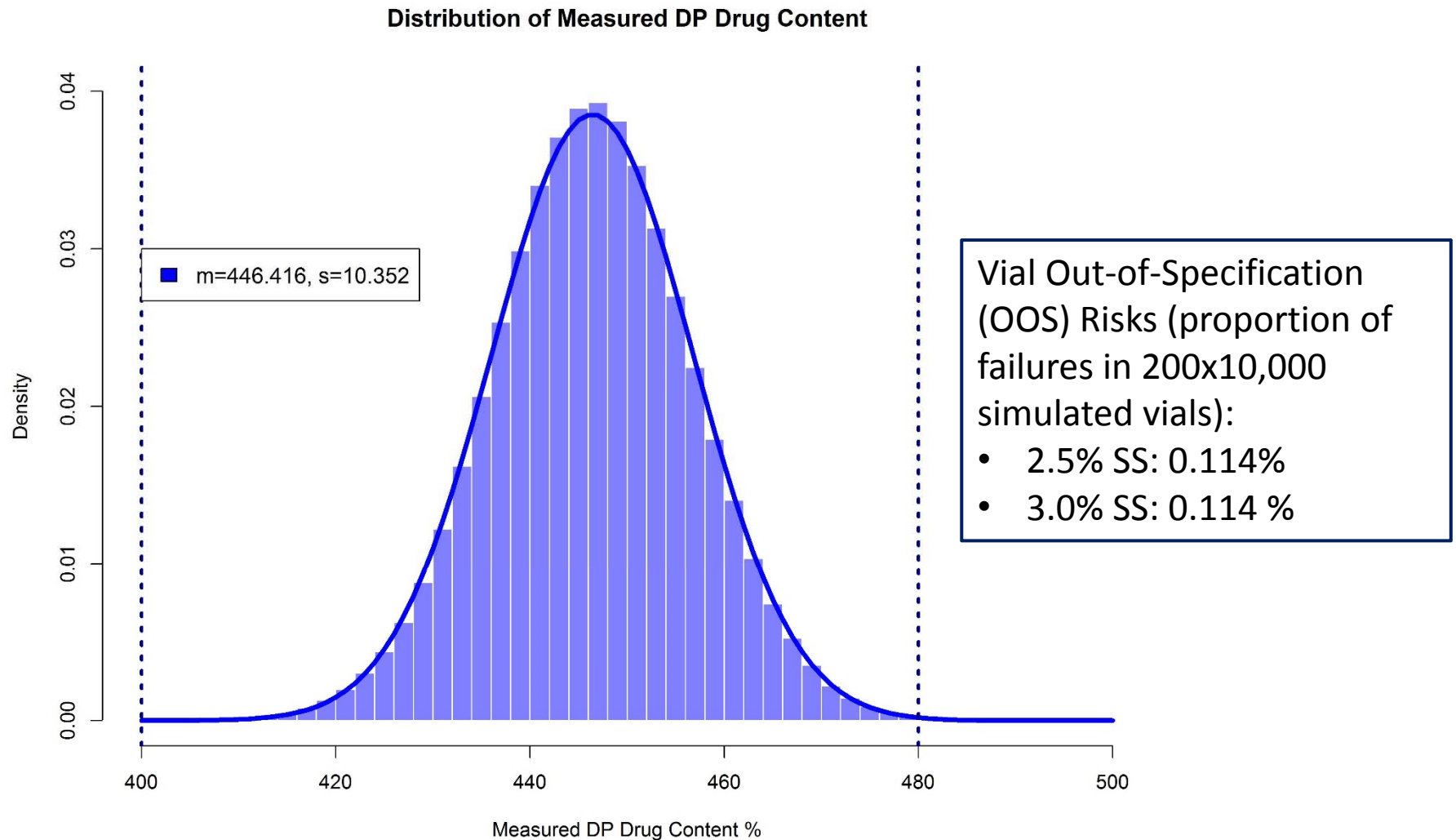
But, is this of critical impact to the product performance?

Simulation Result: DS Protein Concentration



Impact of SS criteria on DS Cpk is relatively small.

Simulation Result: DP Drug Content



Impact of SS criteria on DP OOS risk is small.

Summary and Next Steps

- ❑ Connecting process and analytical performances in a life-cycled manner is critical when establishing risk-based control strategy.
- ❑ Bayesian is a proper modeling tool for risk-based control:
 - Convenient connection of analytical and process components
 - Proper leverage of prior information
 - Predictive inferences about future results
 - Continuous learning capability.
- ❑ A case study illustrated the Bayesian method in modeling the impact of system suitability criterion on capability performance for a protein concentration method.
- ❑ Model potentials:
 - Update the model with accumulated knowledge
 - Expanding to other sources of variances

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Questions?