

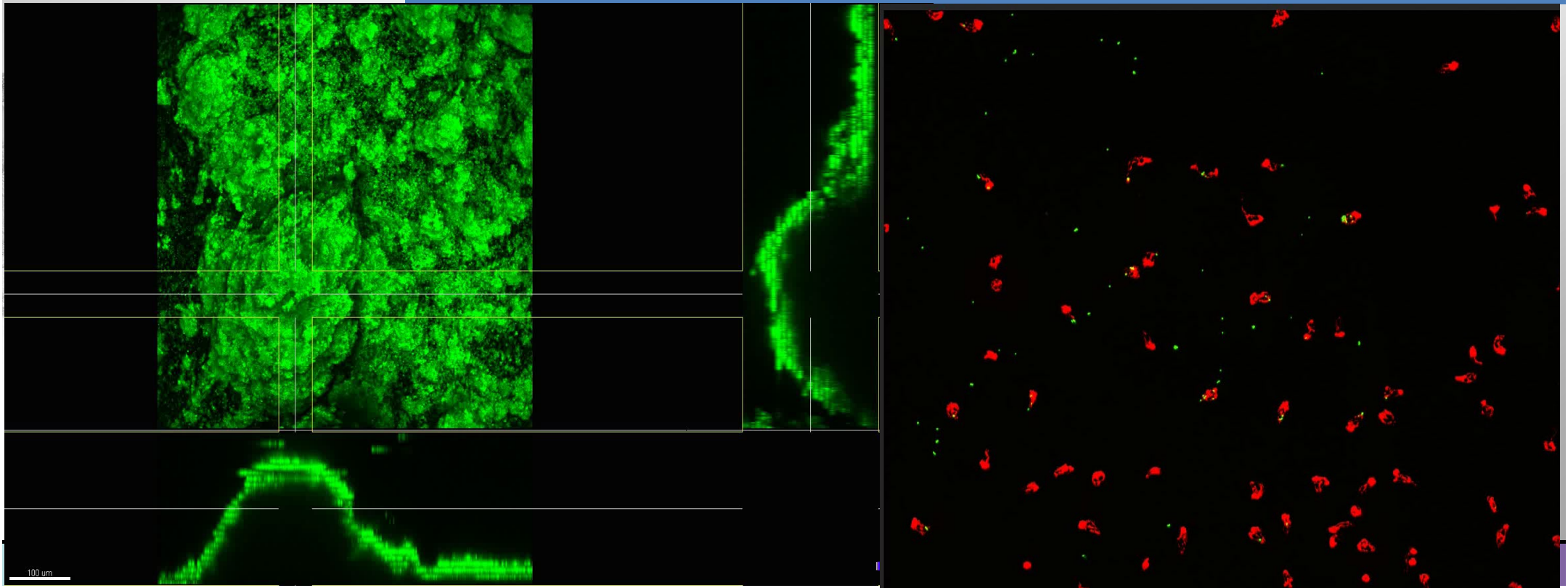


Biofilm Regulatory Toolbox



Basic Stats, Repeatability & Responsiveness 8 Sept, 2026

AI Parker, PhD, Biostatistician, CBE



About me



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- 2019 - present Research Professor, Department of Mathematical Sciences, MSU
- 2008 - present Biostatistician, **Center for Biofilm Engineering**, MSU
- 2008 - present Senior statistician for Office of Pesticide Programs, Biological and Economic Analysis Division, **US EPA**
- 2008 - present Consulting statistician for Committee E35 on Pesticides, Antimicrobials, and Alternative Control Agents, **ASTM International**
- 2008 - 2014 Consulting statistician for Committee M on Antimicrobial Efficacy Testing, **AOAC International**
- 2007 - 2010 Post-doctoral Fellow, Bayesian Statistics, University of Auckland
- 2004 - 2006 Post-doctoral Fellow, Image Analysis, University of California, Santa Cruz

Attributes of an antimicrobial test method: Seven R's

- Relevance
- Reasonableness
- Resemblance (positive controls)
- Repeatability (intra-lab)
- Responsiveness
- Ruggedness
- Reproducibility (inter-lab)



Attributes of an antimicrobial test method: 7 R's + 2

- Relevance
- Reasonableness
- Resemblance (positive controls)
- Repeatability (intra-lab) ISO's "intermediate precision"
- Responsiveness
- Ruggedness
- Reproducibility (inter-lab)
- Unbiasedness ISO's "trueness"
- Limit of Detection

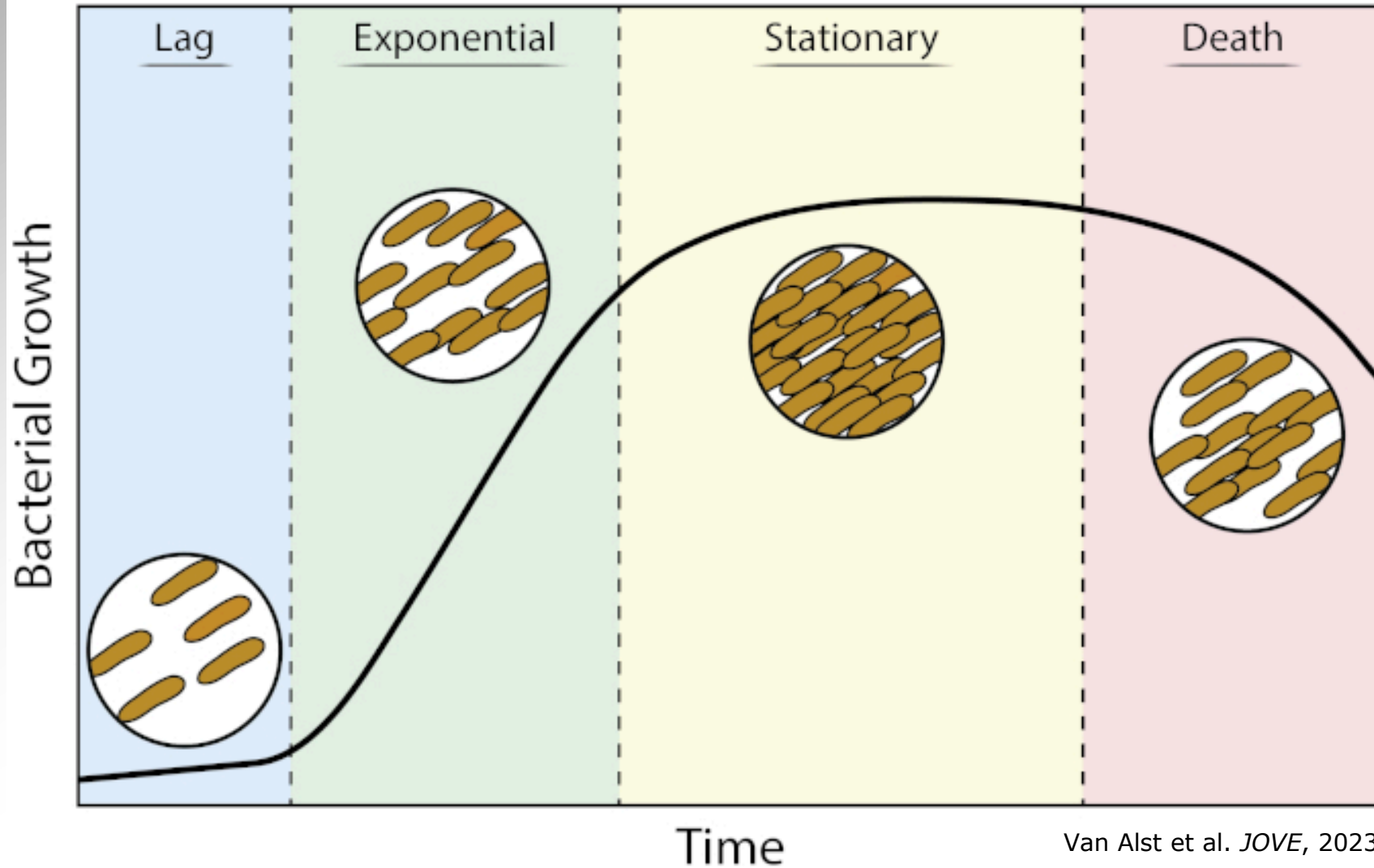


Attributes of an antimicrobial test method: Seven R's



Which phase?

Bacterial Growth Curve



Van Alst et al. *JOVE*, 2023

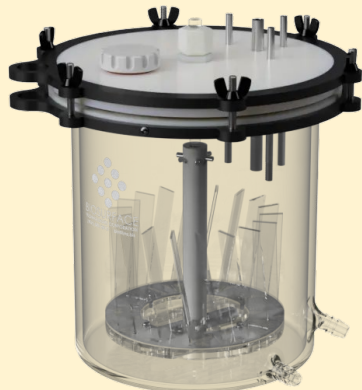
Attributes of an antimicrobial test method: 7 R's + 2

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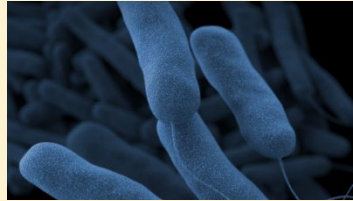


Three R Modules Based on This Talk

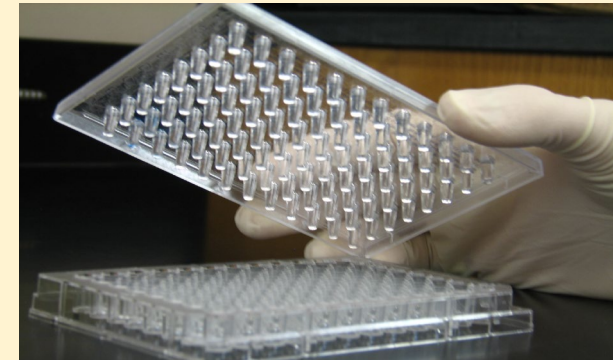
Resemblance (Control Repeatability)



Repeatability

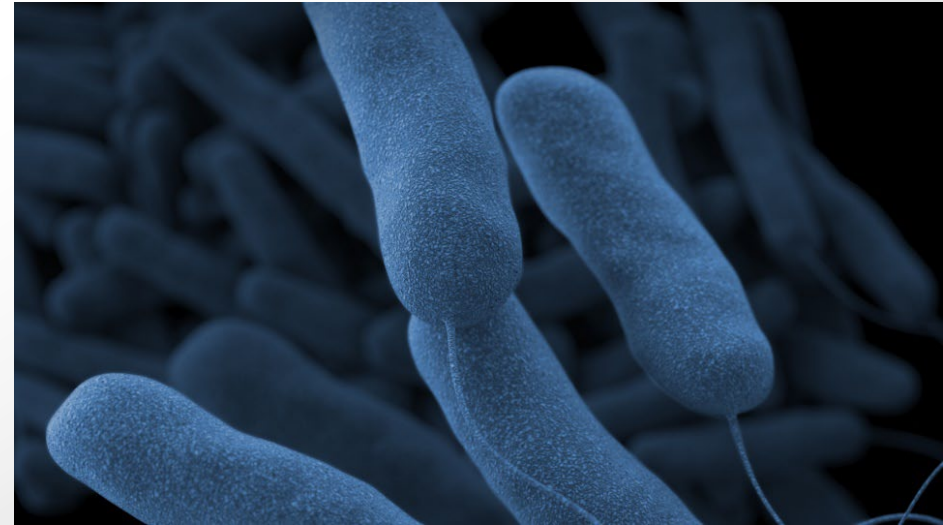


Responsiveness



Attributes of an antimicrobial test method: 7 R's + 2

- Relevance
- Reasonableness
- Resemblance (positive controls)
- Repeatability (intra-lab)
- Responsiveness
- Ruggedness
- Reproducibility (inter-lab)
- Unbiasedness
- Limit of Detection





Legionella **biofilms**

Bodle et al. *Biofilm*, 2026

Resemblance

The **bio-challenge (i.e., positive controls)** should be repeatable within a lab and reproducible across multiple labs, quantified by a small

CS_r = repeatability SD

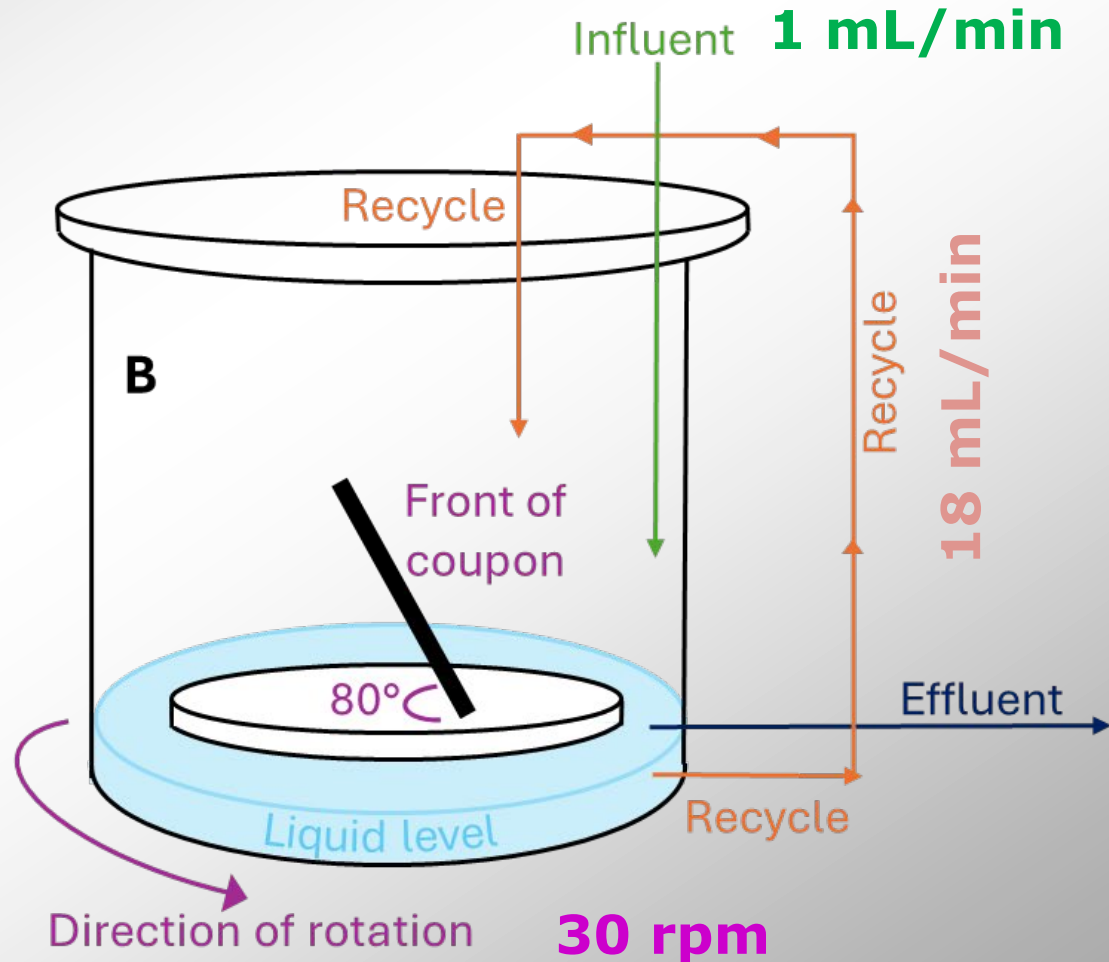
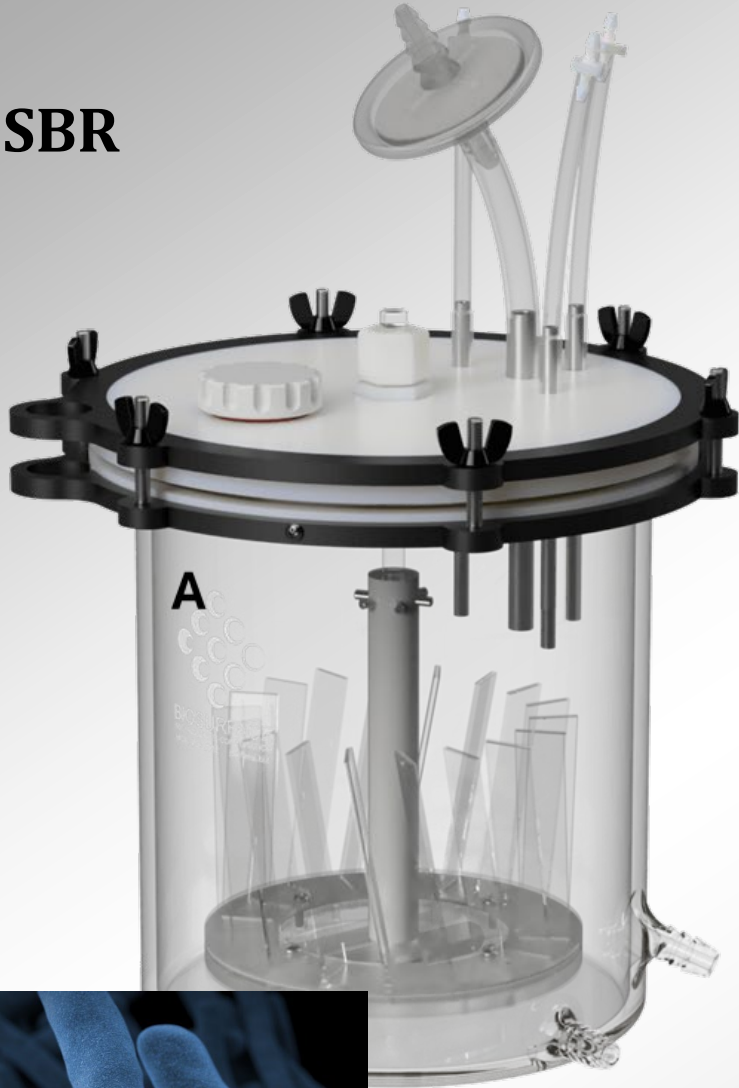
CS_R = reproducibility SD

<https://www.biofilm.montana.edu/documents-reports/knowledge-sharing-articles.html>

Legionella, *Hartmonella* and bacteria found in drinking water formed a biofilm

ISBR

Cooling Tower Model



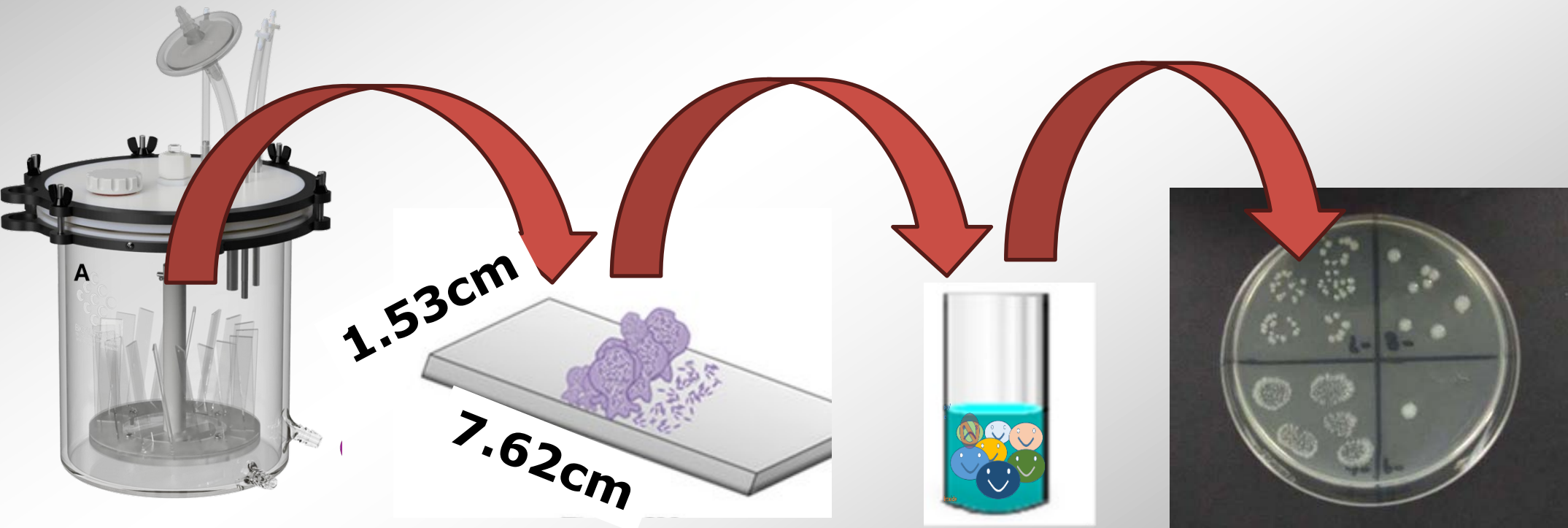
Legionella densities (D) and “log densities” (LD)



$$\begin{aligned}
 \mathbf{D} &= \frac{CFU \times V}{u \times 10^k} = \frac{8 \times 40 \text{ mL}}{0.1 \text{ mL} \times 10^{-2}} = \mathbf{3.2 \times 10^5 \frac{CFU}{\text{coupon}}} \\
 &= 3.2 \times 10^5 \frac{CFU}{1.52 \times 7.62} = \mathbf{27,365 \frac{CFU}{\text{cm}^2}} \\
 \mathbf{LD} &= \log_{10}(27,365) = \mathbf{4.437 \log_{10} \left(\frac{CFU}{\text{cm}^2} \right)}
 \end{aligned}$$

$$\log_{10} (8 \times 40 / (.1 \times 10^{-2}) / (1.53 \times 7.62))$$

www.cdc.gov/legionella



From Fig 1, Floyd et al, PLOS Pathogens, 2015

V=40mL

u=10x10uL drops

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Limit of Detection in Microbiology



$$\begin{aligned}\text{“LOD”} &= \frac{1\text{CFU} \times 40\text{mL}}{0.1\text{mL} \times 10^0} = 400 \frac{\text{CFU}}{\text{coupon}} \\ &= 400 \frac{\text{CFU}}{1.52 \times 7.62} = 34.3 \frac{\text{CFU}}{\text{cm}^2} \\ &= 1.54 \log_{10} \left(\frac{\text{CFU}}{\text{cm}^2} \right)\end{aligned}$$

www.cdc.gov/legionella

$$\log_{10} (1 \times 40 / (.1 \times 10^0) / (1.53 \times 7.62))$$

If there are 400 CFU of *Legionella* on a glass slide in the ISBR then most of the time (51%-63%) they will be detected (CFU>0)

Decrease the LOD by

- decreasing the total volume $V=40\text{mL}$
- increasing the plate volume $u=100\mu\text{L}$

Commonly, $\text{CFU} = \text{LOD} / 2$ or LOD is subbed in for $\text{CFU} = 0$ – but consider better approaches if there are lots of zeros

Limit of Quantification in Microbiology



$$\text{"LOD"} \neq \frac{14CFU \times 40mL}{0.1mL \times 10^0}$$

but maybe ISO considers

$$\text{"LOQ"} = \frac{14CFU \times 40mL}{0.1mL \times 10^0}?$$

Jiang & Parker *European J Parenteral and Pharm Sci* 302 2025.

Data from 1 experiment



Data: viable plate counts of *Legionella* from 3 coupons

Exp	CFU/cm ²	$\log_{10}$ (CFU/cm ²)
1	27,365	4.437
1	27,365	4.437
1	15,490	4.190

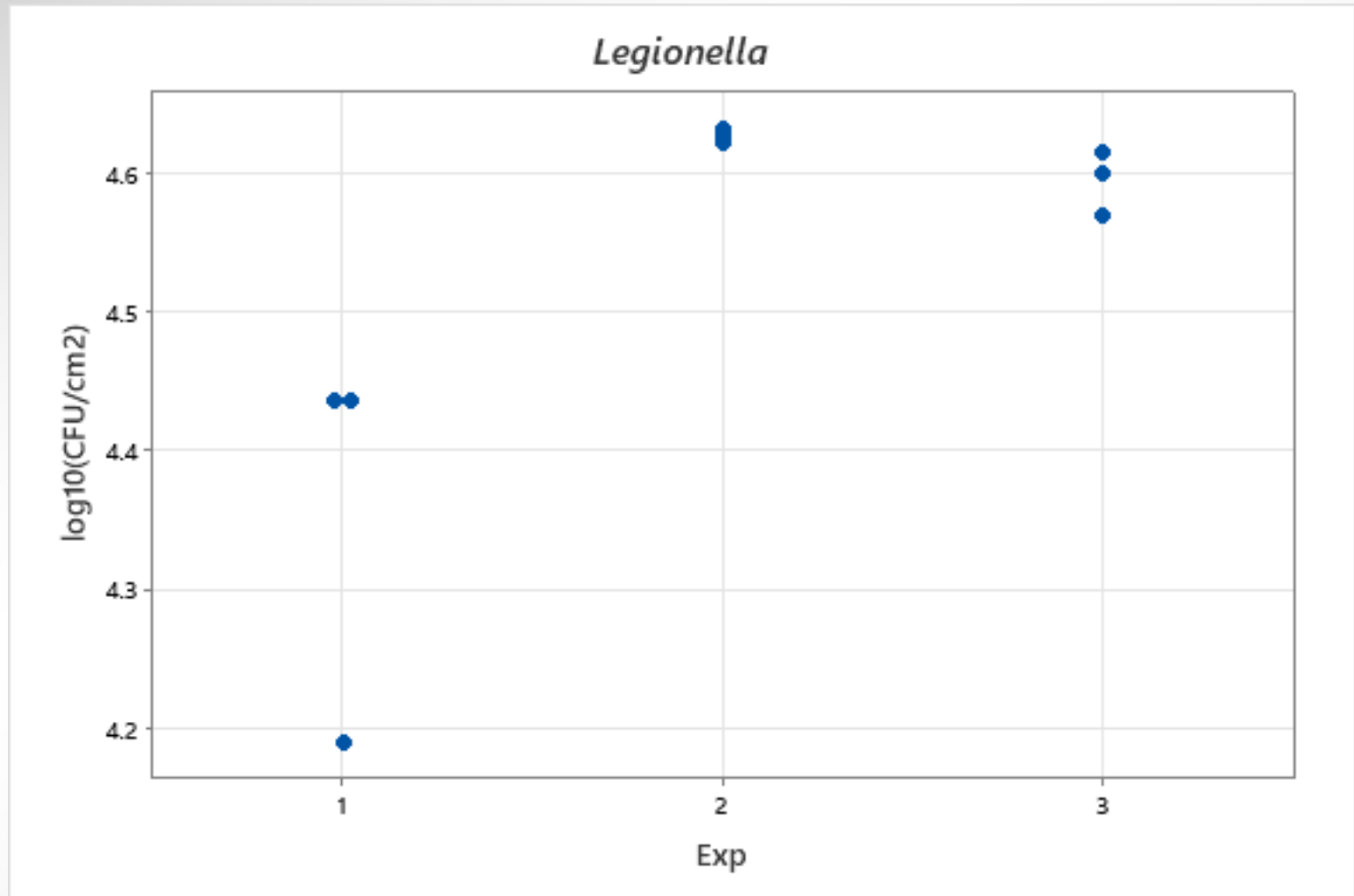
Mean LD = 4.36

Coupon-to-Coupon SD = 0.143

Perform 3 biological replicates

First, always graph the data

Exp	log10 (CFU/cm2)
1	4.437
1	4.437
1	4.190
2	4.632
2	4.627
2	4.621
3	4.632
3	4.627
3	4.621



Bodle et al, in prep

Then Pool and Analyze the Data (in R)

Exp	log10 (CFU/cm2)	mean log10 (CFU/cm^2)	coupon-to- coupon SD (unit-less)
1	4.437		
1	4.437	4.355	0.143
1	4.190		
2	4.632		
2	4.627	4.627	0.005
2	4.621		
3	4.570		
3	4.616	4.595	0.023
3	4.599		

Mean	SE	CS _r
4.53	0.0859	0.1636
95% <i>likelihood profile-CI</i>		
(4.33, 4.72)		
74% Exps, 26% Coupons		
0.74 is coupon correlation		

Random Effect

```
lmer(log10(CFU) ~ (1|Exp), data = Legionella)
```

Pool and Analyze the Data (in Excel!)

Exp	log10 (CFU/cm2)	mean log10 (CFU/cm^2)	coupon-to- coupon SD (unit-less)
1	4.437		
1	4.437	4.355	0.143
1	4.190		
2	4.632		
2	4.627	4.627	0.005
2	4.621		
3	4.570		
3	4.616	4.595	0.023
3	4.599		

Mean	SE	CS _r
4.53	0.0859	0.1636
95% <i>t</i> -CI with DF=2 (WIDER THAN R!)		
(4.16, 4.90)		

Mixed Effects

Model in EXCEL:

$$\text{Overall Mean} = \text{AVERAGE}(4.355, 4.627, 4.627) = 4.53$$

$$S_r = [V_{\text{exp}} + V_{\text{coupon}}]^{0.5} = 0.1636$$

$$V_{\text{coupon}} = \text{AVERAGE}(0.143^2, 0.005^2, 0.023^2)$$

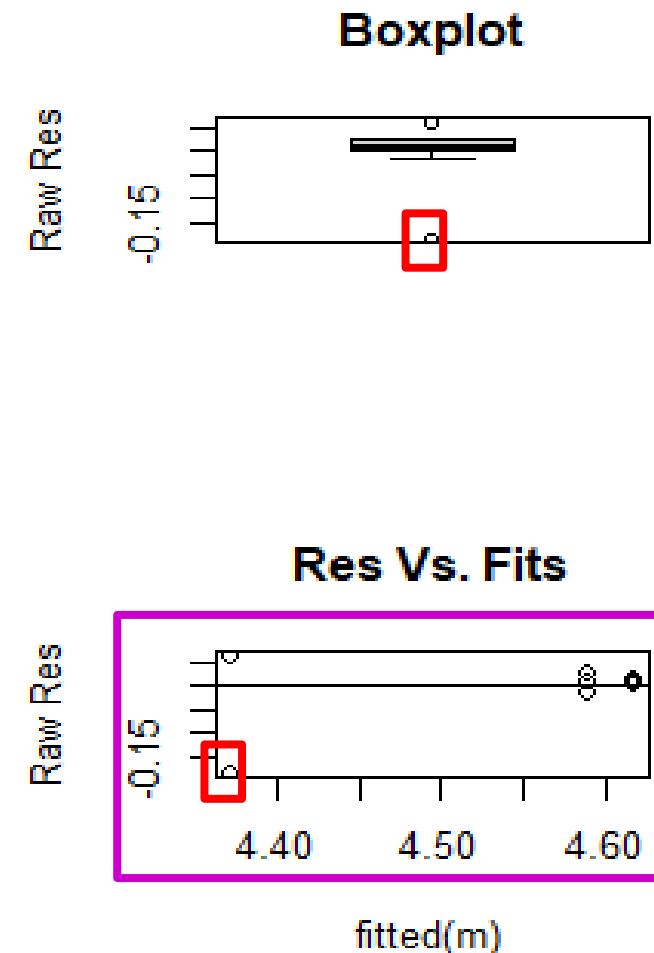
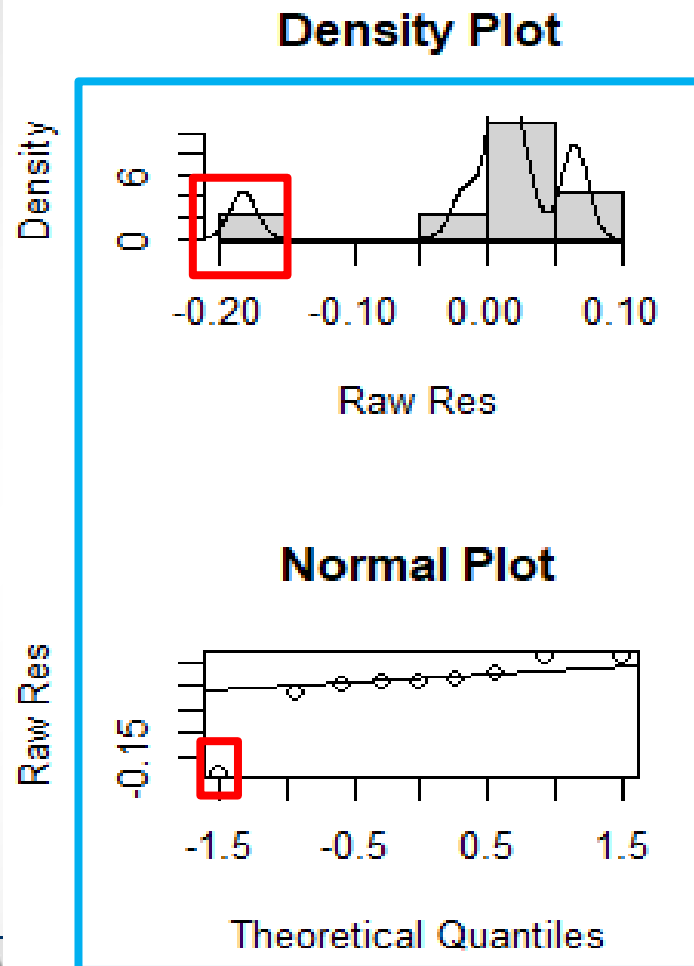
$$V_{\text{exp}} = \text{VAR}(4.355, 4.627, 4.627) - V_{\text{coupon}}/3$$

$$\text{correlation of technical replicates} = V_{\text{exp}} / S_r^2 = 0.74$$

Pooling Data with a Mixed Effects Model in R

```
m = lmer(log10(CFU) ~ (1|Exp), data = Legionella)
diagRES(m)
```

Fitting the
model in R,
we can check
for **constant
variance**,
normality and
outliers



Assess Outlier Influence by temporarily Removing and Refitting!

```
lmer(log10(CFU) ~ (1|Exp), data = Legionella[-3,])
```

Mean	SE	CS _r
4.53	0.0859	0.1636
95% <i>likelihood profile-CI</i>		
(4.33, 4.72)		

Mean	SE	CS _r
4.55	0.0586	0.1021
95% <i>likelihood profile-CI</i>		
(4.42, 4.69)		

My opinion (following ASTM guidance) is to leave outliers in a data set unless there is some deviation from protocol to justify removing them.

Good Repeatability of the Controls?

Does $CS_r = 0.1636$ indicate good repeatability of the untreated *Legionella* controls from the ISBR?

YES: $CS_r \leq 0.5$ indicates good repeatability of untreated biofilm controls

Tilton & Hamilton *JMM* 1999

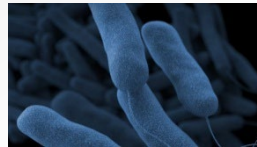
Parker & Hamilton, CBE KSA-11, 2011

Let's compare to standardized biofilm methods

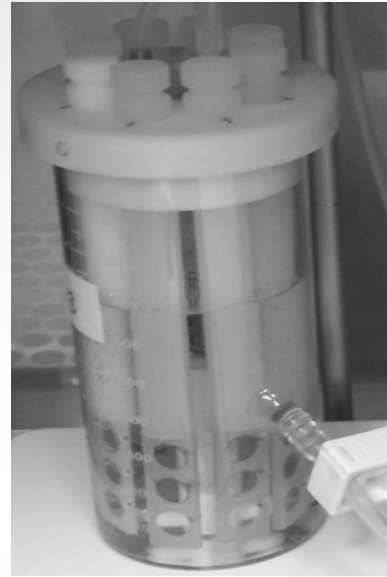


ISBR

not standardized
biofilm on slides
low flow
low shear



Used by researchers

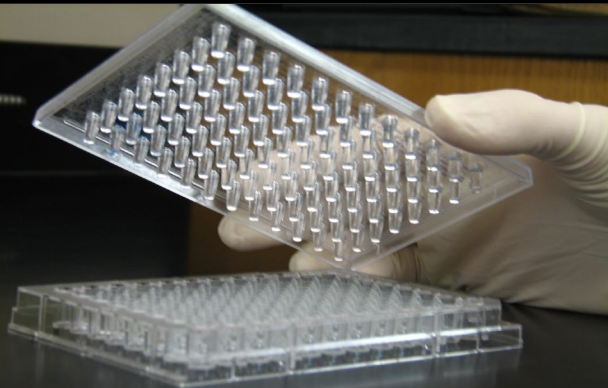


CDC/STM

ASTM E2562/E2871
biofilm on discs
continuous flow
high shear



Used by US EPA

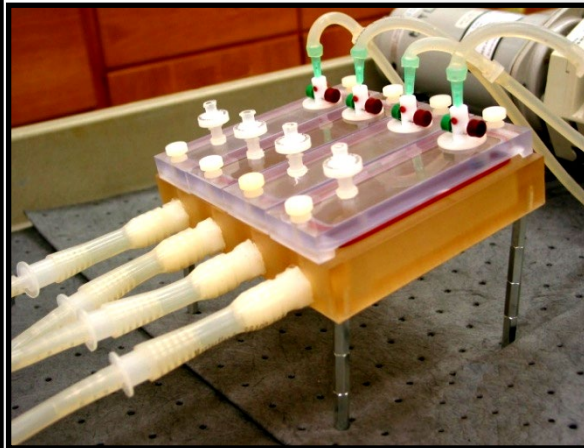


MBEC

ASTM E2799
biofilm on pegs
batch
low shear



Used by Health Canada



DFR

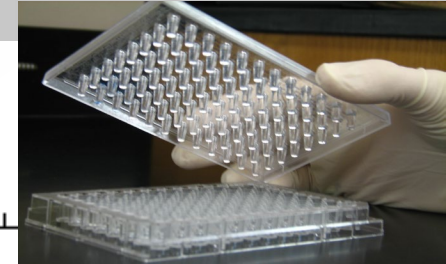
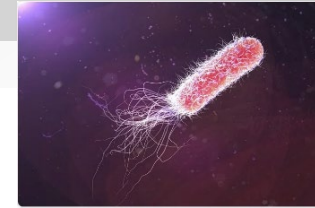
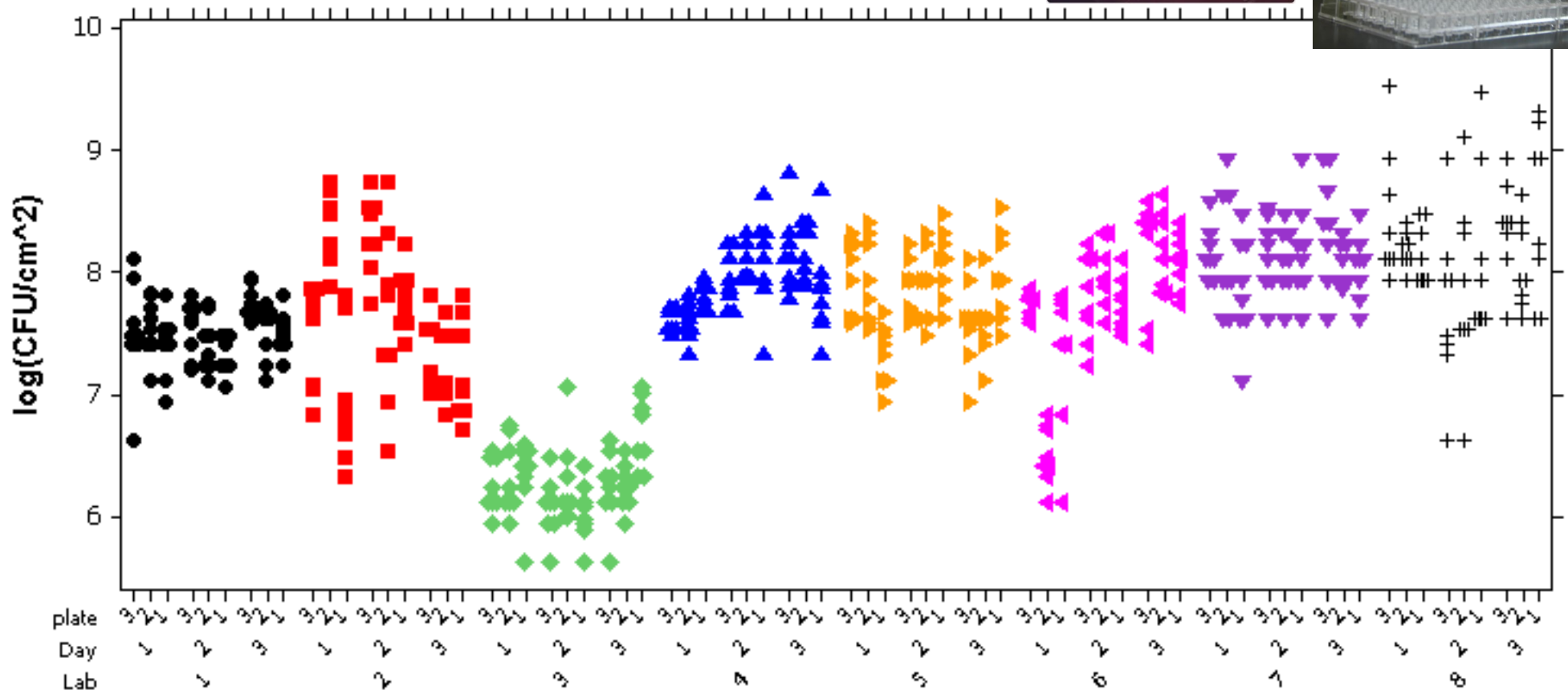
ASTM E2647
biofilm on slides
plug flow
low shear



Used by researchers

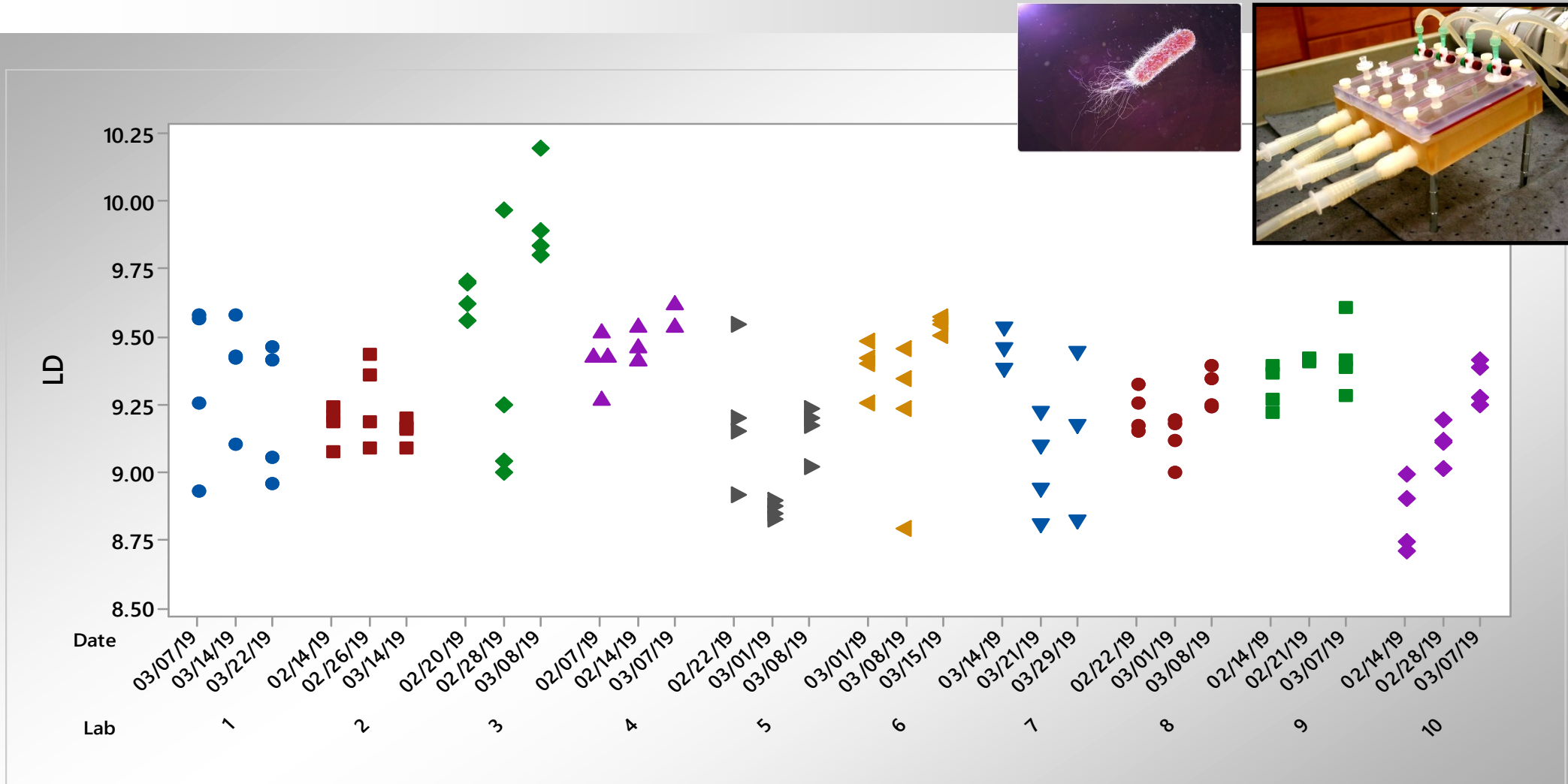
Multi-lab controls for the MBEC (2011)

control data



Parker et al. *JMM*, 2014; ASTM RR:E35-1006, 2011

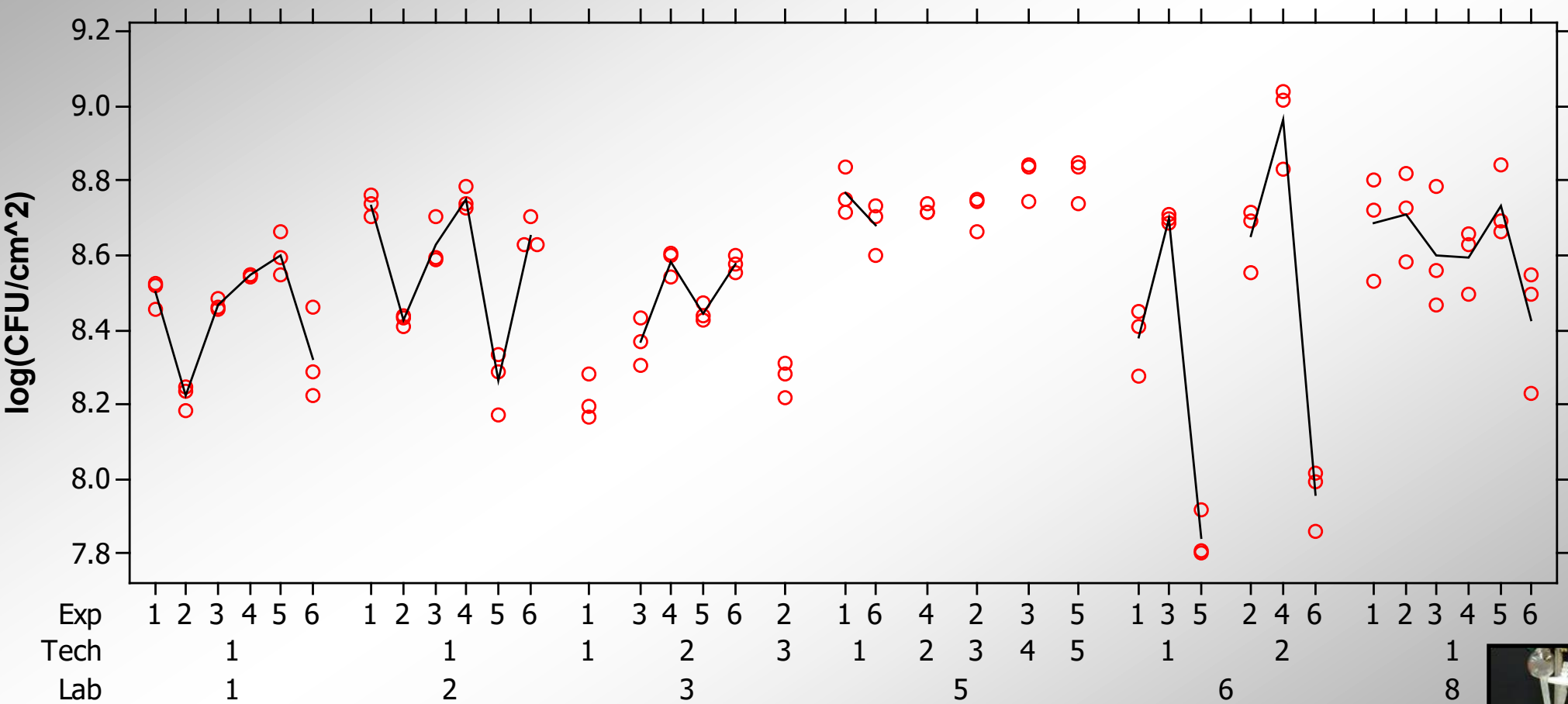
Multi-lab controls for the DFR (2019)



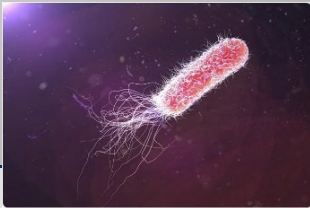
Goeres et al, JMM, 2020; ASTM RR:E35-1015, 2020

Multi-lab controls for the STM/CDC (2012)

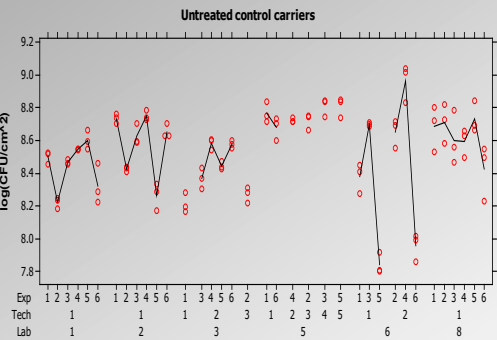
Untreated control carriers



Goeres et al. *JMM*, 2019; ASTM RR:E35-1008, 2013



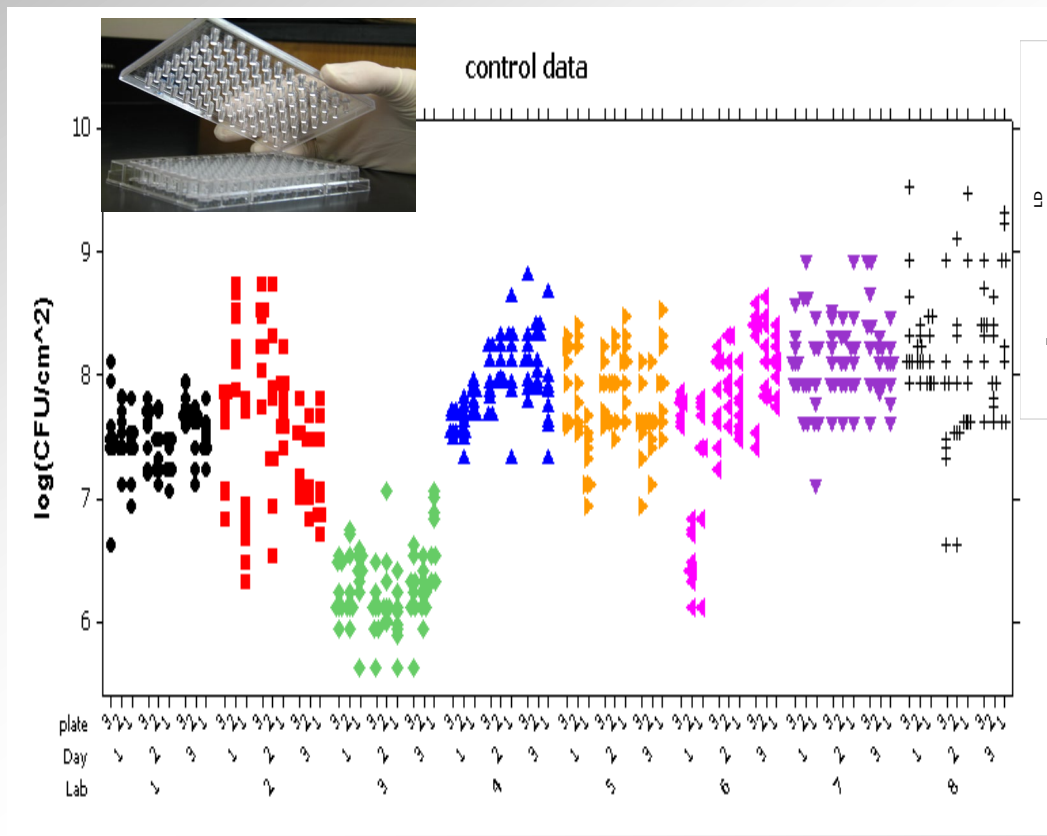
Comparing controls for the STM, MBEC & DFR



STM:

Repeatability SD: 0.221

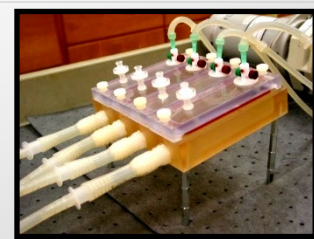
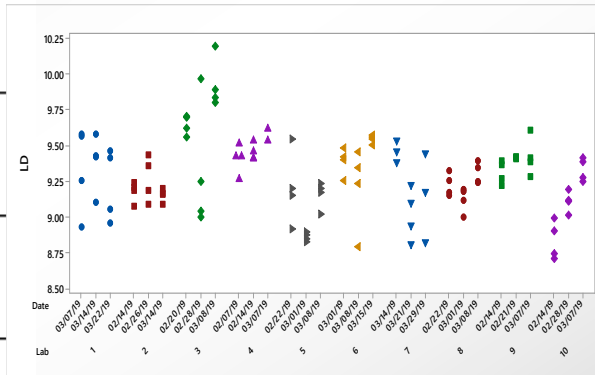
Reproducibility SD: 0.244



MBEC

Repeatability SD: 0.325

Reproducibility SD: 0.667



DFR

Repeatability SD: 0.228

Reproducibility SD: 0.268

Attributes of an antimicrobial test method: 7 R's + 2

- Relevance
- Reasonableness
- Resemblance (positive controls)
- Repeatability (intra-lab)
- Responsiveness
- Ruggedness
- Reproducibility (inter-lab)
- Unbiasedness
- Limit of Detection



Repeatability

Independent repeats of the same experiment in the same laboratory produce nearly the same response, as indicated by a small

repeatability standard deviation

$$S_r = \text{STDEV}(\text{Response for each experiment})$$

<http://www.biofilm.montana.edu/content/ksa-sm-10>



Repeatability Example

Data: log reduction (LR)

$$\text{LR} = \text{mean}(\text{control LDs}) - \text{mean}(\text{treated LDs})$$

Analyze **LRs** instead of the individual **control** and **treated** log(CFU)'s because:

- (1) this normalizes each treatment to the control in each experiment;
- (2) *t*-tests and ANOVA can be applied to LRs;
- (3) usually the **control** and **treated** log(CFU)'s exhibit different variability, which violates the homogeneity of variance assumption of an ANOVA model and the variance assumption of a Poisson model.

Here's the same untreated control data ...

Exp	log10 (CFU/cm2)	mean log10 (CFU/cm^2)	coupon-to- coupon SD (unit-less)
1	4.437	4.355	0.143
1	4.437		
1	4.190		
2	4.632	4.627	0.005
2	4.627		
2	4.621		
3	4.570	4.595	0.023
3	4.616		
3	4.599		

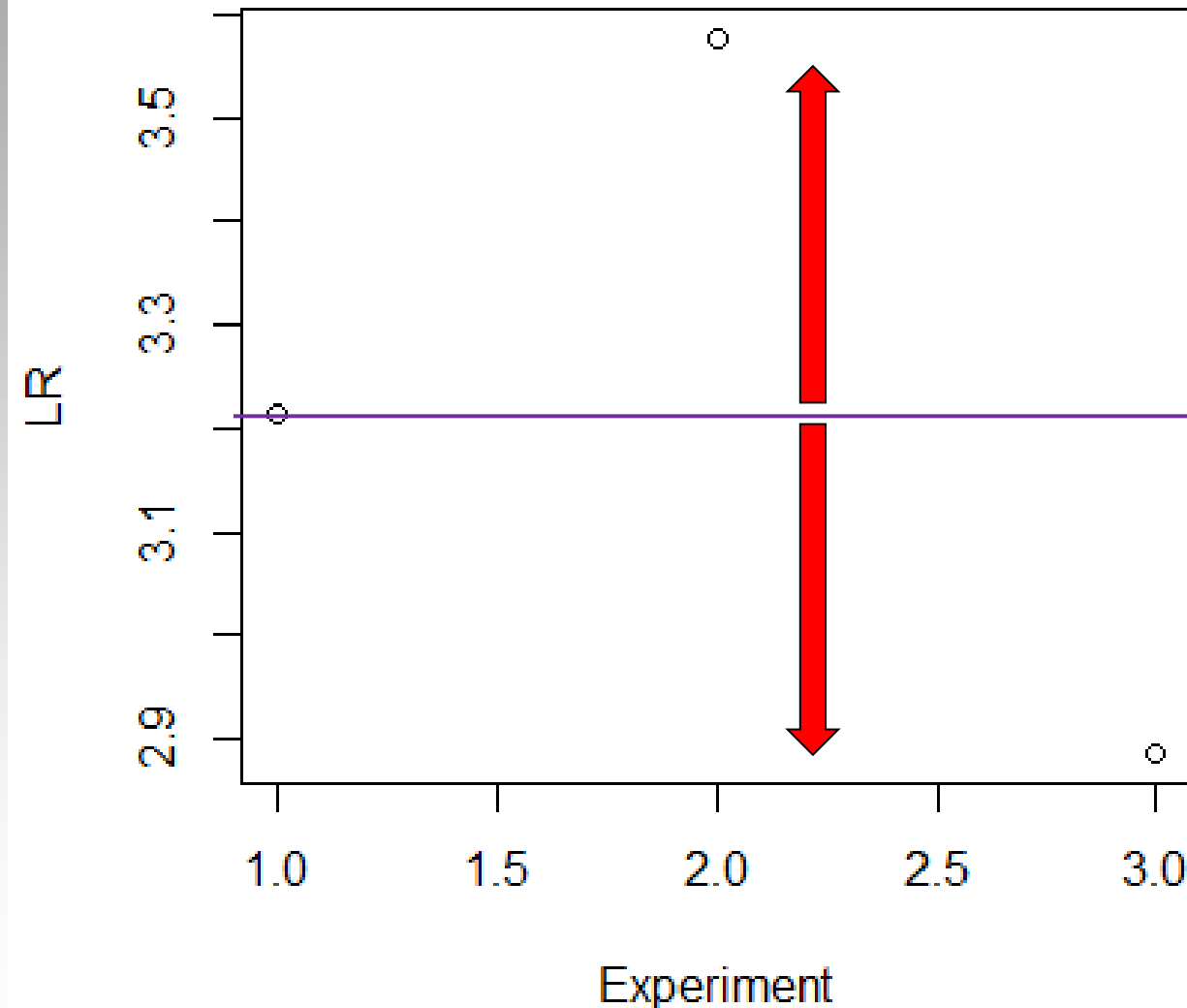
Repeatability Example (synthetic treated)

Exp	coupon LD		Control LD	Treated LD	LR
	control	treated			
1	4.437	1.079			
1	4.437	1.301	4.355	1.141	3.214
1	4.190	1.041			
2	4.632	0.903			
2	4.627	1.041	4.627	1.050	3.577
2	4.621	1.204			
3	4.570	1.740			
3	4.616	1.663	4.595	1.709	2.886
3	4.599	1.724			

Since there is no obvious pairing between the controls and treated coupons in each experiment, get 1 LR for each experiment

Mean LR = 3.23

Repeatability Example



Summary Statistics:

1. Mean LR = 3.23
the best guess for the true mean LR

2. Repeatability SD:

$$S_r = \text{STDEV}(3.21, 3.58, 2.89) \\ = 0.3456$$

the typical distance
between
the LR for a
single experiment and the
true mean LR

Good Repeatability of the LRs in 1 Lab?

Does $S_r = 0.346$ indicate good repeatability of LRs of *Legionella* grown in the ISBR?

YES: $S_r \leq 1.0$ indicates good repeatability of biofilm LRs

Tilton & Hamilton *JMM* 1999

Parker et al *Scientific Reports* 2018

Estimating the True Mean LR in R

```
LR = c(3.214,3.577,2.886)
```

```
mean(LR)
```

```
## [1] 3.225667
```

```
sd(LR)
```

```
## [1] 0.3456477
```

```
t.test(LR)
```

```
## p-value = 0.003806
```

```
## alternative hypothesis: true mean is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## 2.367030 4.084303
```

```
t.test(LR,alternative = "greater", mu=2)
```

```
## p-value = 0.01275
```

```
## alternative hypothesis: true mean is greater than 2
```

```
t.test(LR,alternative = "greater", mu=3)
```

```
## p-value = 0.1877
```

```
## alternative hypothesis: true mean is greater than 3
```


Attributes of an antimicrobial test method: 7 R's + 2

- Relevance
- Reasonableness
- Resemblance (positive controls)
- Repeatability (intra-lab)
- **Responsiveness**
- Ruggedness
- Reproducibility (inter-lab)
- Unbiasedness
- Limit of Detection



Responsiveness

An biofilm test method should be sensitive enough that it can **detect important changes in in the biofilm** (e.g., due to changes in antimicrobial concentration or contact time).

To assess **Responsiveness to Antimicrobials**, experiments should be designed so that at least two efficacy levels are included for each antimicrobial agent

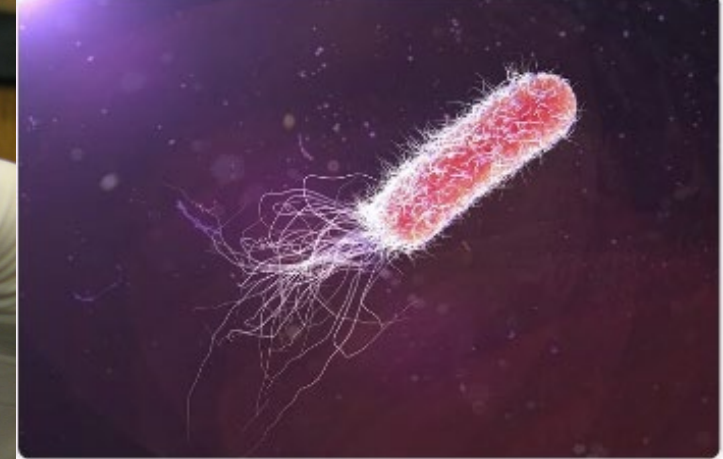
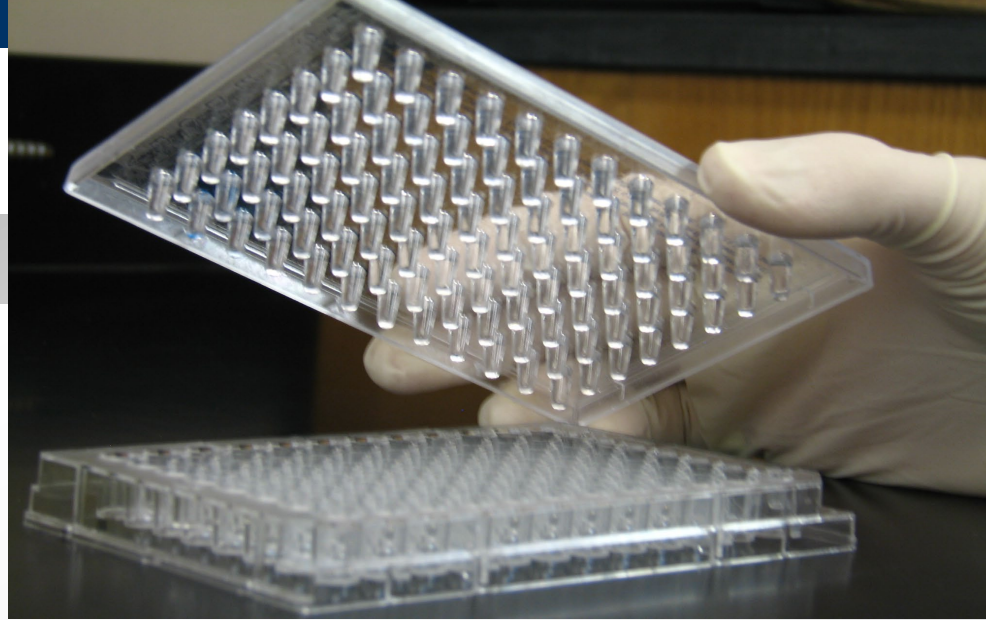
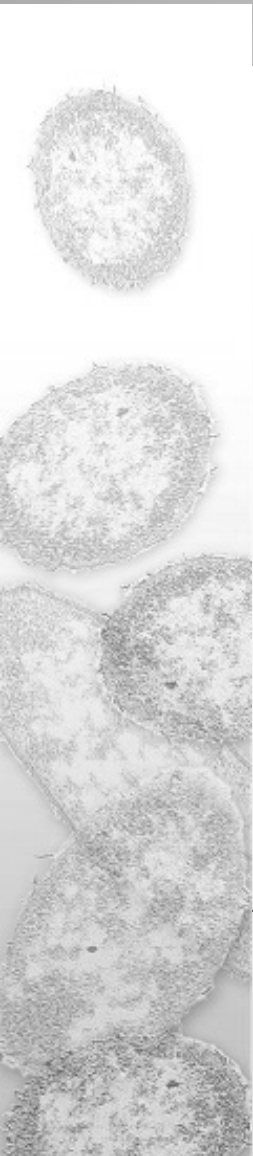
Responsiveness to different efficacy levels

Data: log reduction (LR)

$$\text{LR} = \text{mean}(\text{control log(CFU)'s}) - \text{mean}(\text{disinfected log(CFU)'s})$$

Analyze **LRs** instead of the individual **control** and **treated** log(CFU)'s because:

- (1) this normalizes each treatment to the control in each experiment;
- (2) *t*-tests and ANOVA can be applied to LRs;
- (3) usually the **control** and **treated** log(CFU)'s exhibit different variability, which violates the homogeneity of variance assumption of an ANOVA model and the variance assumption of a Poisson model.



Pseudomonas **biofilms**

Parker et al. *JMM* 2014

MBEC 96 Well Testing Template

A: High Efficacy



H: Low Efficacy

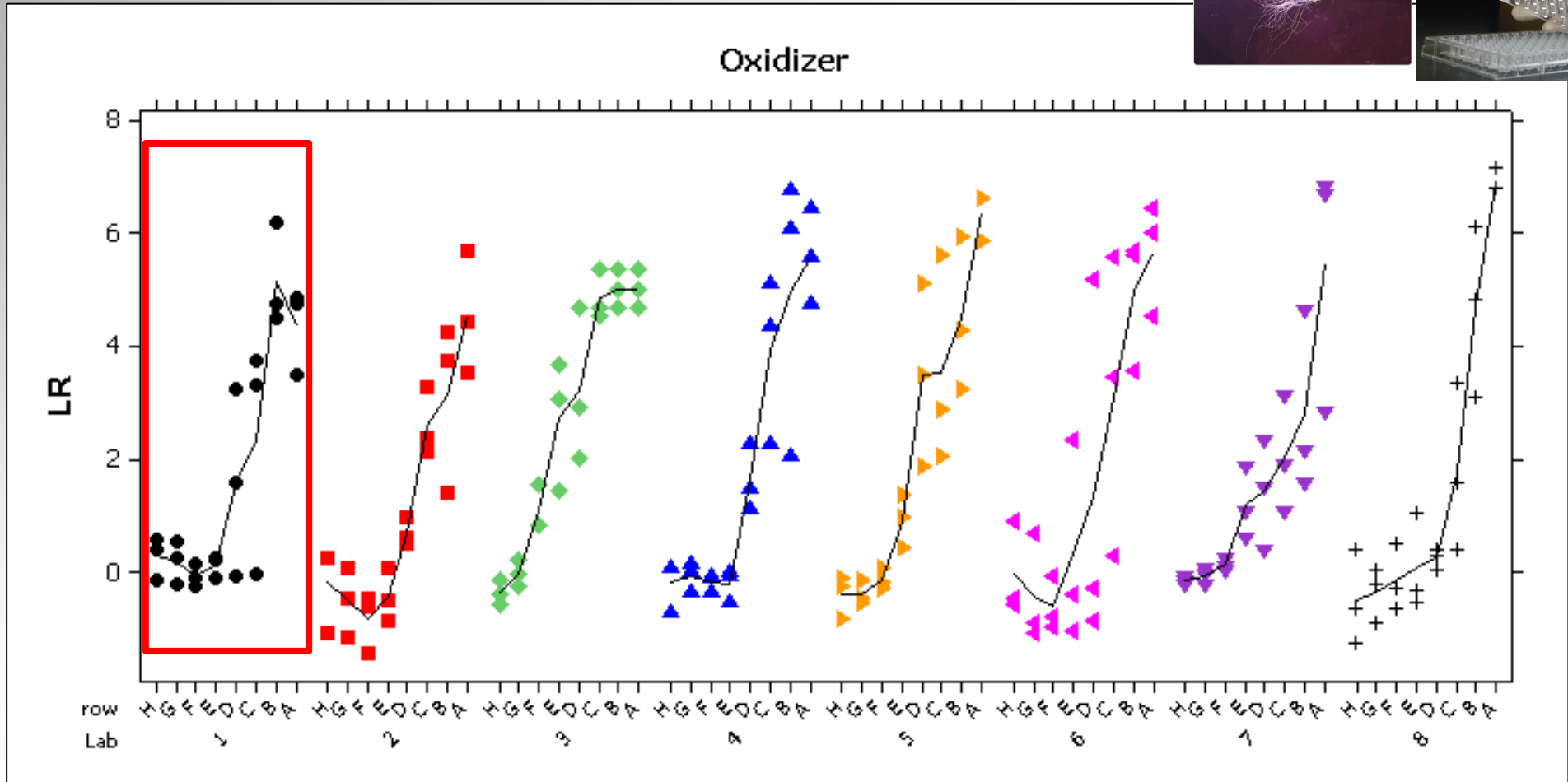
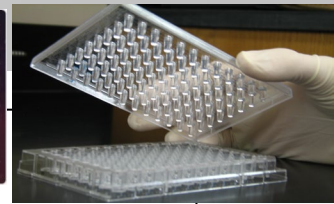
	1	2	3	4	5	6	7	8	9	10	11	12
A	100	100	100	100	100	50:N	N	GC				SC
B	50	50	50	50	50	50:N	N	GC				SC
C	25	25	25	25	25	50:N	N	GC				SC
D	12.5	12.5	12.5	12.5	12.5	50:N	N	GC				
E	6.25	6.25	6.25	6.25	6.25	50:N	N	GC				
F	3.125	3.125	3.125	3.125	3.125	50:N	N	GC				
G	1.563	1.563	1.563	1.563	1.563	50:N	N	GC				
H	0.781	0.781	0.781	0.781	0.781	50:N	N	GC				

disinfectant

neutralizer test

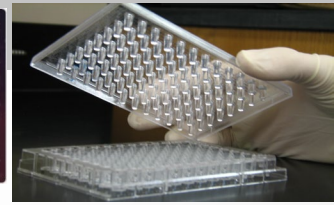
control

MBEC Responsiveness Across 6 Labs



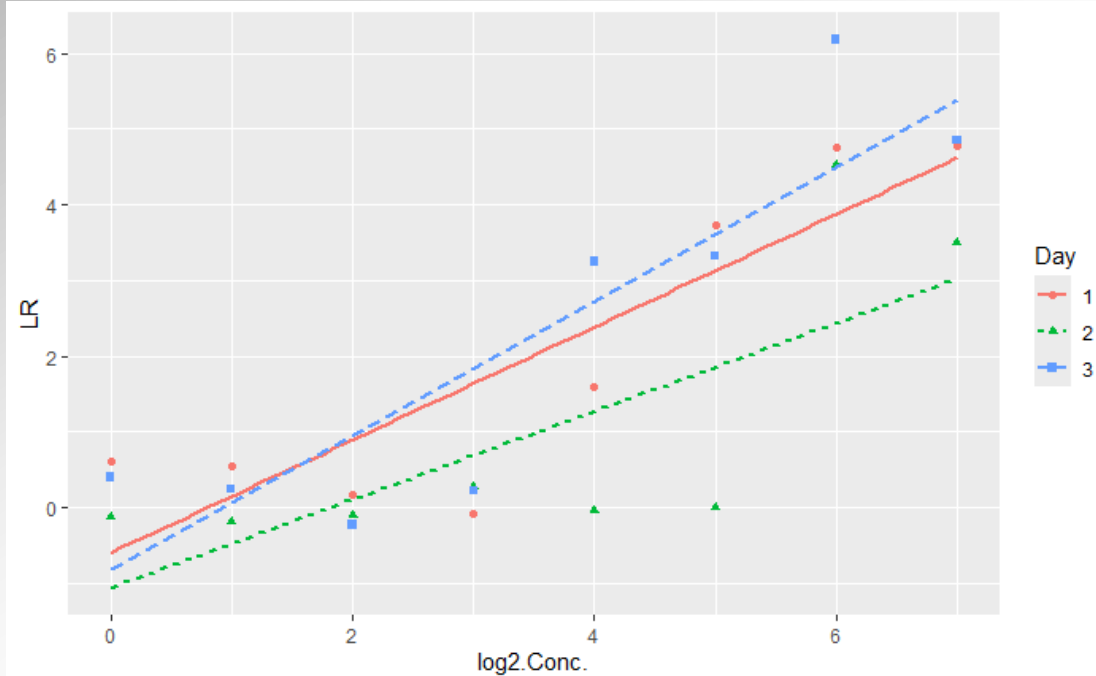
Parker et al. *JMM*, 2014; ASTM RR:E35-1006, 2011

MBEC Responsiveness at Lab 1

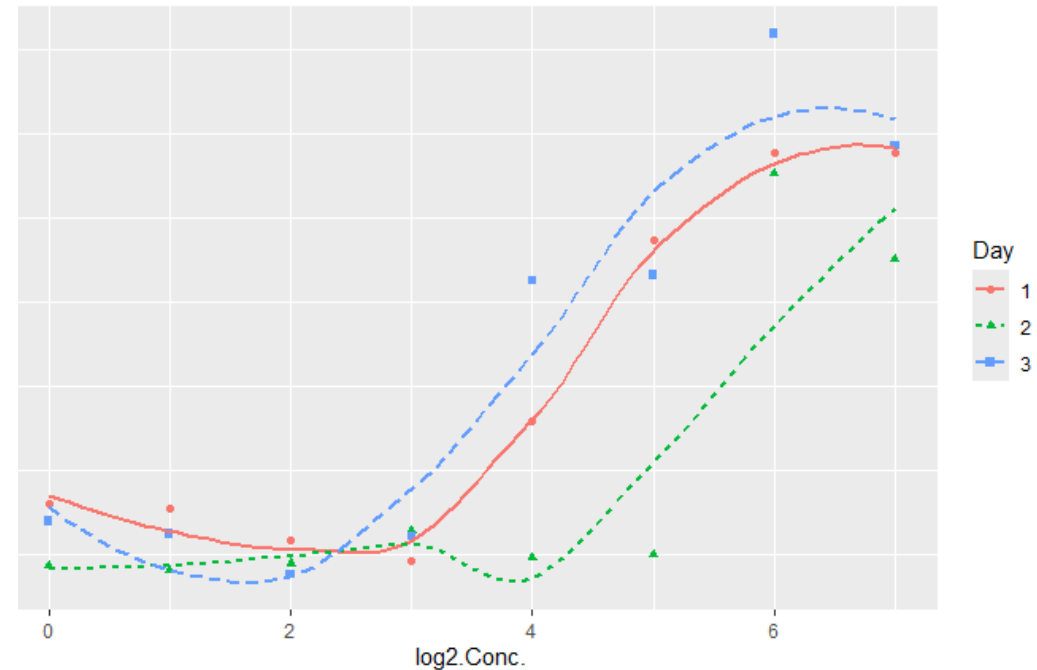


Modeling Increasing Concentrations of an Oxidizer

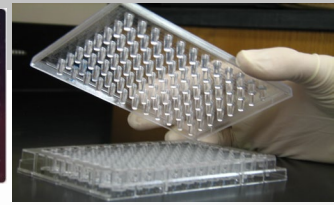
1. Linear Fit



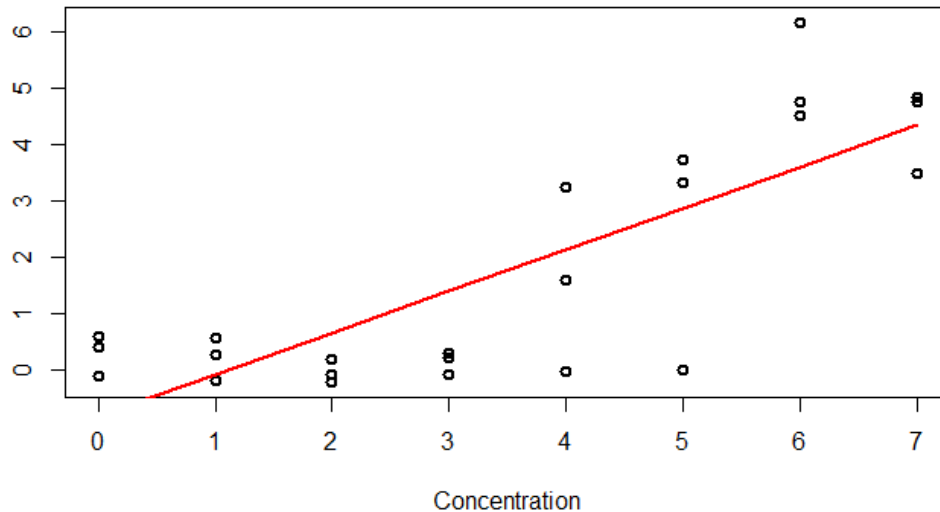
2. Smoother Fit (GAM)



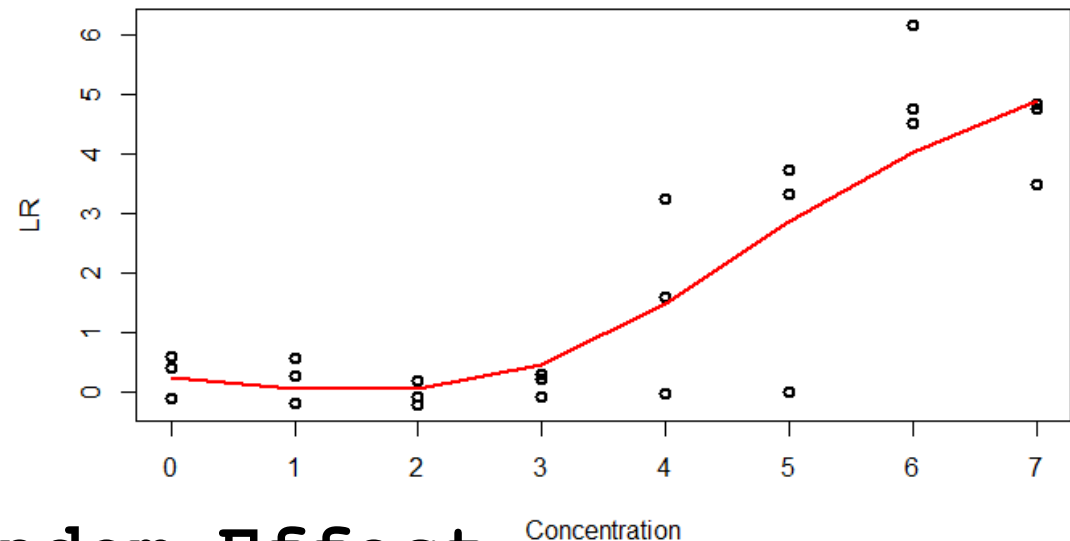
Modeling Responsiveness in R



1. Linear Fit



2. **Smoother** Fit (GAM)

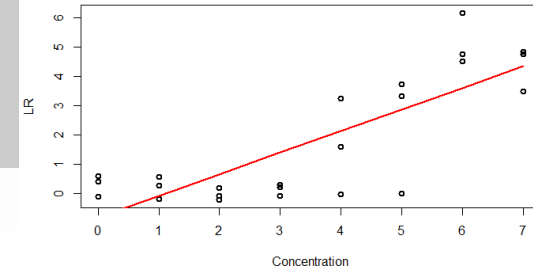


Random Effect

```
lmer(LR~log2.Conc.+(1|Day),  
      data = Pseudomonas)
```

```
gamm(LR~ti(log2.Conc.),  
      random=list(Day=~1),  
      data = Pseudomonas)
```

1. Linear Fit of Responsiveness at Lab 1



```
mean(dt$log2.Conc.)
```

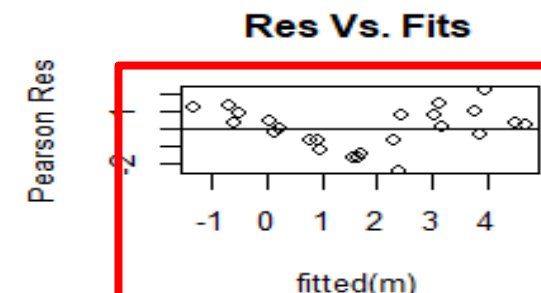
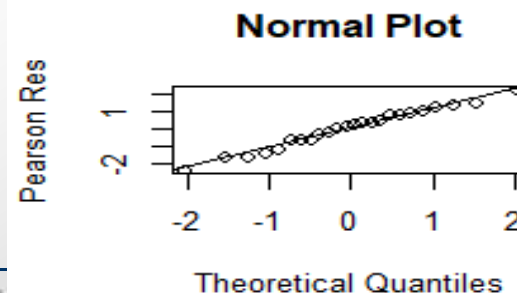
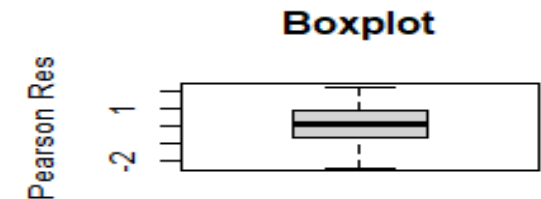
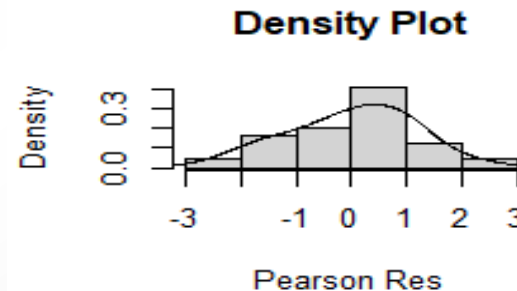
```
## [1] 3.5
```

```
m = lmer(LR ~ I(log2.Conc. - mean(log2.Conc.)) + (1|Day),  
data=dt) summary(m)
```

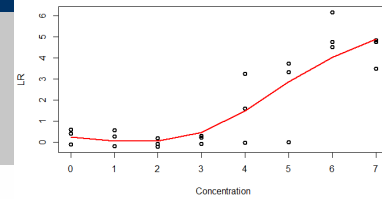
	Estimate	Std. Error	df	tvalue	Pr(> t)	
(Intercept)	1.7575	0.3963	2.0000	4.434	0.0473	*
I(log2.Conc. - mean(log2.Conc.))	0.7383	0.1068	20.0000	6.915	1.03e-06	***

```
diagRES(m)
```

Checking for
inappropriate
fit



2. Smoother Fit of Responsiveness at Lab 1



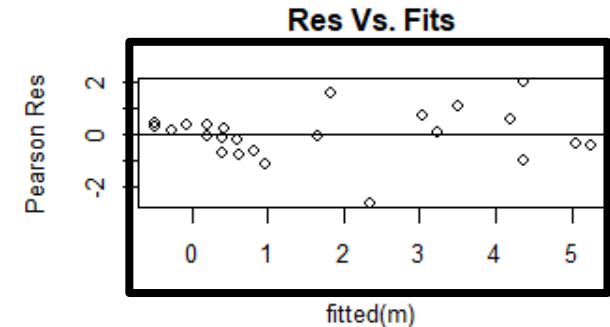
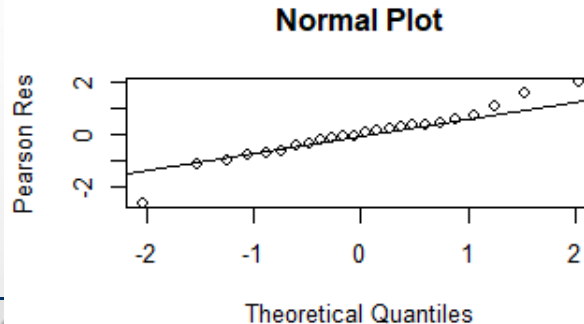
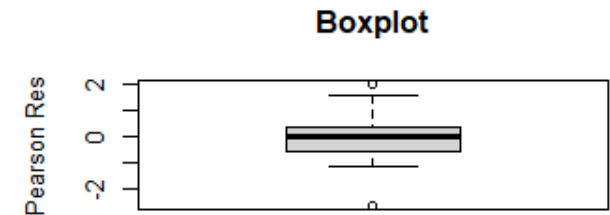
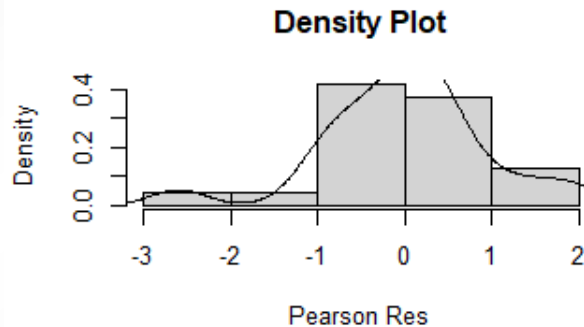
```
g = gamm(LR ~ ti(log2.Conc.), random=list(Day=~1), data=at,
summary(g$gam)
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.7575     0.3306   5.316 3.28e-05 ***
## Approximate significance of smooth terms:
##              edf Ref.df      F p-value
## ti(log2.Conc.) 2.893  2.893 32.82 <2e-16 ***
```

```
diagRES(m)
```

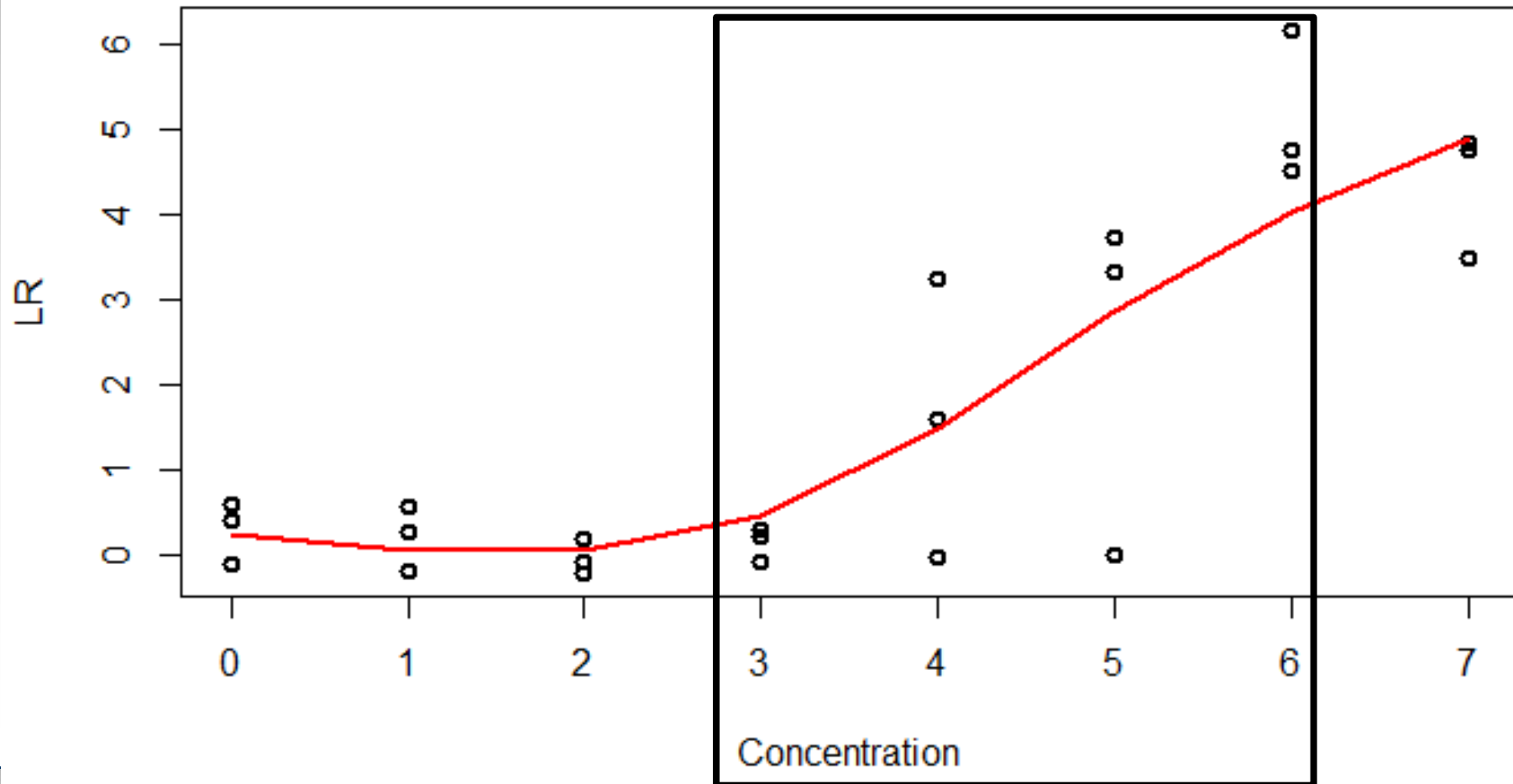
**No quantification of
responsiveness!**

**Is the
fit better?**



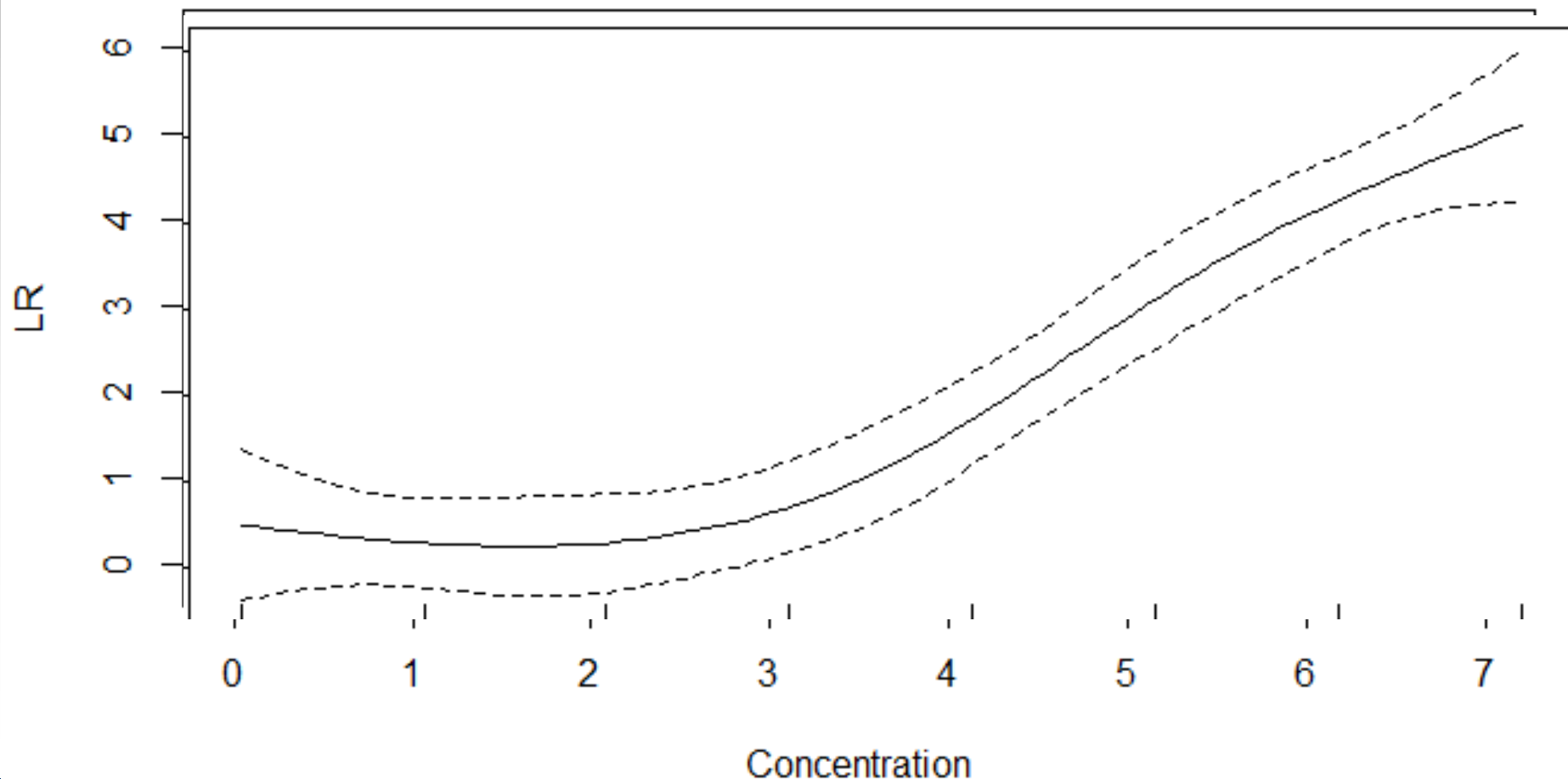
How to quantify responsiveness from a GAM or any ML algorithm?

ANSWER: In Microbiology, look at the Slope of the GAM in the Linear Region – subjective!

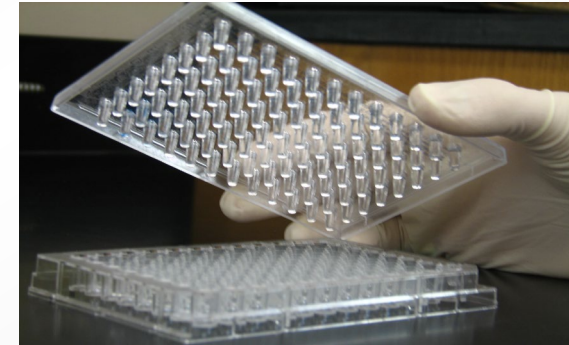
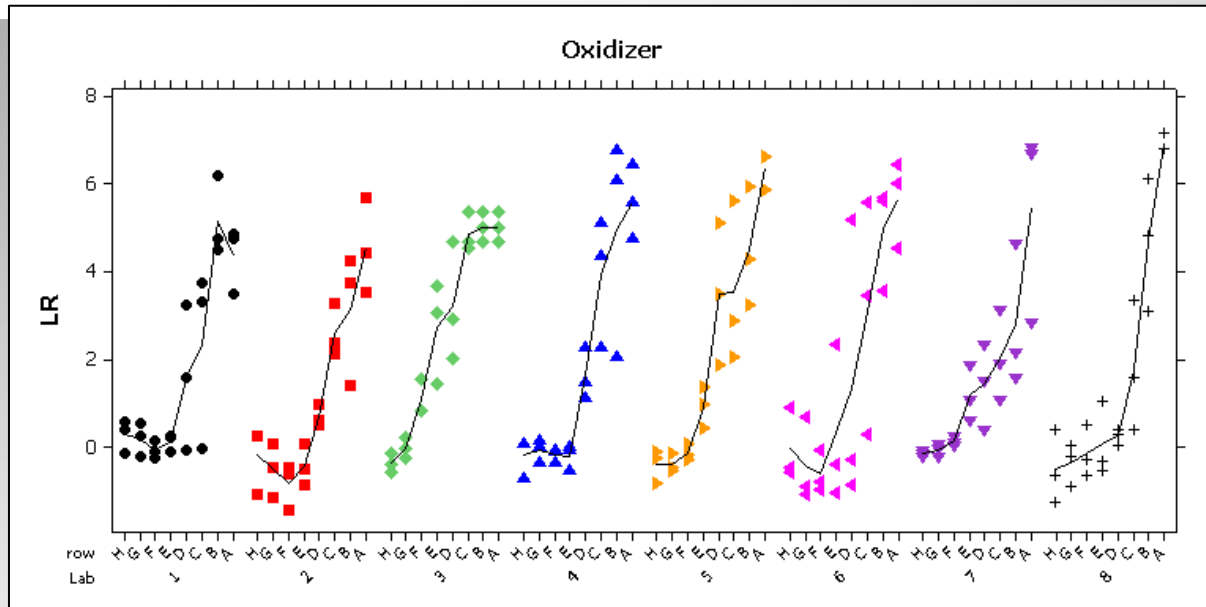


How to quantify uncertainty from a GAM or any ML algorithm?

ANSWER: By putting Error Bars on Predictions



MBEC Responsiveness Across All 6 Labs to 3 Antimicrobials

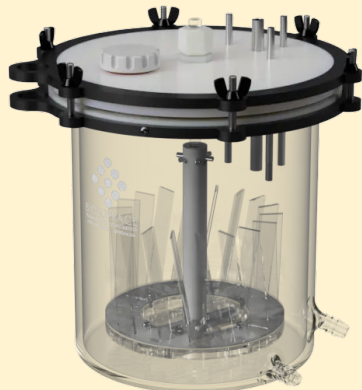


Disinfectant	Trend	SE	p-value
Non-chlorine oxidizer	0.87	0.0379	<0.00005
Phenol	0.87	0.0376	<0.00005
Quat	0.50	0.0275	<0.00005

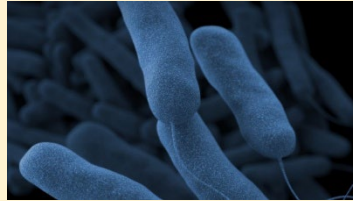
Parker et al. *JMM*, 2014; ASTM RR:E35-1006, 2011

Three R Modules Based on This Talk

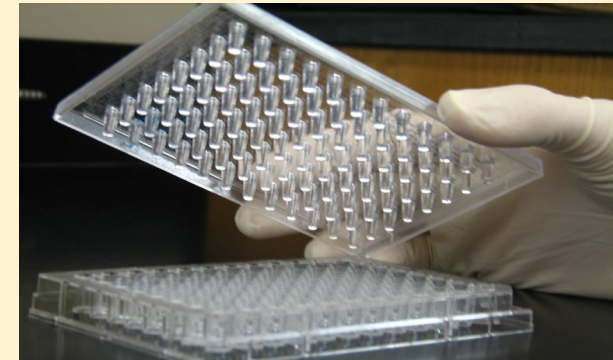
Resemblance (Control Repeatability)



Repeatability



Responsiveness



Any questions?

