All comparisons used Generalized Linear Mixed Models with Gamma (link: log).

SNR vs Stain:

- 1. M1 (7 params): SNR ~ Stain * Tissue + (1|Experiment) + (1|ROI)
- 2. M2 (6 params): SNR ~ Stain + Tissue + (1|Experiment) + (1|ROI) \rightarrow Used because Stain * Tissue (p=0.81) was not significant in previous model M1.
- 3. M3 (5 params): SNR ~ Stain + (1|Experiment) + (1|ROI) \rightarrow Used because Tissue (p=0.19) was not significant in previous model M2.

Model comparison

model	npar	AIC	BIC	logLik	-2*LOG(L)'	Chisq	Df	Pr(>Chisq)
М3	5	1230.44	1248.24	-610.22	1220.44	null	null	null
M2	6	1230.75	1252.11	-609.37	1218.75	1.69	1.00	0.19
M1	7	1232.69	1257.62	-609.35	1218.69	0.06	1.00	0.81

Although statistically not significant, M3 has better metrics compared to others (AIC, BIC and Loglikelihood)

Best model, M3, statistics:

Formula: glmer(SNR~Stain+(1|Experiment)+(1|ROI))

Family: *Gamma (link: log)*Number of observations: *260*Confidence intervals: *boot*Bootstrap Iterations: *1000*

Log-likelihood: -610 AIC: 1230 | BIC: 1248 Residual error: 0.205

Random Effects:		Estimate	CI- low	CI- high	SE	Z-stat	df p
Experiment-sd	(Intercept)	0.097	0.144	0.261			
ROI-sd	(Intercept)	0.064	0.104	0.204			
Residual-sd	Observatio n	0.205	0.218	0.259			

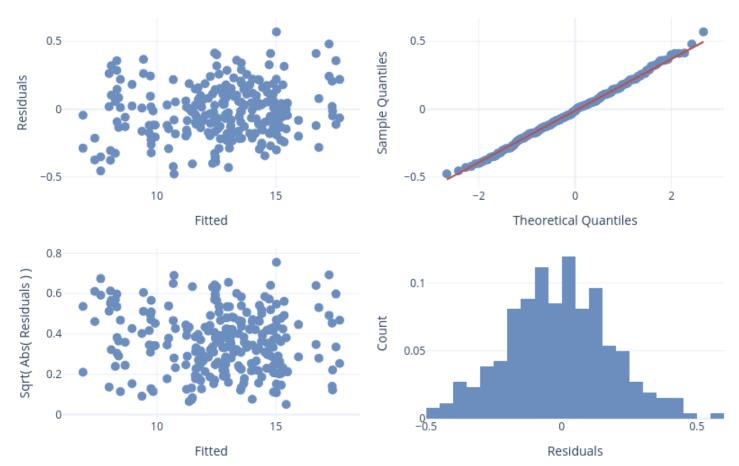
Fixed Effects:

Estimated Marginal Means

Stain	response	SE	asymp_LCL	asymp_UCL
lodine-stained	10.11	1.25	7.66	13.34
PTA-stained	13.65	1.28	11.07	16.83

contrast	ratio	SE	asymp_LCL	asymp_UCL	z_ratio	p_value
Iodine-stained/PTA-stained	0.74	0.10	0.57	0.96	-2.30	0.022

Residual analysis



Mean vs Stain:

- 1. M1 (7 params): Mean ~ Stain * Tissue + (1|Experiment) + (1|ROI)
- 2. M2 (6 params): Mean \sim Stain + Tissue + (1|Experiment) + (1|ROI) Used because Stain * Tissue (p=0.09) was not significant in previous model M1.

Model comparison

	model	npar	AIC	BIC	logLik	-2*LOG(L)'	Chisq	Pr(>Chisq)
Ī	M2	6	2175.38	2196.74	-1081.69	2163.38	null	null
Ī	M1	7	2174.62	2199.55	-1080.31	2160.62	2.75	0.10

Models are statistically not different, metrics performances are also mixed. Choosing M2 as the best model as the Stain*Tissue fixed effect was not significant.

Best model, M2, statistics:

Formula: glmer(Mean~Stain+Tissue+(1|Experiment)+(1|ROI))

Family: *Gamma (link: log)*Number of observations: *260*Confidence intervals: *boot*Bootstrap Iterations: *1000*

Log-likelihood: -1081 AIC: 2175 | BIC: 2196 Residual error: 0.126

Random Effects:		Estimate	CI-low	CI-high	SE	Z-stat	df p
Experiment-sd	(Intercept)	0.059	0.127	0.237			
ROI-sd	(Intercept)	0.047	0.105	0.199			
Residual-sd	Observation	0.126	0.148	0.181			

Fixed Effects:										
	(Intercept)	92.611	3.966	5.005	7.973	52.603	254.0	<.001	***	
	StainPTA-stained	1.331	-0.232	0.879	0.112	3.411	254.0	<.001	***	
	TissueMuscle-serosal	1.182	0.139	0.201	0.017	11.483	254.0	<.001	***	

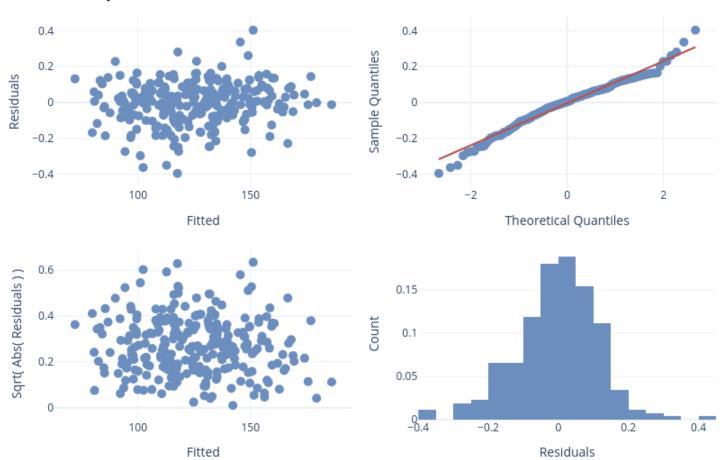
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1

Estimated Marginal Means

Stain	response	SE	asymp_LCL	asymp_UCL
lodine-stained	100.69	8.64	83.11	121.99
PTA-stained	134.01	9.15	115.03	156.12

contrast	ratio	SE	asymp_LCL	asymp_UCL	z_ratio	p_value
Iodine-stained/PTA-stained	0.75	0.06	0.64	0.89	-3.41	0.001

Residual analysis



CNR vs Stain: (offset = 2)

M1: CNR ~ Stain + (1|Experiment) + (1|ROI)

Statistics:

Formula: glmer(CNR~Stain+(1|Experiment)+(1|ROI))

Family: *Gamma (link: log)*Number of observations: *130*Confidence intervals: *boot*Bootstrap Iterations: *1000*

Log-likelihood: -186 AIC: 382 | BIC: 396 Residual error: 0.136

Random Effects:		Estimate	CI-low	CI-high	SE	Z-stat	df p
Experiment-sd	(Intercept)	0.047	0.127	0.240			
ROI-sd	(Intercept)	0.056	0.140	0.258			
Residual-sd	Observation	0.136	0.158	0.204			

Fixed Effects:										
	(Intercept)	6.956	1.504	2.361	0.401	33.617	125.0	<.001	***	
	StainPTA- stained	1.128	-0.285	0.519	0.057	2.392	125.0	0.01823	*	

Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1

Estimated Marginal Means

Stain	response	SE	asymp_LCL	asymp_UCL
lodine-stained	2.92	0.34	2.25	3.80
PTA-stained	3.78	0.37	3.03	4.71

contrast	ratio	SE	asymp_LCL	asymp_UCL	z_ratio	p_value
Iodine-stained/PTA-stained	0.77	0.08	0.63	0.95	-2.47	0.014

Residual analysis

