



**Question:** Does hemolysin production differ between triazole-resistant and susceptible strains, does it change over time, and does the temporal pattern differ between triazole phenotypes?



**Hypothesis:** Triazole-resistant strains will have reduced hemolysin production over time compared to susceptible strains.

**Linear model:** The response variable is hemolysin production (ZOC\_CD). I used a log-scale for this response because the data is right-skewed. This results in proportional effects rather than absolute effects. Fixed effects include the actual triazole phenotype (either resistant or susceptible) and time (24h, 48h, 72h). Random effects are strain backgrounds so that each strain gets its own intercept and can differ in baseline hemolysin production.

```
hemo_mod <- lmer(
```

```
log1p(ZOC_CD) ~ Triazoleclass * Time + (1 | Strain),
```

```
data = hemolysin_long)
```

**Diagnostic plot (qqplot\_hemo):** This shows a Q-Q plot comparing the observed residuals (data points) versus the theoretical normal values (line). This plot shows a heavy lower tail since the min of the scaled residuals is -4.63 (quite large) suggesting a few extreme observations. Middle points are close to a straight line with good alignment, and the upper tail has a slight deviation. I believe my sample size (n=336) can handle minor tail deviations without worrying too much especially because residual SDs is quite small.

