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> #####section 3:statistical analysis####
>
>
> ###Cochran-Mantel-Haenszel (CMH) test of Exopher frequency
>
> # Convert to data frame
> data_df <- as.data.frame(data)
>
> # Convert columns to factors with two levels
> data_df$Trial <- factor(data_df$Trial, levels = unique(data_df$Trial))
> data_df$Treatment <- factor(data_df$Treatment, levels = unique(data_df$Treatment))
> data_df$Exopher <- factor(data_df$Exopher, levels = unique(data_df$Exopher))
>
> # Perform the Mantel-Haenszel test
>
> # Note: The order of the factors matters in running this analysis.
> # mantelhaen.test(x,y,z) where x is the row variable, y is the column variable,
> # and z is the stratifying factor. Generally, x refers to the treatment groups
> # (i.e. control vs. experimental group). y refers to the outcome (is there an exopher?)
> # and z refers to the replicates or trials.
> #
> # Arranging the factors in this order tests for the association of treatment and
> # exopher while controlling for differences between trials. Essentially the Mantel-Haenszel
> # test examines each trial separately before aggregating the the results to conclude
> # if there is a overall association between the treatment and exophers across all
> # trials.
>
> data_CMH <- mantelhaen.test(data_df$Treatment, data_df$Exopher, data_df$Trial)
>
> # Print the result
> print(data_CMH)

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Mantel-Haenszel chi-squared test with continuity correction

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data: data_df$Treatment and data_df$Exopher and data_df$Trial
Mantel-Haenszel X-squared = 16.026, df = 1, p-value = 6.246e-05
alternative hypothesis: true common odds ratio is not equal to 1
95 percent confidence interval:
 2.882464 36.514733
sample estimates:
common odds ratio
 10.25926

```

CMH p-value

Odds ratio from the CMH test, there is a 10.2 times greater chance of producing an exopher in the control group compared to the treatment group.

```

> ##Reformatting the data for logistic regression
> # Define Treatment as a factor and make AD2 (Adult Day 2) your reference dataset
> Treatment_unordered <- factor(data$Treatment, ordered = FALSE) #makes Treatment a factor
> Treatment_unordered <- relevel(Treatment_unordered, ref = "AD2") #makes AD2 within Treatment
>
> ##simple logistic regression
> data_glm <- glm(Exopher ~ Treatment_unordered+factor(Trial), family = binomial(link = "logit"))

```

```
+ data = data)
> summary(data_glm)
```

```
Call:
glm(formula = Exopher ~ Treatment_unordered + factor(Trial),
     family = binomial(link = "logit"), data = data)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.6502	0.3688	-4.474	7.66e-06 ***
Treatment_unorderedAD5	-2.2980	0.6358	-3.614	0.000301 ***
factor(Trial)2	0.7978	0.4594	1.737	0.082433 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 154.55 on 199 degrees of freedom
Residual deviance: 131.66 on 197 degrees of freedom
AIC: 137.66

Number of Fisher Scoring iterations: 6

```
> plot(data_glm)
Hit <Return> to see next plot:
Hit <Return> to see next plot:
Hit <Return> to see next plot:
Hit <Return> to see next plot:
> # Calculate odds ratios
> odds_ratios <- exp(coef(data_glm))
> print(odds_ratios)
```

	(Intercept)	Treatment_unorderedAD5	factor(Trial)2
	0.1920029	0.1004630	2.2206918

```
>
> # Calculate 95% confidence intervals for the odds ratios
> conf_intervals <- exp(confint(data_glm))
waiting for profiling to be done...
> print(conf_intervals)
```

	2.5 %	97.5 %
(Intercept)	0.08724927	0.3768432
Treatment_unorderedAD5	0.02310860	0.3043337
factor(Trial)2	0.92085171	5.6748830

These are the results for the comparison between AD2 (control treatment) and AD5.

Logistic regression results. The estimate is used to calculate the odds ratio. The z-value indicates standard deviations away from the mean and a negative z-value means that the AD5 treatment produces fewer exophers. Pr(>|z|) is the p-value for the logistic.

Odds ratio for the logistic regression. There is only a 10% chance for an exopher to occur on AD5 as compared to AD2.

95% confidence interval for the logistic regression. This range does not include 1 indicating that the odds ratio is statistically significant.