Goals for the Effects doc:

Outline how 5 factors /variables within my MLH1 counts (are not random or constant)

think/outline how they could affect my interpertations/inferences for mean MLH1 differences.

Cell quality

Mouse age

litter

spread / dissection month

room

Inbreeding, F1s

Human Error (how consistant is my counti) – isn’t a variable for this effects document. I’m assuming it apples uniformly across all the data and is more of an inherent factor for the data than – a technical variable to account for.

-XX is another inherent factor.

**Cell Quality**

Human assigned metric, has a bias for best cells (1 to 5, best to worst) to have more MLH1 foci. I tried to keep the scoring to uniformity of staining, completeness of all the SC, lack of background noise -- but I’d score lower for more 0CO bivs, (I don’t know if 0CO bivs are true or from technical noise).

Since it’s human assigned there’s error and looking at replicate data shows that I am not always consistent in assigning scores across the same cell.

The initial purpose was to indicate which cells were kinda of crappy and should have low priority for being used in estimates. (but since not all mice have the same number of cell samples – I wanted to

(I didn’t think this quality range through very well)

Main concern:

Female and male cells have different biases in the CO count quality score relationship. (the effect isn’t equal across sexes – so I’d have to account for this when comparing across the sexes

**Result**: positive correlation with good quality and foci count

Male vs female quality effect!

Impact on inferences --

**Mouse age**

Males

Age range is larger than I would prefer, (if all males could be the same age or within 4 weeks of each other that would have been perfect.

The final dataset does/will exclude old mice above a threshold, but if there are more subtle age effects

Since I was trying to breed many mice – I kept some longer before dissecting – so some strains only have old mice because I couldn’t get them to breed.

Main concern: older mice are biasing the estimated strain effect, all the different age range across the mice in my data are adding noise to the strain RR estimates.

(young and old RR age effects have been shown in previous publications)

Result: (modeling the effect of age and tracking the curve of age

Reassurances-

It seems unlikely that age effects – are discontinuous for the age ranges I have (i.e. there would be a window when the RR jumps up then goes back down.

Also, the general male pattern seems to be the RR is highly elevated or near the minimum. This is the main signal I’m trying to detect, --- it might be unlikely that I’d miss an elevated strain due to the age effect.

(I have at least 1 3-9 week mice for each of the strains)

(include age in MM? but it’s so unbalanced)

**Age (female)**

Getting embryos was diffecult (impossible) for some strains – also logistically impossible – so almost all of my female data came from neonates ( < 24 hours old)

I did try a few mice over 24 hours old (SPIC?) (MOLF?)

Main concerns;

1.Collect data / distinguish data (based on meta.data sheet)

2. run logistic regression for nMLH1 ~ female.age (emb | neonate)

**Room**

We had to switch rooms, Biotech, cut off ~1mar17 (summer, june 17). This would be a concern if there was a room affect

I successfully collected/ collated the data for strains housed in different rooms. I ran wilcox tests for the cell counts and mouse averages. The adjusted p values are NS, but I don’t quite understand how the p values are adjusted.

\*\*play with the compare means – try coding in a different way\*\*

The adjusted p values for the mlh1 counts, indicate there are significant effects, but the pvalues still look strange to me. The adjusted p values for mouse averages indicate there is not a significant room effect. I should also cite other papers for showing that strains raised in different institutions have similar MLH1 counts.

**Litter (maternal effect) (maternal age)**

Maternal age:

Collected – X number of observations

The range of maternal ages across categories might not be sufficient

(facet sex \* subsp)

I have so few ages for Dom male and female, (kicking myself)

I think I’ll conclude --- that I don’t have enough mice.

**Dissection and spread (dissection date)**

(dissection month – might cause effects from humidity), (for total SC –previous Peromyscus results indicate this might be a thing)

-I’ve made draft plots for MLH1 and total SC, write up these summaries

Main concern:

\*age effects\* (male, maternal age)

\*litter effect\*

\*mouse room effect\* (Charmony, MSC)

\*quantification repeatability\*

\*spread batch and staining effects\*

\*power analysis on number of cells\*

\*time of year effect (on spread)\*

\*dominant effect\* (F1s)

(estimated room changes)

**WSB** (check if raised in Charmony)

Female: 10 precut off, 4 post cut off (these might have been Charmony

Male: 12 all precut off

**LEW**

Female: 8 precut off, 1 post cut off

Male: 6 precutt off, 2 post (2 intermediate, 8may17)

**MSM**

Female: 5 precut, 8 post, 3 intermediate

Male: 5 precut off, 2 post, 2 intermediate

Only WSB, LEW, and MSM will give mice where the room effects can be compared.

Have to check if I have any of these grown in Charmony (WSB female litter)

PERC male: 24aug17

**PWD**

Female: 15 pre cut off, 0 post cut off

Male: 8 pre cut off, 0 post cut off

**MOLF**

all post

**SKIVE**

All post