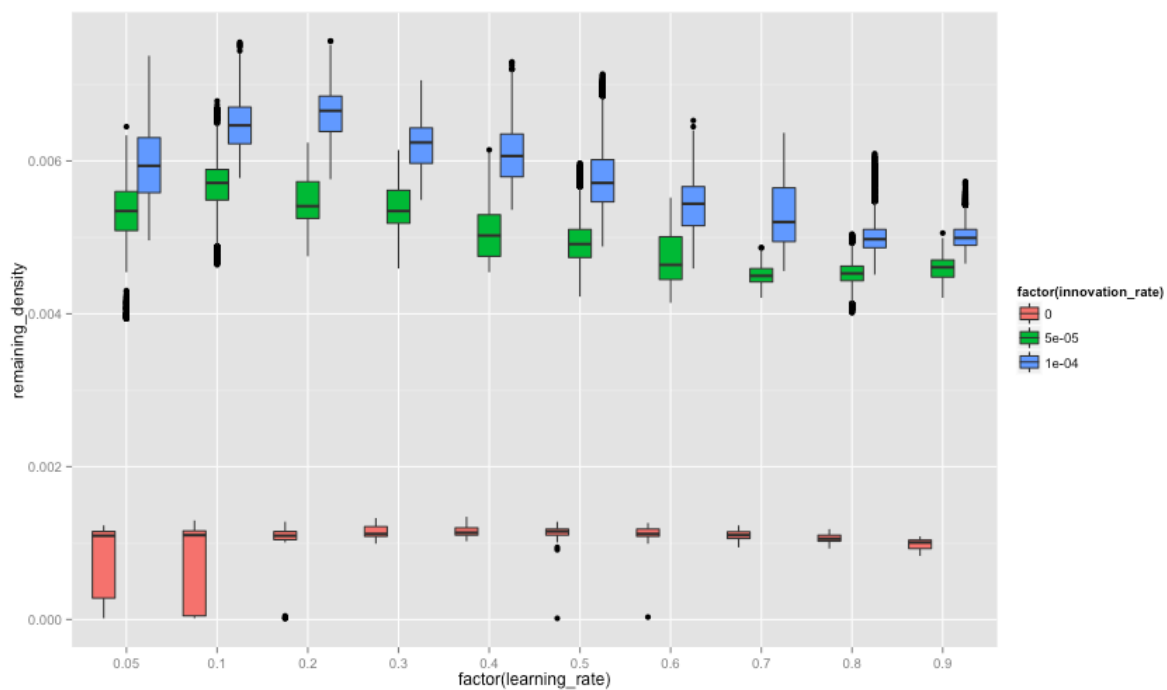


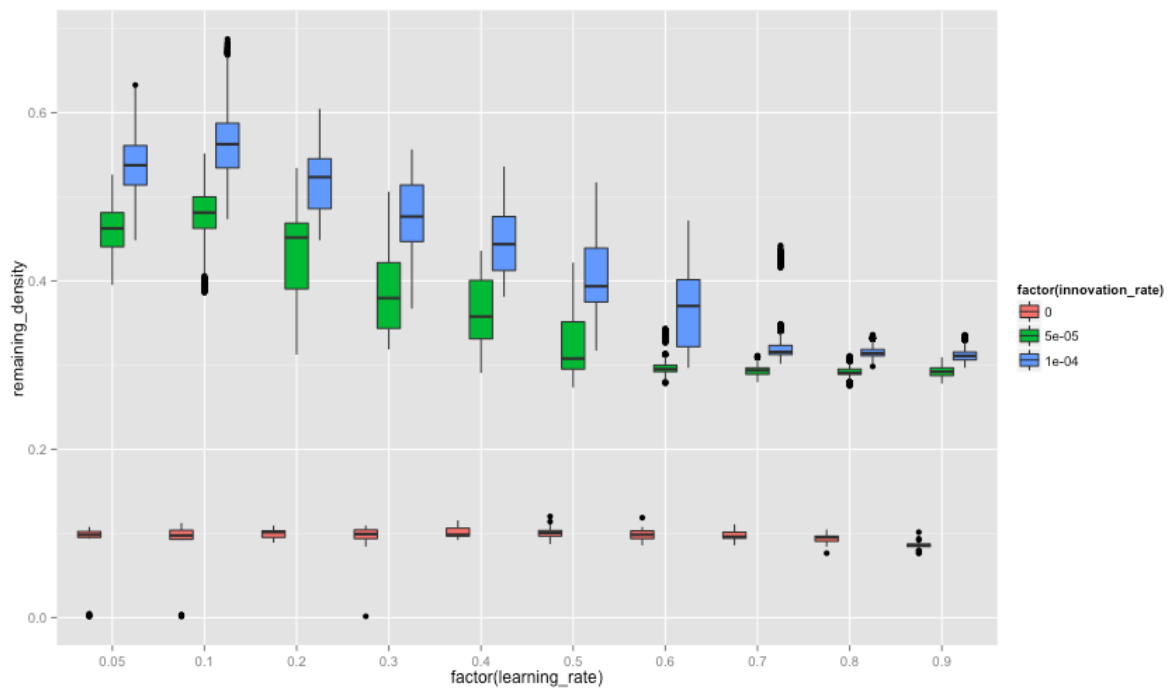
There's very definitely some interesting stuff happening with the remaining density if we look in a single size of state space – in this case, our largest.

```
p <- ggplot(data = ss5516, aes(y = remaining_density,  
x = factor(learning_rate),  
fill = factor(innovation_rate)))  
p + geom_boxplot(notch = FALSE)
```



And, at a much smaller state space, we see the same shape but at a much higher fraction of remaining density.

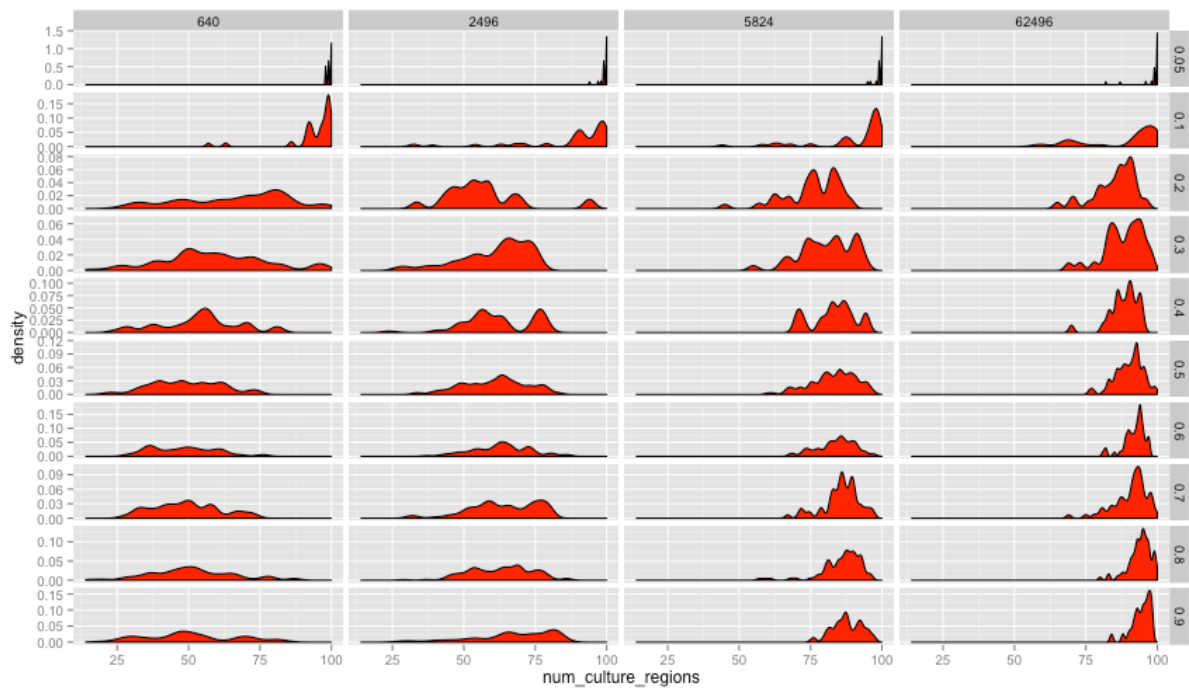
```
p <- ggplot(data = ss3316, aes(y = remaining_density,  
x = factor(learning_rate),  
fill = factor(innovation_rate)))  
p + geom_boxplot(notch = FALSE)
```



## 16 Trees, Low Innovation Level

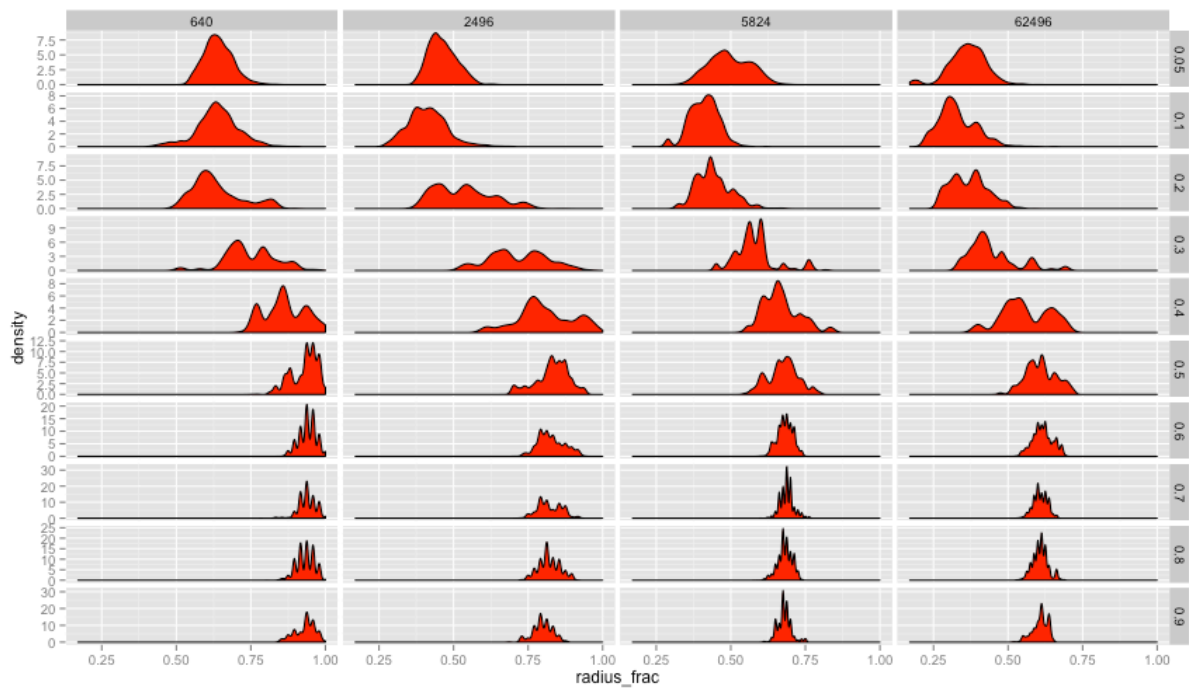
Now, let's just look at the state spaces with 16 trees, and with the medium level of innovation, 5e-05. This is just density of culture solutions, broken down by size space size (but all state spaces having 16 trees), and learning rate. There seems to be a clear effect, more variance in smaller state spaces, and higher means in larger learning rates?

```
p <- ggplot(ss16midinnov, aes(x =
num_culture_regions)) + geom_density(fill = "red")
p + facet_grid(learning_rate ~ size_trait_space, scale
= "free_y")
```



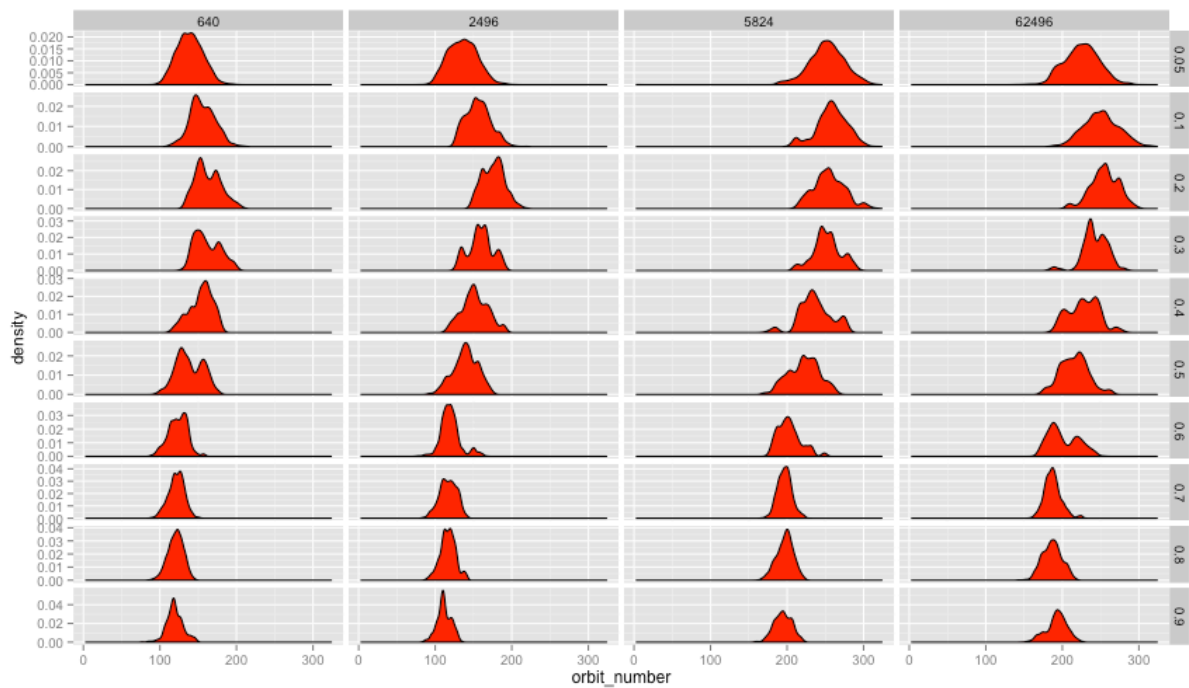
Now let's look at the radius fraction. Again, these all have 16 trait trees, but some of them are depth 3 and some depth 5. So what's interesting is the ratio to the maximum. This seems like a clear effect, but with the size of the state space, the entire pattern just shifts left, to occupy less of the state space.

```
p <- ggplot(ss16midinnov, aes(x = radius_frac)) +
  geom_density(fill = "red")
p + facet_grid(learning_rate ~ size_trait_space, scale
= "free_y")
```



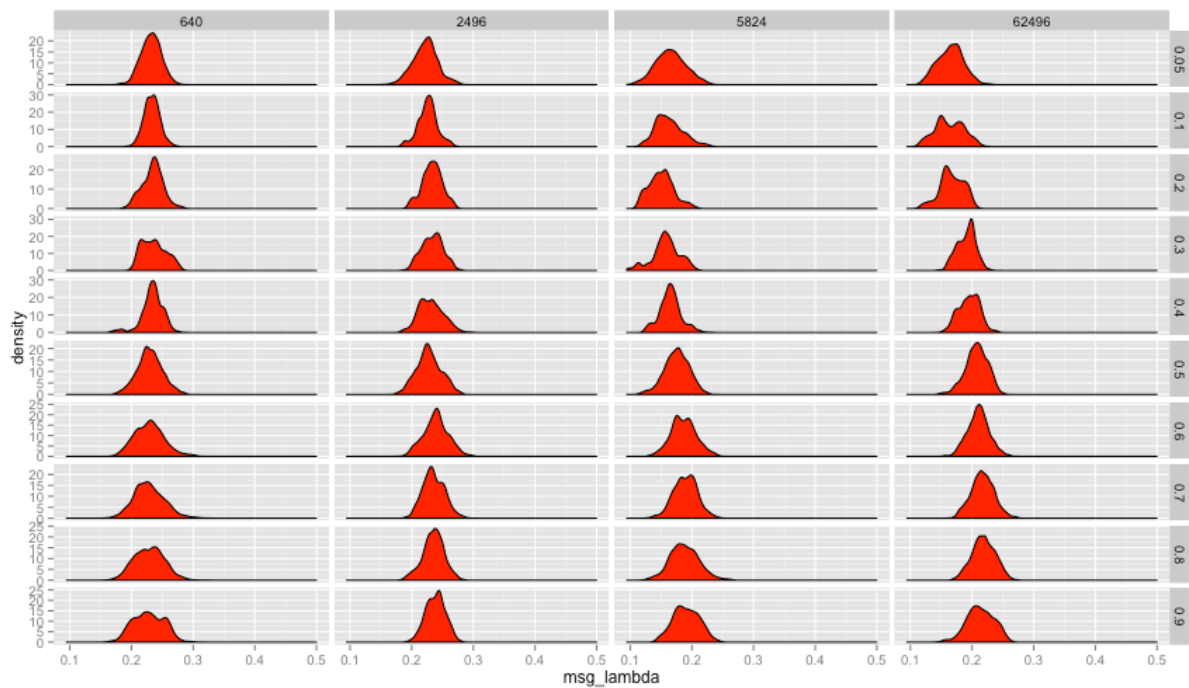
Finally let's see what's going on with symmetry measures. First, the raw orbit number:

```
p <- ggplot(ss16midinnov, aes(x = orbit_number)) +
  geom_density(fill = "red")
p + facet_grid(learning_rate ~ size_trait_space, scale = "free_y")
```



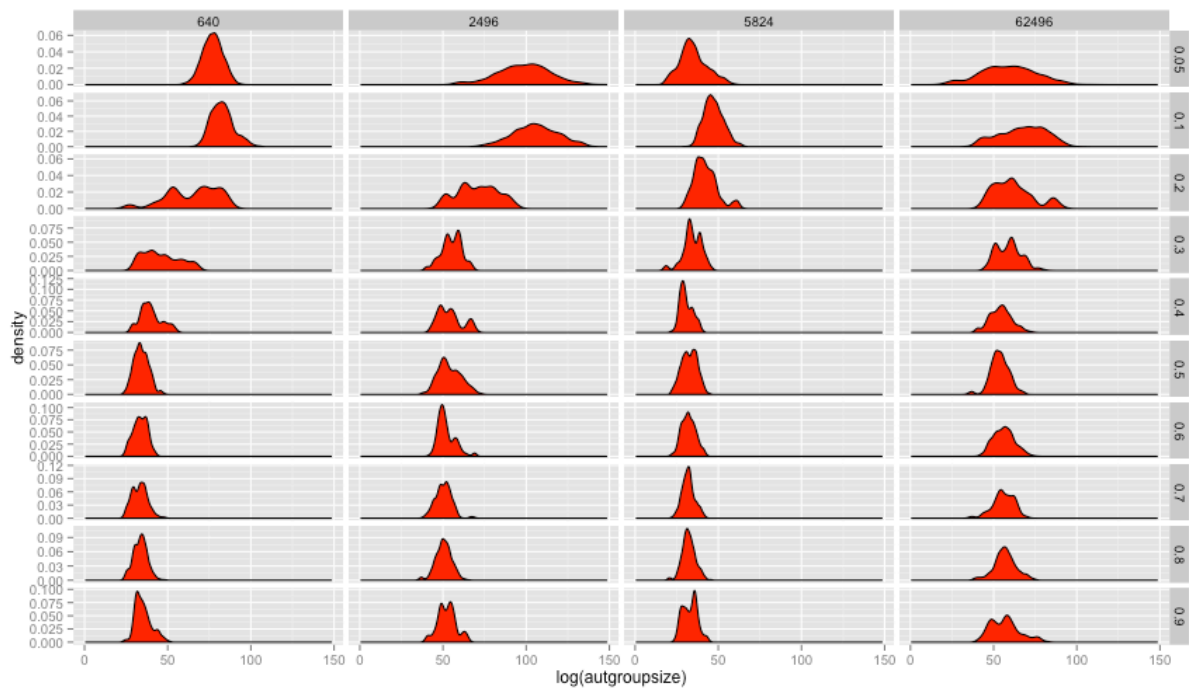
And now the lambda function:

```
p <- ggplot(ss16midinnov, aes(x = msg_lambda)) +
  geom_density(fill = "red")
p + facet_grid(learning_rate ~ size_trait_space, scale
= "free_y")
```



And now the automorphism group size:

```
p <- ggplot(ss16midinnov, aes(x = log(autgroupsize)))
+ geom_density(fill = "red")
p + facet_grid(learning_rate ~ size_trait_space, scale
= "free_y")
```



How does the final tree size compare?

```
p <- ggplot(ss16midinnov, aes(x = order)) +
  geom_density(fill = "red")
p + facet_grid(learning_rate ~ size_trait_space, scale = "free_y")
```

