



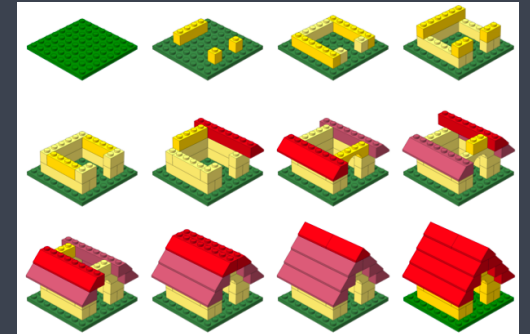
```
dds <- DESeqDataSetFromMatrix(countData = cts,  
                              colData = coldata,  
                              design= ~ batch + condition)  
  
dds <- DESeq(dds)  
resultsNames(dds) # lists the coefficients  
res <- results(dds, name="condition_trt_vs_untrt")  
# or to shrink log fold changes association with condition:  
res <- lfcShrink(dds, coef="condition_trt_vs_untrt", type="apeglm")
```

# Introduction to Differential Gene Expression Analysis

Harvard Chan Bioinformatics Core

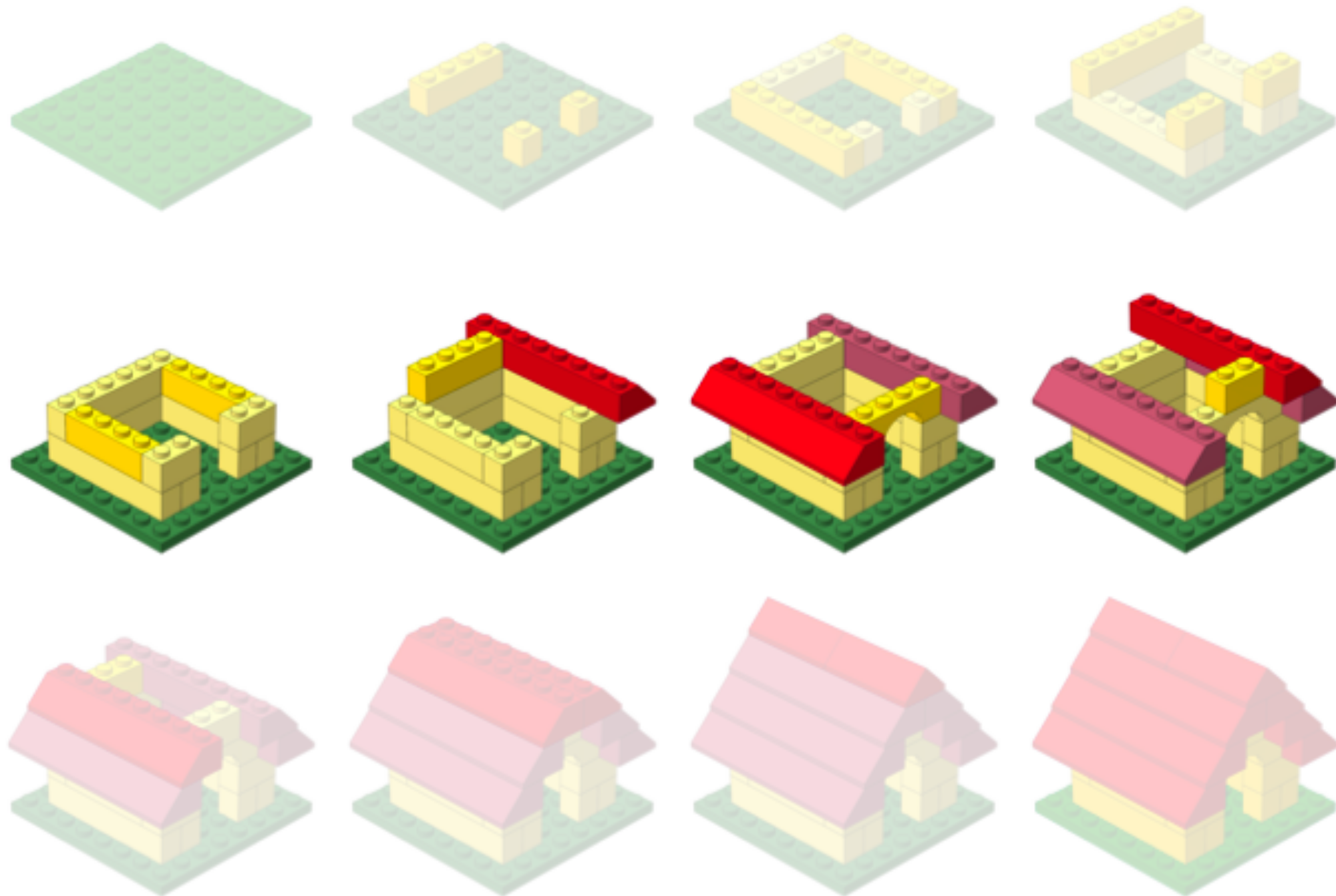
<https://tinyurl.com/hbc-dge-online>

# Workshop Scope



## Differential Gene Expression analysis

- ✓ Understand the considerations for performing statistical analysis on RNA-seq data
- ✓ Start with gene counts (after alignment and counting)
- ✓ Perform QC on count data
- ✓ Use DESeq2 to perform differential expression analysis on the count data and obtain a list of significantly different genes
- ✓ Visualize results of the analysis
- ✓ Perform functional analysis on the lists of differentially expressed genes



<http://anoved.net/tag/lego/page/3/>

# Bioinformatics data analysis

# Exit survey

<https://tinyurl.com/DGE-exit-survey>

# Contact us!

*HBC webpage:* <http://bioinformatics.sph.harvard.edu>

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