



```
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")
```

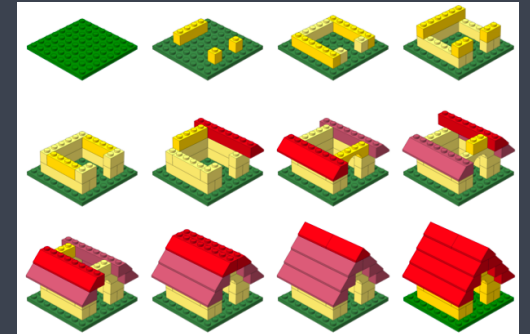
# Bulk RNA-seq Analysis Part II

## *Differential Gene Expression*

Harvard Chan Bioinformatics Core

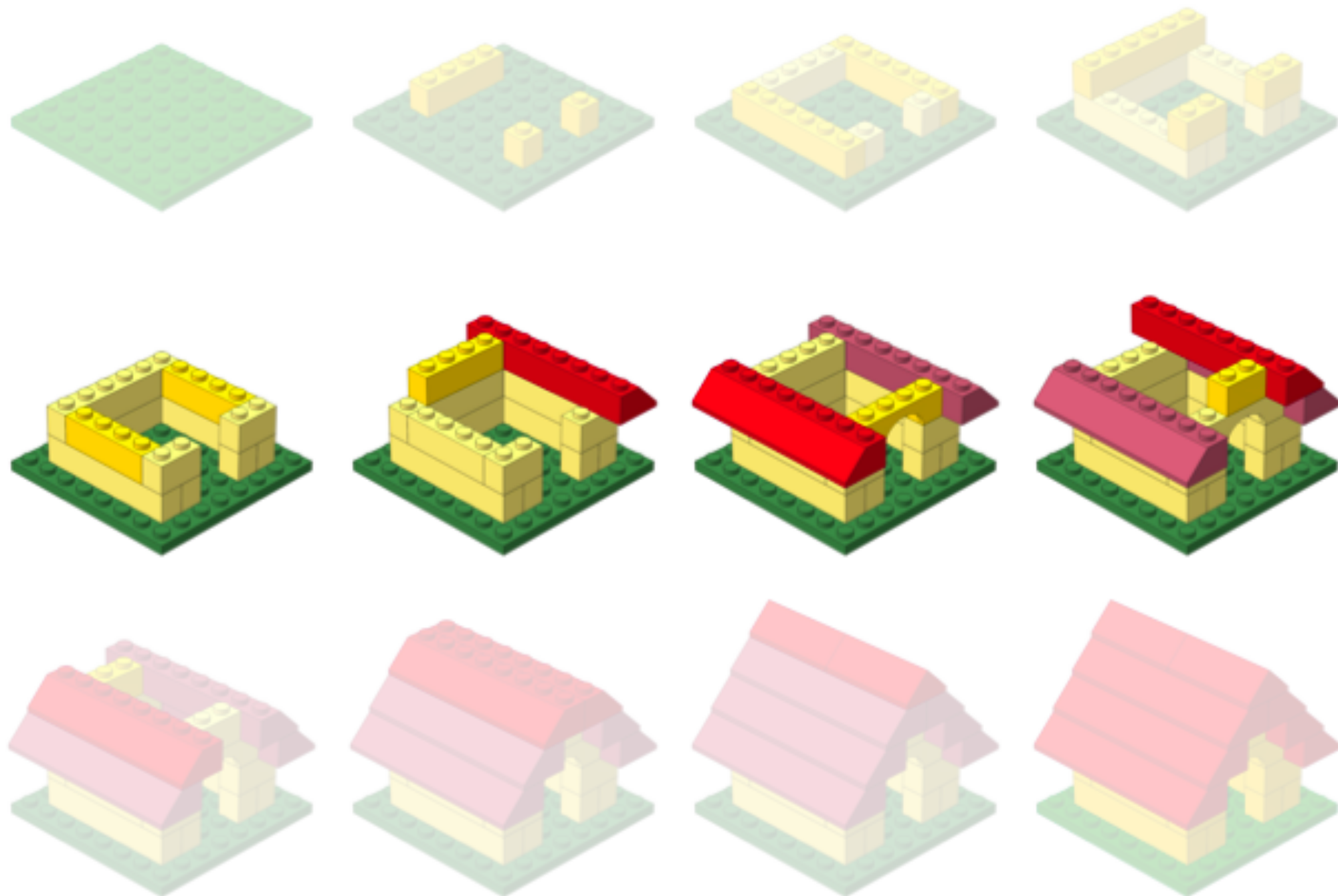
<https://tinyurl.com/hbc-dge-online>

# 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>

# Office hours

- 30 minute office hours for trainees
- Every other Wednesday at 11 AM or 11:30 AM
- Sign up form will be emailed to you

# Interested in additional training?

All workshop materials are online: <https://hbctraining.github.io/main>

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Upcoming relevant courses from our partners

Countway Libraries -

1. Research Data Management: Tips and Tools (May 18th)

HMS Research Computing -

Intro to Python	Wednesday, May 18, 2022
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# Get (stay) in touch with us!

*Sign up for our mailing list:*

<https://tinyurl.com/hbc-training-mailing-list>

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