



```
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")
```

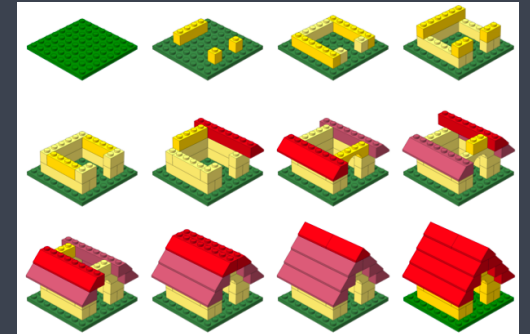
Bulk RNA-seq Analysis Part II

Differential Gene Expression

Harvard Chan Bioinformatics Core

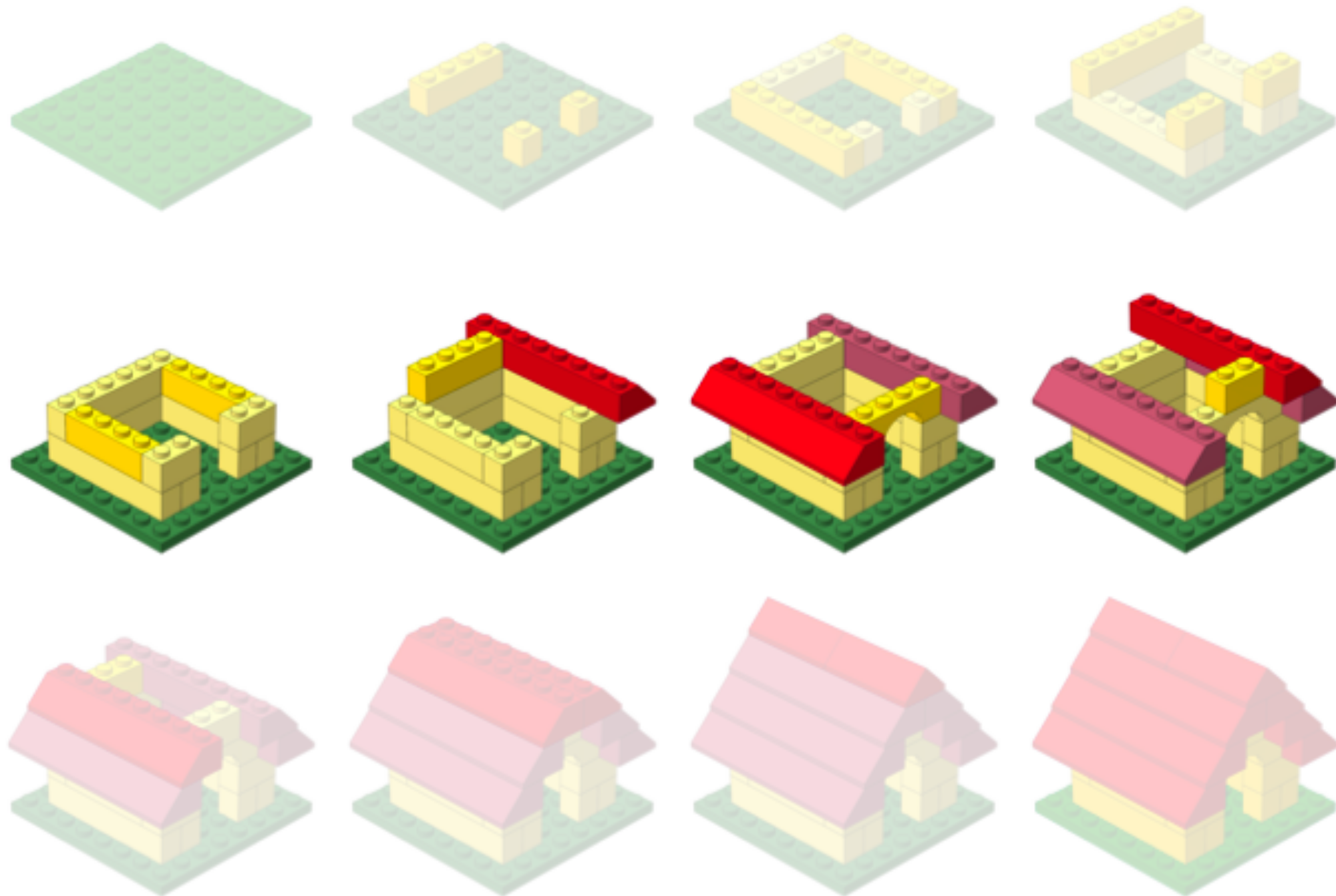
<https://tinyurl.com/hbc-dge-online>

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>

Interested in additional training?

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

Sign up for our mailing list:

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

Data Management

- HMS Data management -
 - Webpage: <https://datamanagement.hms.harvard.edu/>
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 - Check out the [training schedule](#) for short workshops
- Harvard-wide Research Data Management -
<https://researchdatamanagement.harvard.edu/>

Get (stay) in touch with us!

Training email: hbctraining@hsph.harvard.edu

Consulting email: bioinformatics@hsph.harvard.edu

Twitter: [@bioinfocore](https://twitter.com/bioinfocore)