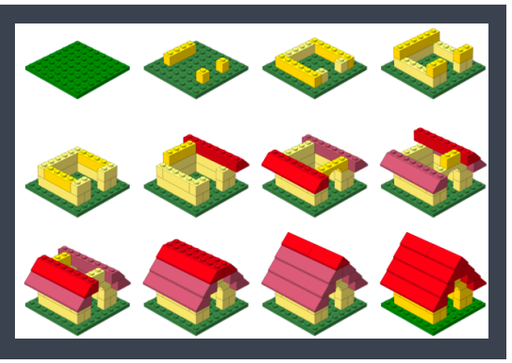
```
dds <- DESeqDataSetFromMatrix(countData = cts,
                              colData = coldata,
                              design= ~ batch + condition)
dds <- DESeq(dds)
resultsNames(dds) # lists the coefficients
res <- results(dds, name="condition_trt_vs_untrt")
# or to shrink log fold changes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

Introduction to Differential Gene Expression Analysis

Harvard Chan Bioinformatics Core

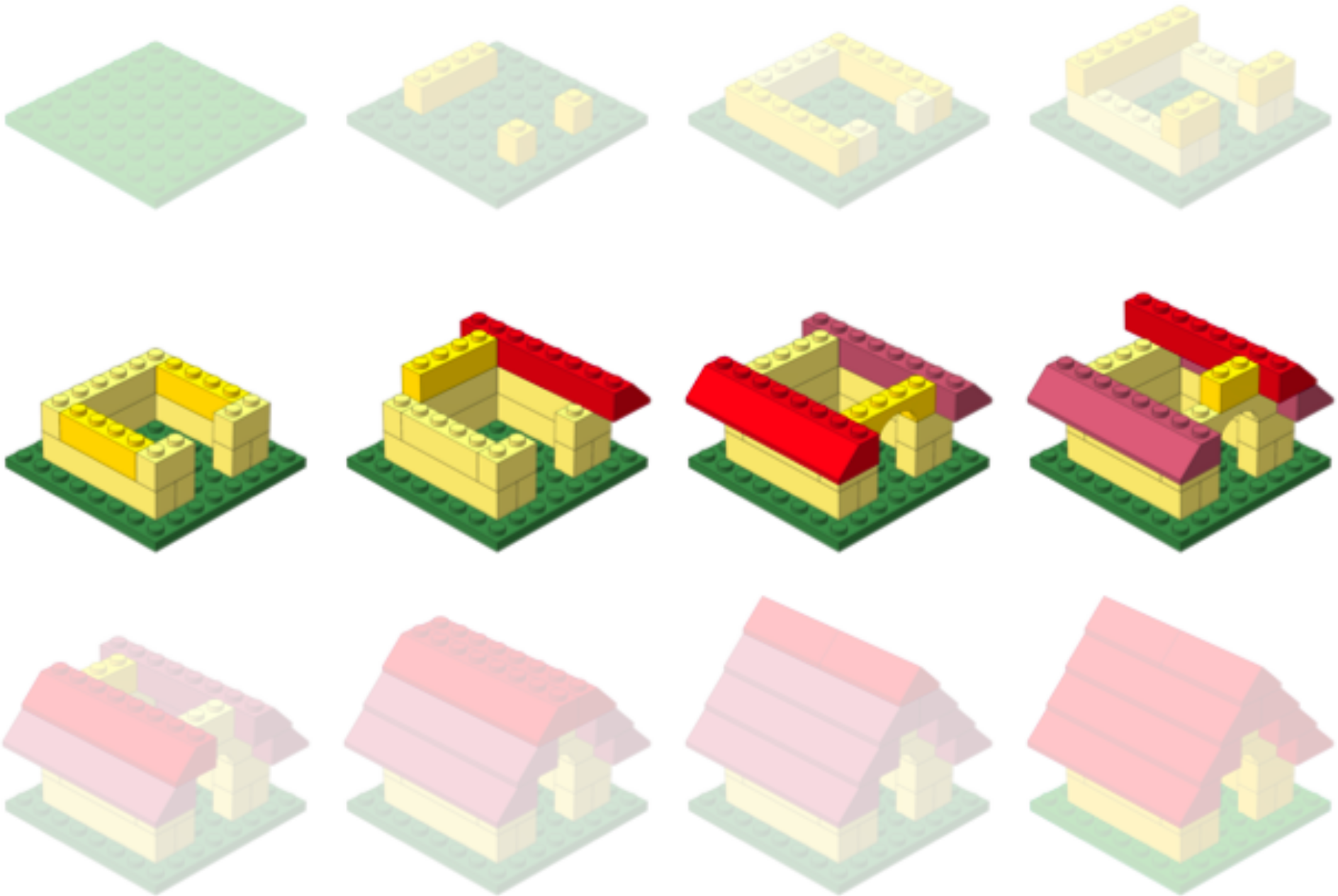
https://tinyurl.com/hbc-dge-online

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/dfhcc-dge-exit

Upcoming free, monthly, 3hr workshops

Introduction to Python

August 28th

1pm - 4pm

Registration link coming soon!

Interested in additional training?

All workshop materials available at:

https://hbctraining.github.io/main

Next DF/HCC workshops:

- R
- scRNA-seq

Office hours

- 30 minute office hours for trainees
- Every other Friday at 10 AM or 10:30 AM
- Sign up form will be emailed to you

Get (stay) in touch with us!

Sign up for our mailing list:

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

Training email: hbctraining@hsph.harvard.edu

Consulting email: bioinformatics@hsph.harvard.edu

Twitter: @bioinfocore