```
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")
```

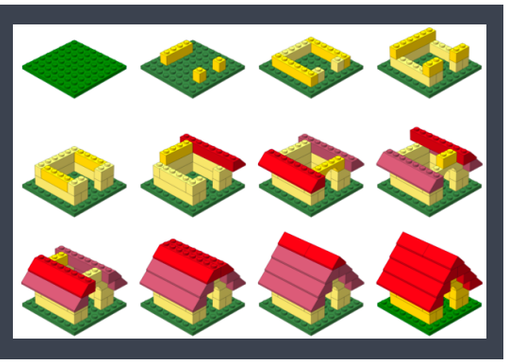
Bulk RNA-seq Analysis Part II

Differential Gene Expression

Harvard Chan Bioinformatics Core

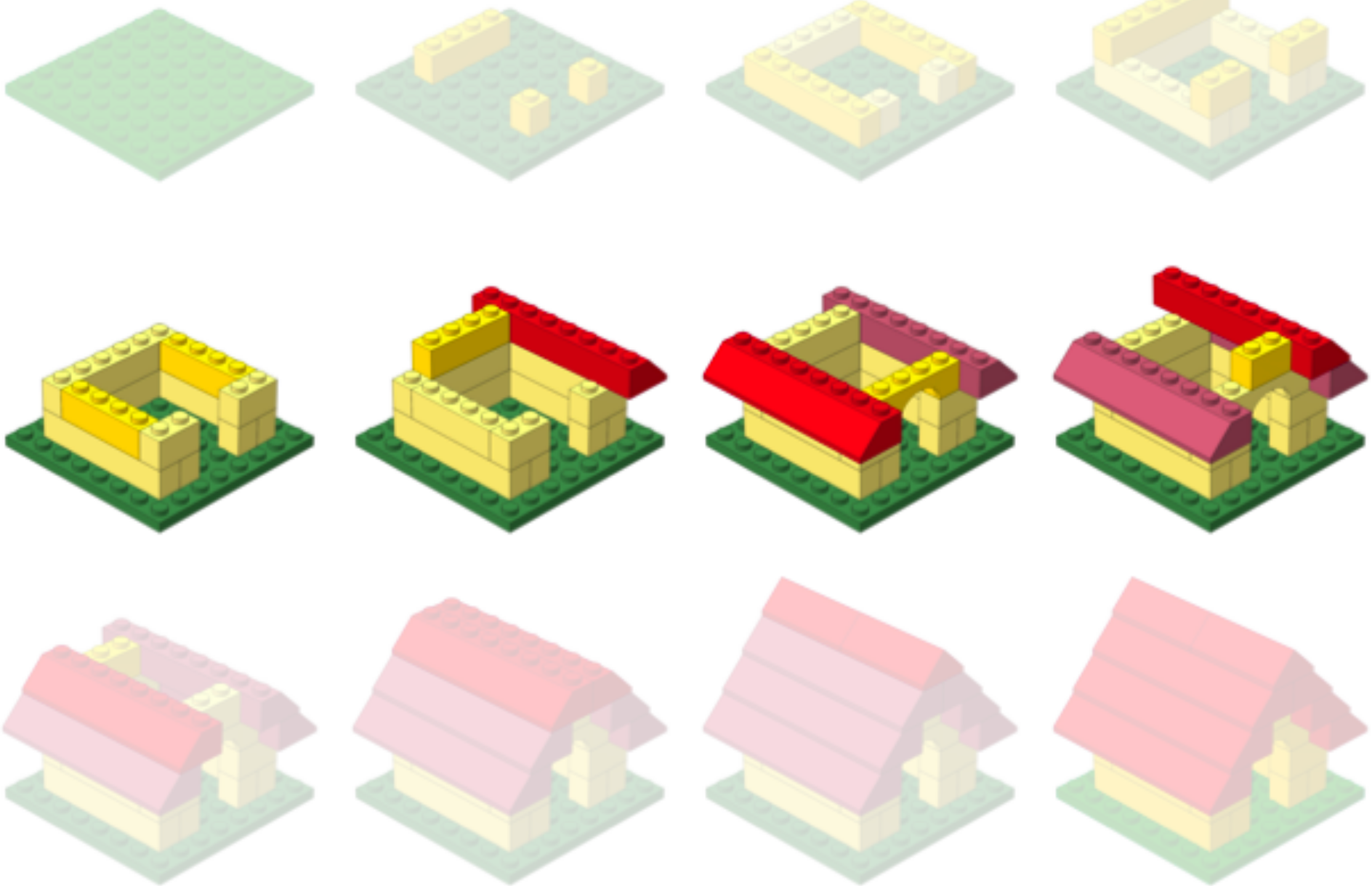
https://tinyurl.com/hbc-dge-online

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

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Sign up for our mailing list:

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

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https://bioinformatics.sph.harvard.edu/current-bioinformatics-topics-workshops

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- Hands-on workshops - be prepared with your MAC or Windows computer
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- HMS Data management -
  - Webpage: https://datamanagement.hms.harvard.edu/
  - Click here to sign up for data management related emails
  - Check out the training schedule for short workshops

- Harvard-wide Research Data Management - https://researchdatamanagement.harvard.edu/

Get (stay) in touch with us!

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Consulting email: bioinformatics@hsph.harvard.edu

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