



```
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")
```

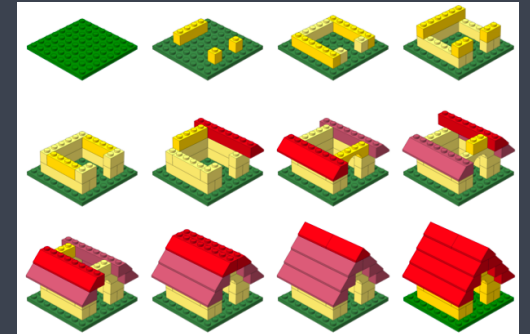
# Bulk RNA-seq Analysis Part II

## *Differential Gene Expression*

Harvard Chan Bioinformatics Core

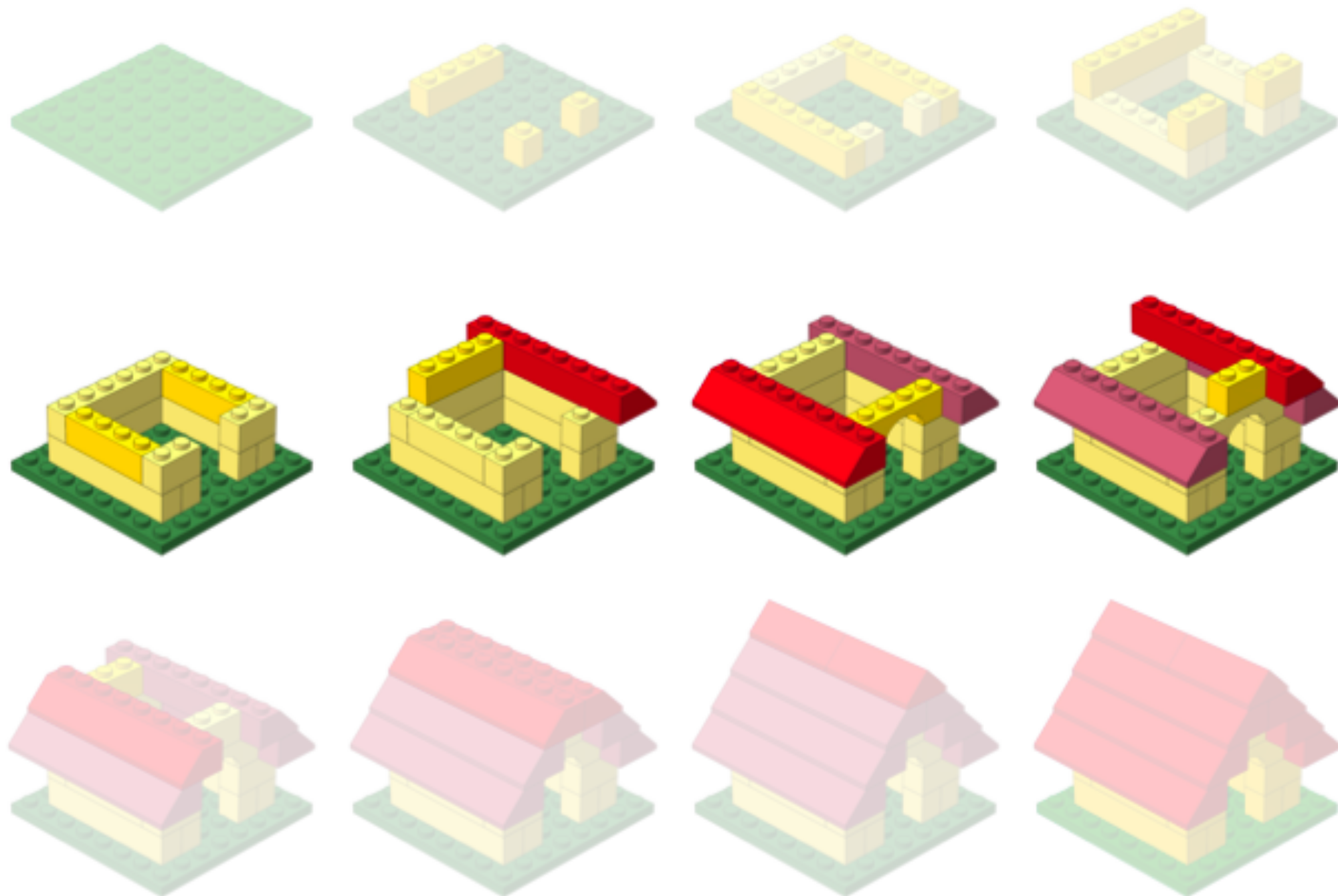
<https://tinyurl.com/hbc-dge-online>

# 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>

# Data Management

- 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/>

# Interested in additional training?

<https://hbctraining.github.io/Training-modules/>

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## Short workshops: Current Topics in Bioinformatics

These workshops are free and open to all researchers at Harvard University and affiliated institutions.

- **Workshops** on bioinformatics methods & related skills.
- Once a month for 3 hours
- Hands-on workshops - be prepared with your MAC or Windows computer
- **Free and open to everyone at Harvard University and its affiliates**
- Will meet the **first Wednesday of the month** (with one exception) **online via Zoom**
- **Sign up at the links below to receive the workshop Zoom link**

# Interested in additional training?

<https://hbctraining.github.io/Training-modules/>

Current Topics in Bioinformatics workshops 2023 Schedule (1pm - 4pm):

Topic and Link(s) to lessons	Prerequisites	Date	Registration
<a href="#">Basics of Python</a>	None	6/21/2023	<a href="#">Sign up!</a>
<a href="#">R Basics</a>	None	7/19/2023	<a href="#">Sign up!</a>
<a href="#">R Intermediate</a>	Beginner R or <a href="#">Online R course - Harvard Catalyst</a>	8/16/2023	<a href="#">Sign up!</a>
<a href="#">Publication Perfect: Part I</a>	Beginner R or <a href="#">Completion of the Intro to R online resource</a>	9/20/2023	Coming soon
<a href="#">Publication Perfect: Part II</a>	<a href="#">Publication Perfect: Part I</a>	10/18/2023	Coming soon
<a href="#">Rmarkdown</a>	Beginner R or <a href="#">Online R course - Harvard Catalyst</a>	11/15/2023	Coming soon



# Data Management Short Workshops

Date	Time	Event	Location
May 31	12pm	<b>Closing Out Your Research: Data Transfer</b>	Zoom (libcal.countway.harvard.edu...)
Jun 7	10am	<b>Intro to Git/GitHub</b>	TMEC 328

<https://datamanagement.hms.harvard.edu/about/news-events/rdmwg-calendar>

# Get (stay) in touch with us!

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