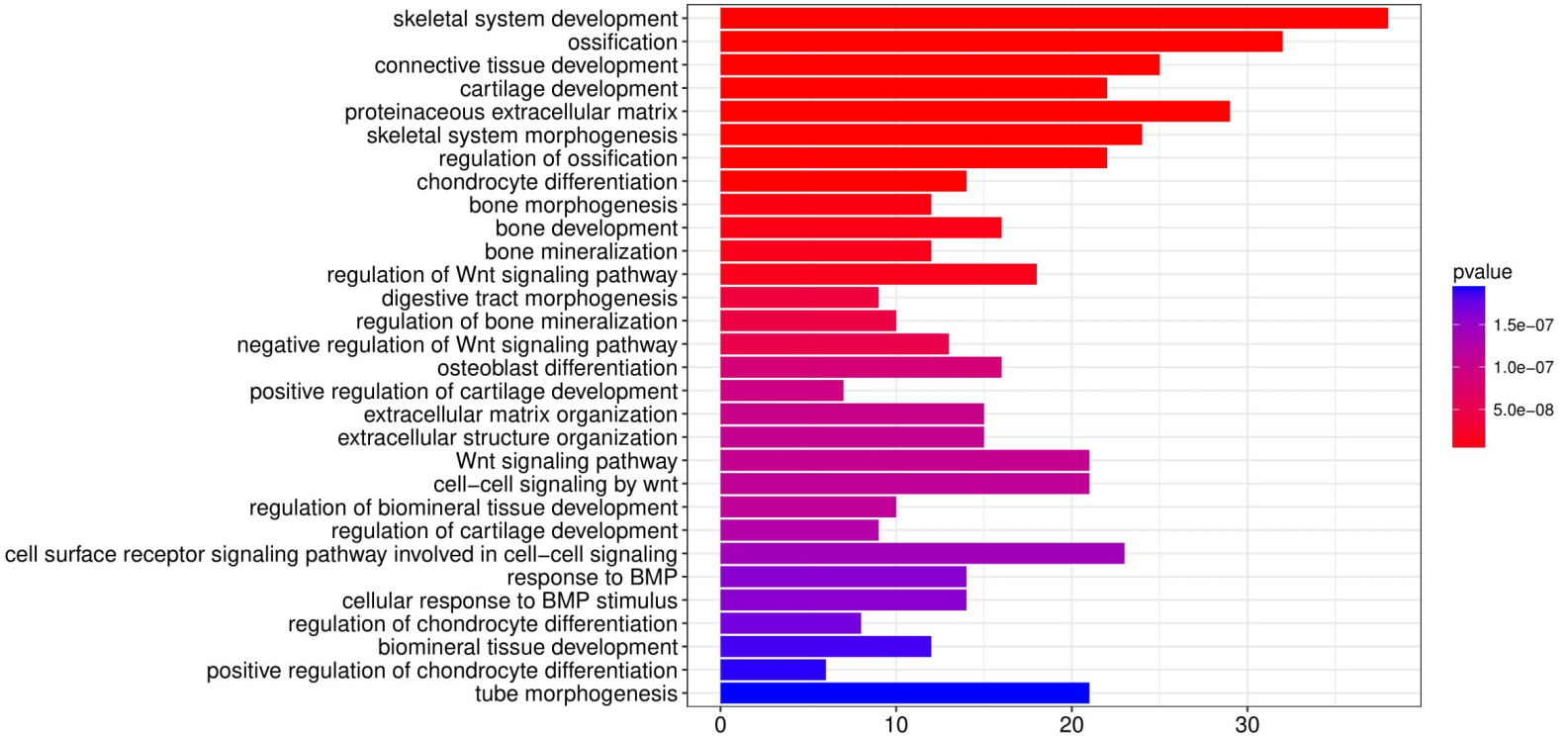
GO enrichment analysis

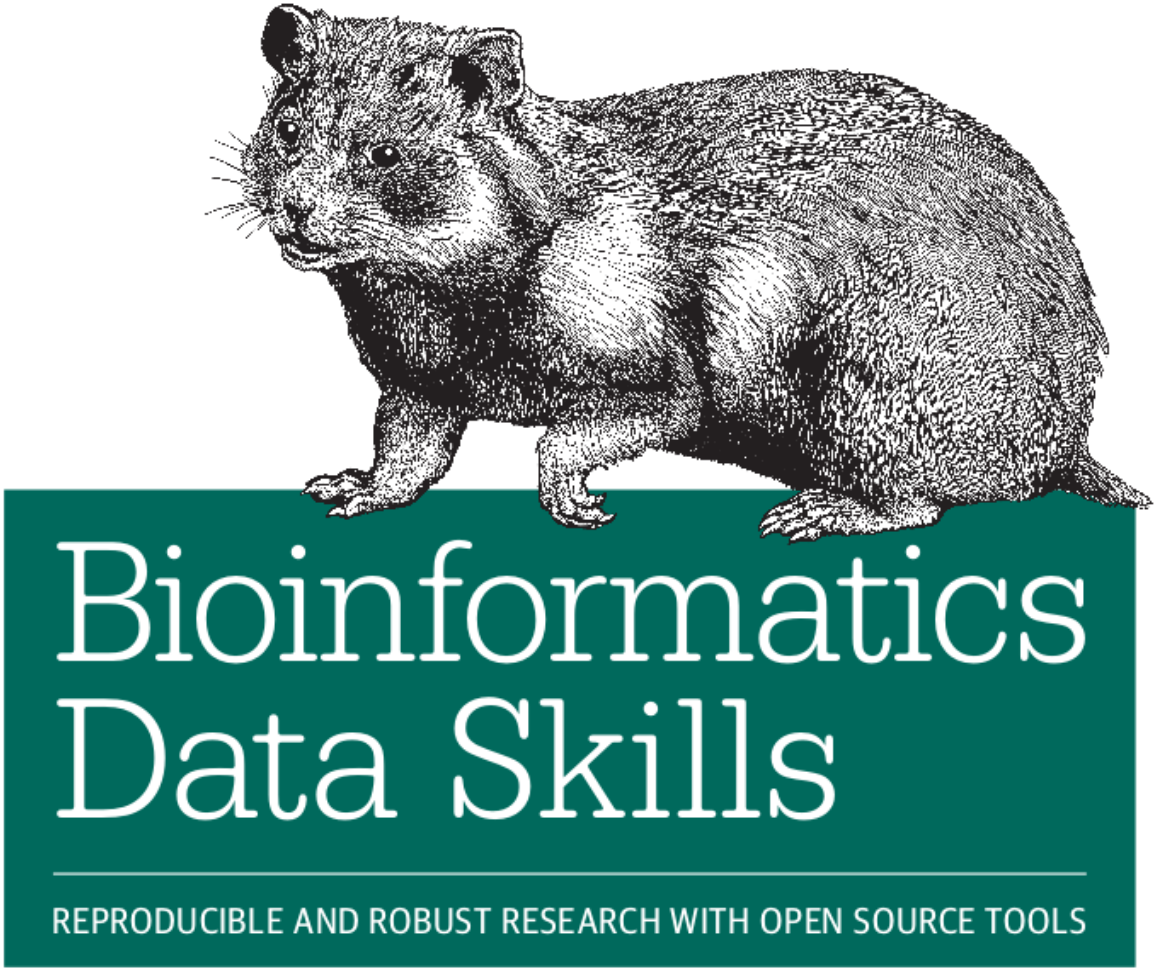
```
library(gProfileR)

de  <-  read.csv("./results/de_results.csv", header = TRUE)

goresults  <-  gprofiler(as.character(de$external_gene_name),
                         organism = "mmusculus",
                         ordered_query = F, significant = T, exclude_iea = F, underrep = F,
                         evcodes = F, region_query = F, max_p_value = 0.05, min_isect_size = 0,
                         correction_method = "gSCS", hier_filtering =  "strong", domain_size = "annotated",
                         #custom_bg = as.character(df_final$external_gene_name),
                         numeric_ns = "", png_fn = NULL, include_graph = F, src_filter = "GO")
```

```
goview <- function(goresults){
ggplot2::ggplot(data=goresults, aes(x=reorder(term.name, -p.value), y=overlap.size,fill=p.value))+
geom_bar(stat="identity")+
scale_fill_gradient2(mid='red', high='blue', space='Lab')+
labs(title="GO enrichment", x ="GO terms", y = "number of genes", fill = "P value")+
theme(plot.title = element_text(hjust = 0.5, size = 12))+
coord_flip()
}
```



Work with range data

Bioinformatics Data Skills



https://github.com/vsbuffalo/bds-files

Course Materials

All materials are available on the Coursera website as well as on the course GitHub page. The materials on the GitHub website will be updated continuously as needed, whereas the materials hosted on Coursera will not change after the course has started.

The course consists of a number of video lecture. Most of the video lectures are supported by a script in R markdown which we render in HTML and we provide the stand-alone R code. We recommend reading these lectures following the HTML links. Changes and improvements to these scripts are welcome at the class GitHub repository.

There is a few number of video lectures supported by slides made in Google Slides. We link to the original slides and provide them in HTML.

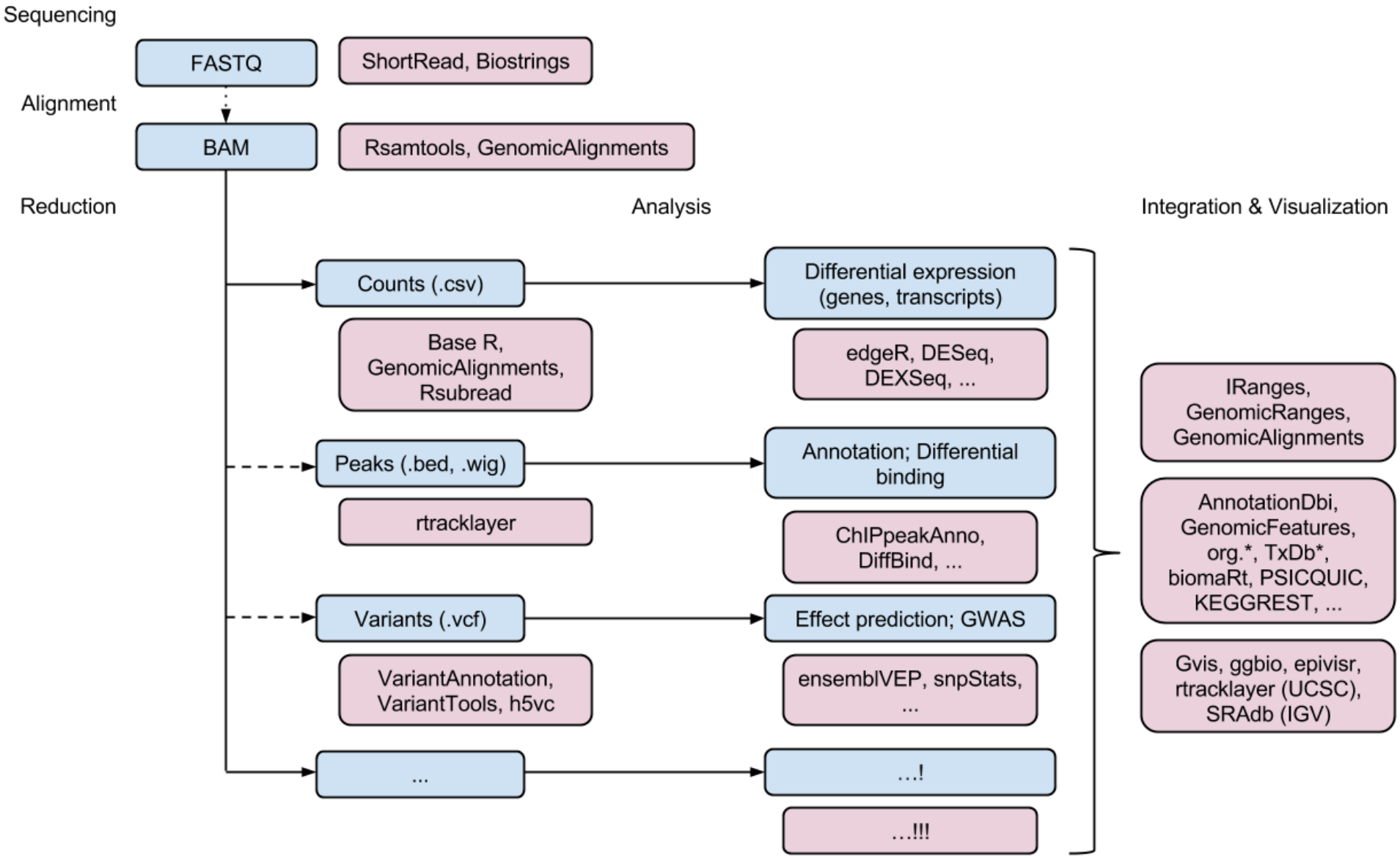
Videos are available both on the Coursera website as well as on Youtube. Links are provided to both locations.

Week 1

N	Lecture	Time	Coursera	Youtube	Material	Code	Source
1	What is Bioconductor	(7:18)	Video	Youtube	PDF	NA	Google Slides
2	Installing Bioconductor	(3:39)	Video	Youtube	HTML	NA	R markdown (On GitHub)
3	The Bioconductor Website	(9:56)	Video	Youtube	HTML	NA	R markdown (On GitHub)
4	Useful Online Resources	(5:08)	Video	Youtube	HTML	NA	R markdown (On GitHub)
5	R Base Types	(18:11)	Video	Youtube	HTML	R code	R markdown (On GitHub)
6	GRanges - Overview	(4:42)	Video	Youtube	PDF	NA	Google Slides
7	IRanges - Basic Usage	(12:12)	Video	Youtube	HTML	R code	R markdown (On GitHub)
8	GenomicRanges - GRanges	(8:44)	Video	Youtube	HTML	R code	R markdown (On GitHub)
9	GenomicRanges - Basic GRanges Usage	(8:14)	Video	Youtube	HTML	R code	R markdown (On GitHub)

http://kasperdanielhansen.github.io/genbioconductor/

Bioconductor



http://bioconductor.org/packages/release/BiocViews.html#___Software