## set the proper directory
setwd(CHANGEME)

## Foreword slide 5
library(IRanges)
?Classes
?Methods
getClass("RleList")
names(completeSubclasses(getClass("XStringSet")))
head(showMethods(classes="RleList",printTo=FALSE))
showMethods("values",includeDefs=TRUE)

## Foreword slide 7
library(GenomicRanges)
library(genomeIntervals)
grngs <- GRanges(seqnames=c("chr1","chr2","chr1"),
ranges=IRanges(start=c(3,4,1),end=c(7,5,3)),
strand=c("+","+","-"),
seqlengths = c("chr1"=24,"chr2"=18))
reduce(grngs)
showMethods(reduce)
search()
detach(package:genomeIntervals)
detach(package:intervals)
showMethods(reduce)
reduce(grngs)

## IRanges slide 17
library(IRanges)
f.list <- showMethods(classes="Rle",printTo=FALSE)
sapply(
   strsplit( f.list[grep("Function",f.list)],' '),
   function(l){gsub('"|:','',l[[2]])}
)

## IRanges slide 20
library(ShortRead)
library(EatonEtAlChIPseq)
fl <- system.file("extdata",
   "GSM424494_wt_G2_orc_chip_rep1_S288C_14.mapview.txt.gz",
   package="EatonEtAlChIPseq")
aln <- readAligned(fl, type = "MAQMapview")
cover <- coverage(aln)
cover
cover[["S288C_14"]]
head(runValue(cover[["S288C_14"]]))
head(runLength(cover[["S288C_14"]]))
as.integer(cover[["S288C_14"]][1:7])
smoothCover <- round(runmean(cover,75,endrule="constant"))
class(smoothCover)
smoothCover
## IRanges slide 21

```r
islands <- slice(smoothCover,lower=10)
islandsWithWidePeaks <- islands[viewMaxs(islands) >= 20L & width(islands) >= 500L]
islandsWithWidePeaks
```

## Biostrings slide 24

```r
library(Biostrings)
getClass("XString")
```

## Biostrings slide 25

```r
data(package="Biostrings")
data(yeastSEQCHR1)
class(yeastSEQCHR1)
nchar(yeastSEQCHR1)
DNAString(yeastSEQCHR1)
alphabet(DNAString(yeastSEQCHR1))
```

## Biostrings slide 26

```r
GENETIC_CODE
AMINO_ACID_CODE
RNA_GENETIC_CODE
IUPAC_CODE_MAP
```

## Biostrings slide 27

```r
names(completeSubclasses(getClass("XStringSet")))
data(srPhiX174)
class(srPhiX174)
srPhiX174
```

## Biostrings slide 28

```r
getSlots("XString")
getSlots("XStringSet")
```

## Biostrings slide 30

```r
alphabetFrequency(DNAString(yeastSEQCHR1))
alphabetFrequency(DNAString(yeastSEQCHR1),baseOnly=TRUE)
dinucleotideFrequency(DNAString(yeastSEQCHR1))
head(trinucleotideFrequency(DNAString(yeastSEQCHR1)),20)
head(oligonucleotideFrequency(DNAString(yeastSEQCHR1),6),14)
```

## Biostrings slide 31

```r
head(narrow(srPhiX174,1,9))
head(reverse(narrow(srPhiX174,1,9)))
head(reverseComplement(narrow(srPhiX174,1,9)))
head(translate(narrow(srPhiX174,1,9)))
alphabetFrequency(chartr("C","T",DNAString(yeastSEQCHR1)),baseOnly=TRUE)
alphabetFrequency(DNAString(yeastSEQCHR1),baseOnly=TRUE)
```

## Biostrings slide 32
snippet <- subseq(head(sort(srPhiX174), 5), 1, 10)
snippet
consensusMatrix(snippet, baseOnly=TRUE)
consensusString(snippet)
consensusString(snippet, ambiguityMap = "N", threshold = 0.5)
?consensusString

## Biostrings slide 33
data(phiX174Phage)
phiX174Phage
geno <- phiX174Phage["NEB03"]
negPhiX174 <- reverseComplement(srPhiX174)
posCounts <- countPDict(PDict(srPhiX174), genome)
negCounts <- countPDict(PDict(negPhiX174), genome)
table(posCounts, negCounts)
macthPDict(PDict(srPhiX174[posCounts > 0]), genome)

## Biostrings slide 34
posScore <- pairwiseAlignment(srPhiX174, genome, type = "global-local",
scoreOnly = TRUE)
negScore <- pairwiseAlignment(negPhiX174, genome, type = "global-local",
scoreOnly = TRUE)
which(pmin(posScore) < pmin(negScore))
pairwiseAlignment(srPhiX174[932], genome, type = "global-local")
pairwiseAlignment(negPhiX174[932], genome, type = "global-local")