A quick overview of the S4 class system

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June 2016
What is S4?

S4 from an end-user point of view

Implementing an S4 class (in 4 slides)

Extending an existing class

What else?
Outline

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The S4 class system

- The *S4 class system* is a set of facilities provided in R for OO programming.
- Implemented in the *methods* package.
- On a fresh *R* session:
  ```r
  > sessionInfo()
  ...
  attached base packages:
  [1] stats graphics grDevices utils datasets
  [6] methods base
  
  R also supports an older class system: the *S3 class system*.
A different world

The syntax

> foo(x, ...)

not:

> x.foo(...)

like in other OO programming languages.

The central concepts

- The core components: classes\(^1\), generic functions and methods
- The glue: method dispatch (supports simple and multiple dispatch)

\(^1\)also called formal classes, to distinguish them from the S3 classes aka old style classes
The result

```r
> ls('package:methods')

[1] "addNextMethod"        "allGenerics"
[3] "allNames"             "Arith"
[5] "as"                   "as<-"
[7] "asMethodDefinition"   "assignClassDef"
...
[211] "testVirtual"         "traceOff"
[213] "traceOn"             "tryNew"
[215] "unRematchDefinition" "validObject"
[217] "validSlotNames"
```

- Rich, complex, can be intimidating
- The classes and methods we implement in our packages can be hard to document, especially when the class hierarchy is complicated and multiple dispatch is used
Heavily used. In BioC 3.3: 3158 classes and 22511 methods defined in 609 packages! (out of 1211 software packages)

Top 10: 128 classes in *ChemmineOB*, 98 in *flowCore*, 79 in *IRanges*, 68 in *rsbml*, 61 in *ShortRead*, 58 in *Biostrings*, 51 in *rtracklayer*, 50 in *oligoClasses*, 45 in *flowUtils*, and 40 in *BaseSpaceR*.

For the end-user: it's mostly transparent. But when something goes wrong, error messages issued by the S4 class system can be hard to understand. Also it can be hard to find the documentation for a specific method.

Most Bioconductor packages use only a small subset of the S4 capabilities (covers 99.99% of our needs)
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Where do S4 objects come from?

From a dataset

```r
> library(graph)
> data(apopGraph)
> apopGraph

A graphNEL graph with directed edges
Number of Nodes = 50
Number of Edges = 59
```

From using an object constructor function

```r
> library(IRanges)
> IRanges(start=c(101, 25), end=c(110, 80))

IRanges object with 2 ranges and 0 metadata columns:

<table>
<thead>
<tr>
<th>start</th>
<th>end</th>
<th>width</th>
</tr>
</thead>
<tbody>
<tr>
<td>101</td>
<td>110</td>
<td>10</td>
</tr>
<tr>
<td>25</td>
<td>80</td>
<td>56</td>
</tr>
</tbody>
</table>
```
From a coercion

```r
> library(Matrix)
> m <- matrix(3:-4, nrow=2)
> as(m, "Matrix")
```

2 x 4 Matrix of class "dgeMatrix"

```
[1,]  3  1 -1  -3
[2,]  2  0 -2  -4
```

From using a specialized high-level constructor

```r
> library(GenomicFeatures)
> makeTxDbFromUCSC("sacCer2", tablename="ensGene")
```

TxDb object:

```
# Db type: TxDb
# Supporting package: GenomicFeatures
# Data source: UCSC
# Genome: sacCer2
# Organism: Saccharomyces cerevisiae
# Taxonomy ID: 4932
# UCSC Table: ensGene
# UCSC Track: Ensembl Genes
...```
From using a high-level I/O function

```r
> library(ShortRead)
> path_to_my_data <- system.file(  
+   package="ShortRead",  
+   "extdata", "Data", "C1-36Firecrest", "Bustard", "GERALD")
> lane1 <- readFastq(path_to_my_data, pattern="s_1_sequence.txt")
> lane1

class: ShortReadQ
length: 256 reads; width: 36 cycles

Inside another object

```r
> sread(lane1)

A DNAStringSet instance of length 256
   width  seq
[1] 36 GGACTTTGTAGGATACCCTCGCTTTCCTCCTGT
[2] 36 GATTTCTTACCTATTAGTGGTTGAACAGCATCGGAC
[3] 36 GCGGTGGTCTATAGTGTTATTAATATCAATTTGGGT
[4] 36 GTTACCATGATGTTATTTCTTCATTTGGAGGTAAAA
[5] 36 GTATGTTTCTCCTGCTTATCACCTTCTTGAAGGCTT
...  ...  ...
[252] 36 GTTTAGATATGAGTGATACACATTGTGTTTGATGGTAGAGT
[253] 36 GTTTTACAGACACCTAAAGCTACATCGTCAACGTTA
How to manipulate S4 objects?

Low-level: getters and setters

```r
> ir <- IRanges(start=c(101, 25), end=c(110, 80))
> width(ir)

[1] 10 56

> width(ir) <- width(ir) - 5
> ir

IRanges object with 2 ranges and 0 metadata columns:

<table>
<thead>
<tr>
<th>start</th>
<th>end</th>
<th>width</th>
</tr>
</thead>
<tbody>
<tr>
<td>101</td>
<td>105</td>
<td>5</td>
</tr>
<tr>
<td>25</td>
<td>75</td>
<td>51</td>
</tr>
</tbody>
</table>
```

High-level: plenty of specialized methods

```r
> qa1 <- qa(lane1, lane="lane1")
> class(qa1)

[1] "ShortReadQQA"
attr(,"package")
[1] "ShortRead"
```
How to find the right man page?

- `class?graphNEL` or equivalently `?`graphNEL-class` for accessing the man page of a class

- `?qa` for accessing the man page of a generic function

- The man page for a generic might also document some or all of the methods for this generic. The `See Also:` section might give a clue. Also using `showMethods()` can be useful:

  ```r
  > showMethods("qa")
  
  Function: qa (package ShortRead)
  dirPath="ShortReadQ"
  dirPath="SolexaPath"
  dirPath="character"
  dirPath="list"
  ```

- `?qa,ShortReadQ-method` to access the man page for a particular method (might be the same man page as for the generic)

- In doubt: `??qa` will search the man pages of all the installed packages and return the list of man pages that contain the string `qa`
Inspecting objects and discovering methods

- class() and showClass()

```r
> class(lane1)
[1] "ShortReadQ"
attr(,"package")
[1] "ShortRead"

> showClass("ShortReadQ")
Class "ShortReadQ" [package "ShortRead"]

Slots:

Name: quality sread id
Class: QualityScore DNAStringSet BStringSet

Extends:
Class "ShortRead", directly
Class ".ShortReadBase", by class "ShortRead", distance 2

Known Subclasses: "AlignedRead"
```

- str() for compact display of the content of an object
- showMethods() to discover methods
- selectMethod() to see the code
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Class definition and constructor

Class definition

```r
> setClass("SNPLocations",
+   slots=c(
+     genome="character", # a single string
+     snpid="character", # a character vector of length N
+     chrom="character", # a character vector of length N
+     pos="integer"     # an integer vector of length N
+   )
+ )
```

Constructor

```r
> SNPLocations <- function(genome, snpid, chrom, pos)
+   new("SNPLocations", genome=genome, snpid=snpid, chrom=chrom, pos=pos)

> snplocs <- SNPLocations("hg19",
+   c("rs0001", "rs0002"),
+   c("chr1", "chrX"),
+   c(224033L, 1266886L))
```
Getters

Defining the `length` method

```r
> setMethod("length", "SNPLocations", function(x) length(x@snpid))
> length(snplocs)  # just testing
[1] 2
```

Defining the slot getters

```r
> setGeneric("genome", function(x) standardGeneric("genome"))
> setMethod("genome", "SNPLocations", function(x) x@genome)

> setGeneric("snpid", function(x) standardGeneric("snpid"))
> setMethod("snpid", "SNPLocations", function(x) x@snpid)

> setGeneric("chrom", function(x) standardGeneric("chrom"))
> setMethod("chrom", "SNPLocations", function(x) x@chrom)

> setGeneric("pos", function(x) standardGeneric("pos"))
> setMethod("pos", "SNPLocations", function(x) x@pos)

> genome(snplocs)  # just testing
[1] "hg19"

> snpid(snplocs)  # just testing
[1] "rs0001" "rs0002"
```
Defining the `show` method

```r
> setMethod("show", "SNPLocations",
+   function(object)
+       cat(class(object), "instance with", length(object),
+           "SNPs on genome", genome(object), "\n")
+ )
```

```r
> snplocs  # just testing

SNPLocations instance with 2 SNPs on genome hg19
```

Defining the `validity` method

```r
> setValidity("SNPLocations",
+   function(object) {
+     if (!is.character(genome(object)) ||
+         length(genome(object)) != 1 || is.na(genome(object)))
+       return("'genome' slot must be a single string")
+     slot_lengths <- c(length(snpid(object)),
+                       length(chrom(object)),
+                       length(pos(object)))
+     if (length(unique(slot_lengths)) != 1)
+       return("lengths of slots 'snpid', 'chrom' and 'pos' differ")
+     TRUE
+   }
+ )
```

```r
> snplocs@chrom <- LETTERS[1:3]  # a very bad idea!
> validObject(snplocs)

Error in validObject(snplocs) :
  invalid class "SNPLocations" object: lengths of slots 'snpid', 'chrom' and 'pos' differ
```
Defining slot setters

```r
> setGeneric("chrom<-", function(x, value) standardGeneric("chrom<-"))
> setReplaceMethod("chrom", "SNPLocations",
+    function(x, value) {x@chrom <- value; validObject(x); x})
> chrom(snplocs) <- LETTERS[1:2]  # repair currently broken object
> chrom(snplocs) <- LETTERS[1:3]  # try to break it again
Error in validObject(x) :
  invalid class "SNPLocations" object: lengths of slots 'snpid', 'chrom'
  and 'pos' differ
```

Defining a coercion method

```r
> setAs("SNPLocations", "data.frame",
+    function(from)
+    data.frame(snpid=snpid(from), chrom=chrom(from), pos=pos(from))
+ )
> as(snplocs, "data.frame")  # testing

   snpid chrom  pos
1 rs0001    A 224033
2 rs0002    B 1266886
```
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Slot inheritance

- Most of the time (but not always), the child class will have additional slots:
  ```r
  > setClass("AnnotatedSNPs",
  +   contains="SNPLocations",
  +   slots=c(
  +     geneid="character"  # a character vector of length N
  +   )
  + )
  ```

- The slots from the parent class are inherited:
  ```r
  > showClass("AnnotatedSNPs")
  
  Class "AnnotatedSNPs" [in ".GlobalEnv"]

  Slots:

  Name:  geneid   genome   snpid   chrom   pos
  Class:  character character character character integer

  Extends: "SNPLocations"

- Constructor:
  ```r
  > AnnotatedSNPs <- function(genome, snpid, chrom, pos, geneid)
  + { 
  +   new("AnnotatedSNPs",
  +       SNPLocations(genome, snpid, chrom, pos),
  +       geneid=geneid)
  + }
Method inheritance

Let’s create an AnnotatedSNPs object:
```r
> snps <- AnnotatedSNPs("hg19",
+ c("rs0001", "rs0002"),
+ c("chr1", "chrX"),
+ c(224033L, 1266886L),
+ c("AAU1", "SXW-23"))
```

All the methods defined for SNPLocations objects work out-of-the-box:
```r
> snps
AnnotatedSNPs instance with 2 SNPs on genome hg19
```

But sometimes they don’t do the right thing:
```r
> as(snps, "data.frame") # the 'geneid' slot is ignored

   snpid chrom  pos
1     rs0001 chr1 224033
2     rs0002 chrX 1266886
```
Being a SNPLocations object vs being a SNPLocations instance:

> is(snps, "AnnotatedSNPs")  # 'snps' is an AnnotatedSNPs object
[1] TRUE

> is(snps, "SNPLocations")   # and is also a SNPLocations object
[1] TRUE

> class(snps)                # but is *not* a SNPLocations *instance*
[1] "AnnotatedSNPs"
attr("package")
[1] ".GlobalEnv"

Method overriding: for example we could define a show method for AnnotatedSNPs objects. `callNextMethod` can be used in that context to call the method defined for the parent class from within the method for the child class.

Automatic coercion method:

> as(snps, "SNPLocations")
SNPLocations instance with 2 SNPs on genome hg19
The validity method for AnnotatedSNPs objects only needs to validate what's not already validated by the validity method for SNPLocations objects:

```r
> setValidity("AnnotatedSNPs",
+ function(object) {
+     if (length(object@geneid) != length(object))
+         return("'geneid' slot must have the length of the object")
+     TRUE
+ }
+ )
```

In other words: before an AnnotatedSNPs object can be considered valid, it must first be a valid SNPLocations object.
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Other important S4 features

- Virtual classes: equivalent to abstract classes in Java
- Class unions (see `?setClassUnion`)
- Multiple inheritance: a powerful feature that should be used with caution. If used inappropriately, can lead to a class hierarchy that is very hard to maintain

Resources

- The Extending RangedSummarizedExperiment section of the SummarizedExperiment vignette in the SummarizedExperiment package.
- Note: S4 is not covered in the An Introduction to R or The R language definition manuals\(^2\)
- The Writing R Extensions manual for details about integrating S4 classes to a package
- The R Programming for Bioinformatics book by Robert Gentleman\(^3\)

\(^2\)http://cran.fhcrc.org/manuals.html
\(^3\)http://bioconductor.org/help/publications/books/r-programming-for-bioinformatics/