Microarray Informatics at the EBI

Alvis Brazma Group

BIOCEP Project

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Grant's Principal Investigators: Wolfgang Huber, Misha Kapushesky

What do we need ?

- Provide tools and frameworks for Bioconductor packages automatic exposure as Web Services

- Provide a scalable, robust architecture for R integration within ArrayExpress Warehouse and Expression Profiler

State of the art

- **SJava and rJava/JRI**
  - Basic mapping via JNI of the R C API
- **TypeInfo**
  - Plug meta descriptions to R functions
- **RWebservices**
  - Generated Java Beans for basic R Types / S4 Classes
  - Axis Web Services based on SJava and ActiveMQ
- **JavaGD**
  - R devices connection to Java (JGR)
- **Rserve**
  - TCP/IP interface to R

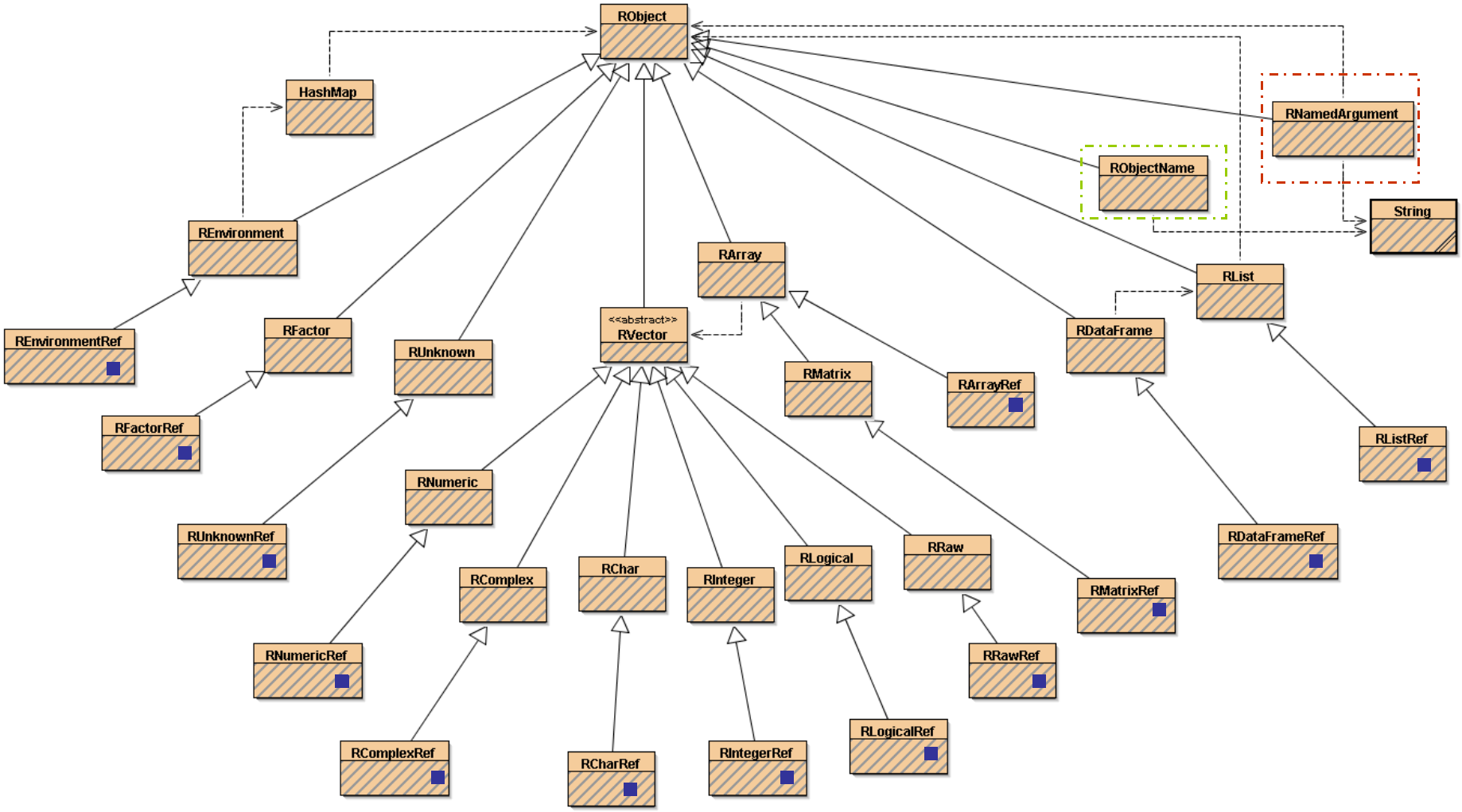
What is missing ?

- High Level Java API for Accessing R
- Stateful, Resuable, Remotable R Components
- Scalable, Distributed, R Based Infrastructure
- Safe multiple clients framework for components usage as a pool of indistinguishable Remote Resources
- User friendly Interface for the remote resources creation, tracking and debugging

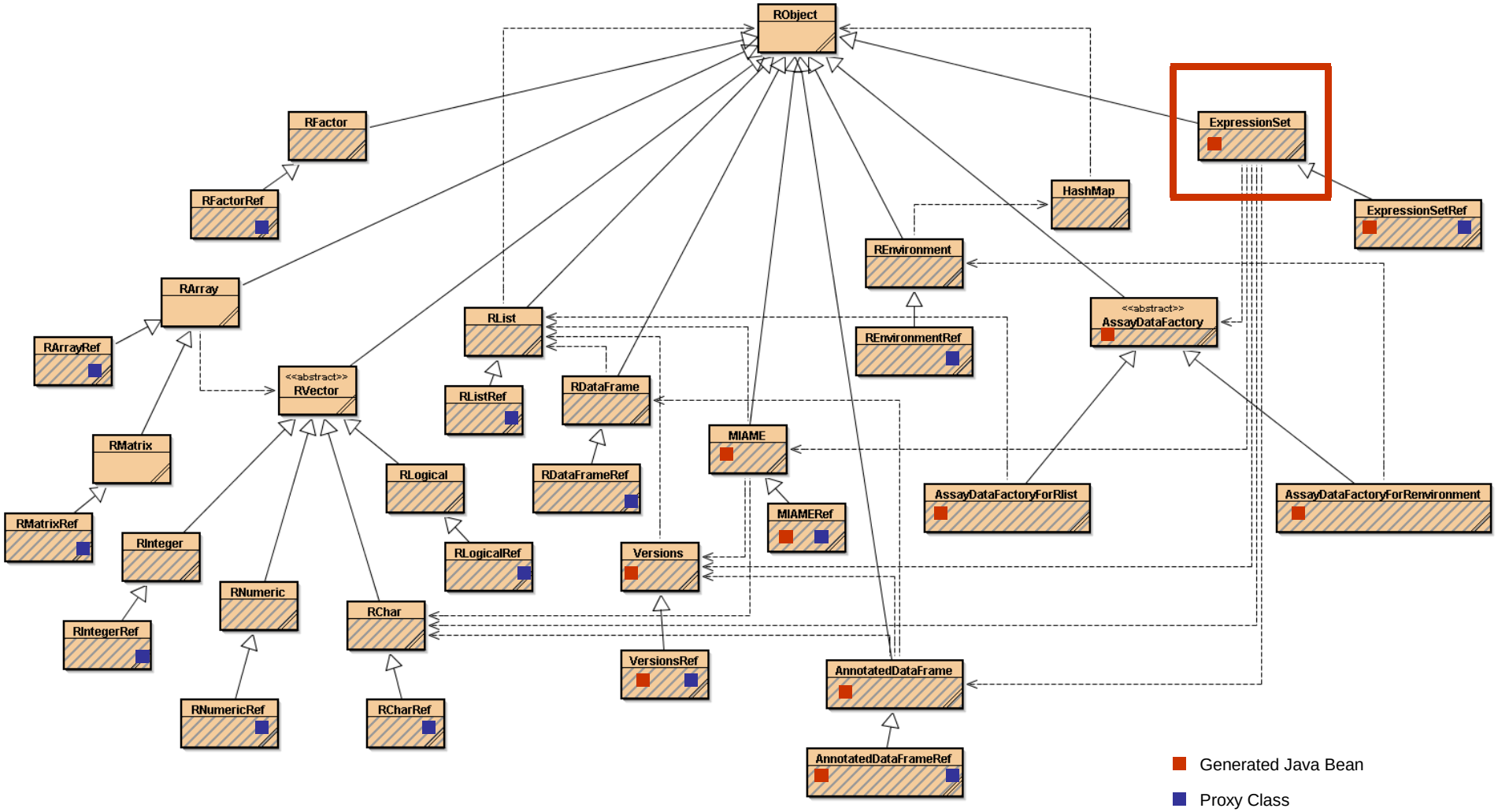
What is missing ?

- Generated light-weight Java proxies for R Types / S4 Classes
- On-demand mapping and deployment of R pacakges as RMI Components or as JAX-WS Web Services
- Remotable R Graphics / Swing Components for R
- Remote R components files exchange API
- Semi-thick client (applet) for web based tools using R

Standard R objects mapping to Java



Generated beans for ExpressionSet



High Level API for Accessing R

public interface RServices extends ManagedServant {

public String evaluate(String expression) throws RemoteException;
...
public RObject call(String methodName, RObject... args) throws RemoteException;
...
public RObject callAsReference(String methodName, RObject... args) throws RemoteException;
...
public RObject evalAndGetObject(String expression) throws RemoteException;
...
public RObject evalAndGetObjectAsReference(String expression) throws RemoteException;
...
public RObject putObjectAndGetReference(RObject obj) throws RemoteException;
...
public void putObjectAndAssignName(RObject obj, String name) throws RemoteException;
...
public RPackage getPackage(String packageName) throws RemoteException;
...
public void setCallBack(RCallback callback) throws RemoteException;
...
public GDDevice newDevice(int w, int h) throws java.rmi.RemoteException;
...
public byte[] readWorkingDirectoryFileBlock(String fileName, long offset, int blocksize) ..
...
public String getStatus() throws RemoteException;
...

Remote Resource Pool Framework

- Generic Standalone framework
- Pooling of any RMI components and if combined with JNI of any library / open architecture

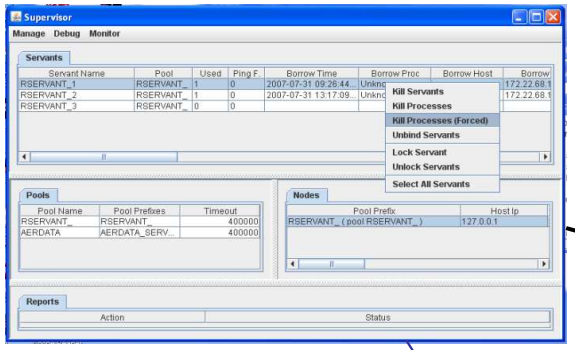
- New Remote Object Registry based on Derby | Oracle | MySql

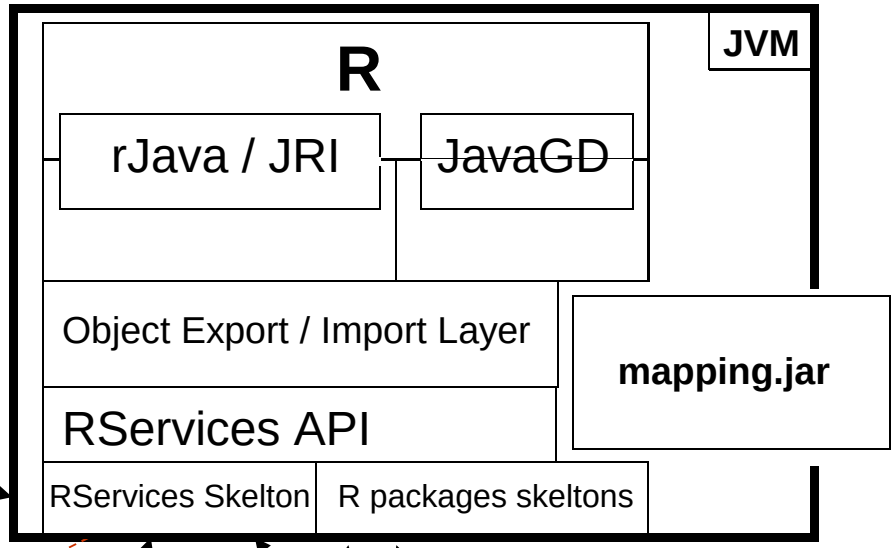
- Three implementations available
  - rmiregistry / mono-node / single client process
  - rmiregistry / multinodes / single client process
  - database ROR / multinodes / multiple client processes

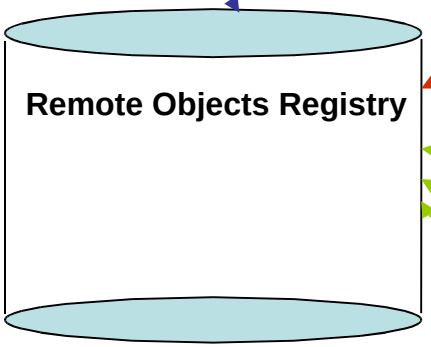
- User friendly interface for the remote resources creation, tracking and debugging, nodes and pools management

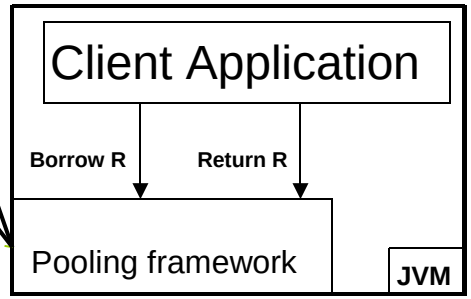
Architecture I

Supervisor

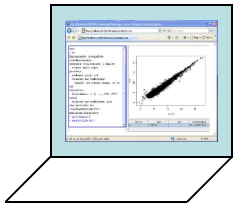




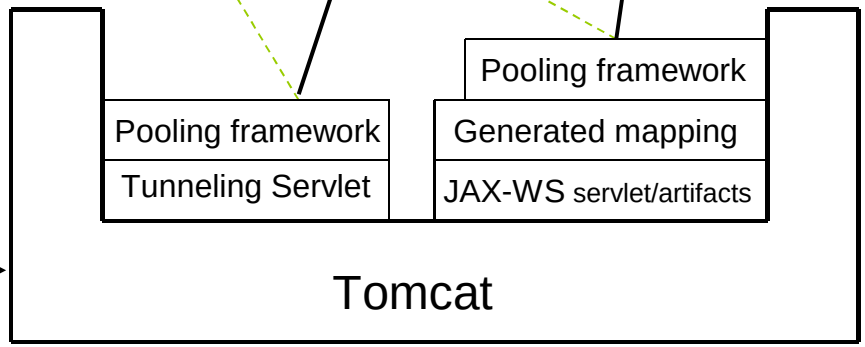




Web Browser (java plugins (applet))



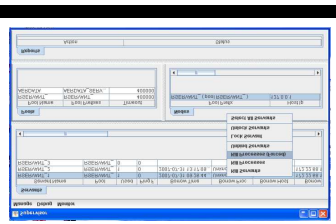
Http Tunneling



SOAP

.NET, Perl..
Application

Architecture II



Remote Objects Registry

Pooling framework
Tunneling Servlet
Generated mapping
JAX-WS servlet/artifacts
Tomcat

Node 1 : 64 bits machine / Linux

Node 2 : Windows XP

Node 3 : Mac OS

R
rJava / JRI
JavaGD
Object Export / Import Layer
RServices API
mapping.jar
RServices Skelton
R packages skeltons
JVM

Parallel Computing

```
final double[][] m=..;
Future<Double>[] result=new Future[m.length];
ExecutorService exec = Executors.newFixedThreadPool(50);
for (int i=0; i<result.length; ++i) {
        final double[] v=m[i];
        result[i]= exec.submit(
    new Callable<Double>() {
        public Double call() throws Exception {
          RServices r=null;
          try {
            r=(RServices)ServantProviderFactory.getFactory().getServantProvider().borrowServantProxy();
            Rnumeric mean=(RNumeric)r.call("mean", new RNumeric(v));
            return mean.getValue()[0];
          } finally { ServantProviderFactory.getFactory().getServantProvider().returnServantProxy(r); }
        }
    });
}
while(true) {
        int count=0; for (int i=0; i<result.length; ++i) if (result[i].isDone()) ++count; if (count==result.length) break;
        Thread.sleep(100);
}
for (int i=0; i<result.length; ++i) System.out.println(result[i].get());
```

Web Services Generation

Script / globals.r

```
square ← function(x) {return(x^2) }
typeInfo(square) ← SimultaneousTypeSpecification(
TypedSignature(x = "numeric"), returnType = "numeric")
```

Script / rjmap.xml

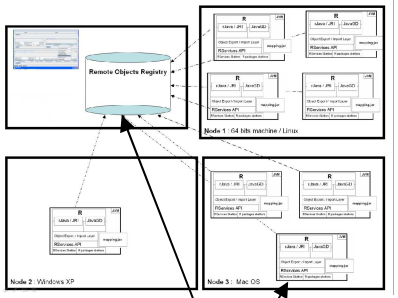
```
<rj>
  <publish>
    <functions> <function name="square" forWeb="true"/> </functions>
  </publish>
  <scripts>  <initScript name="globals.r" embed="true"/> </scripts>
</rj>
```

ant demogen

mapping.war

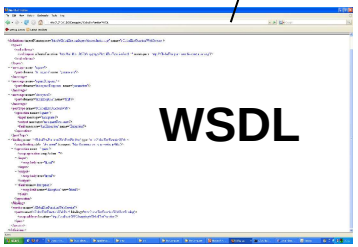
+ mapping.jar
+ pooling framework
+ R Java Bridge
+ **JAX-WS**
  - Servlets
  - Generated artifacts

Deploy

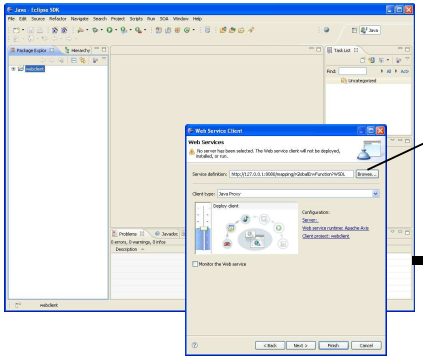


mapping.war

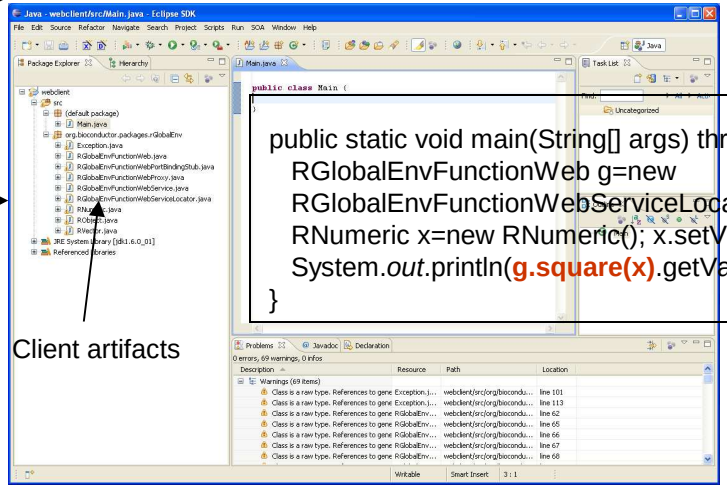
tomcat



http://127.0.0.1:8080/mapping/rGlobalEnvFunction?WSDL



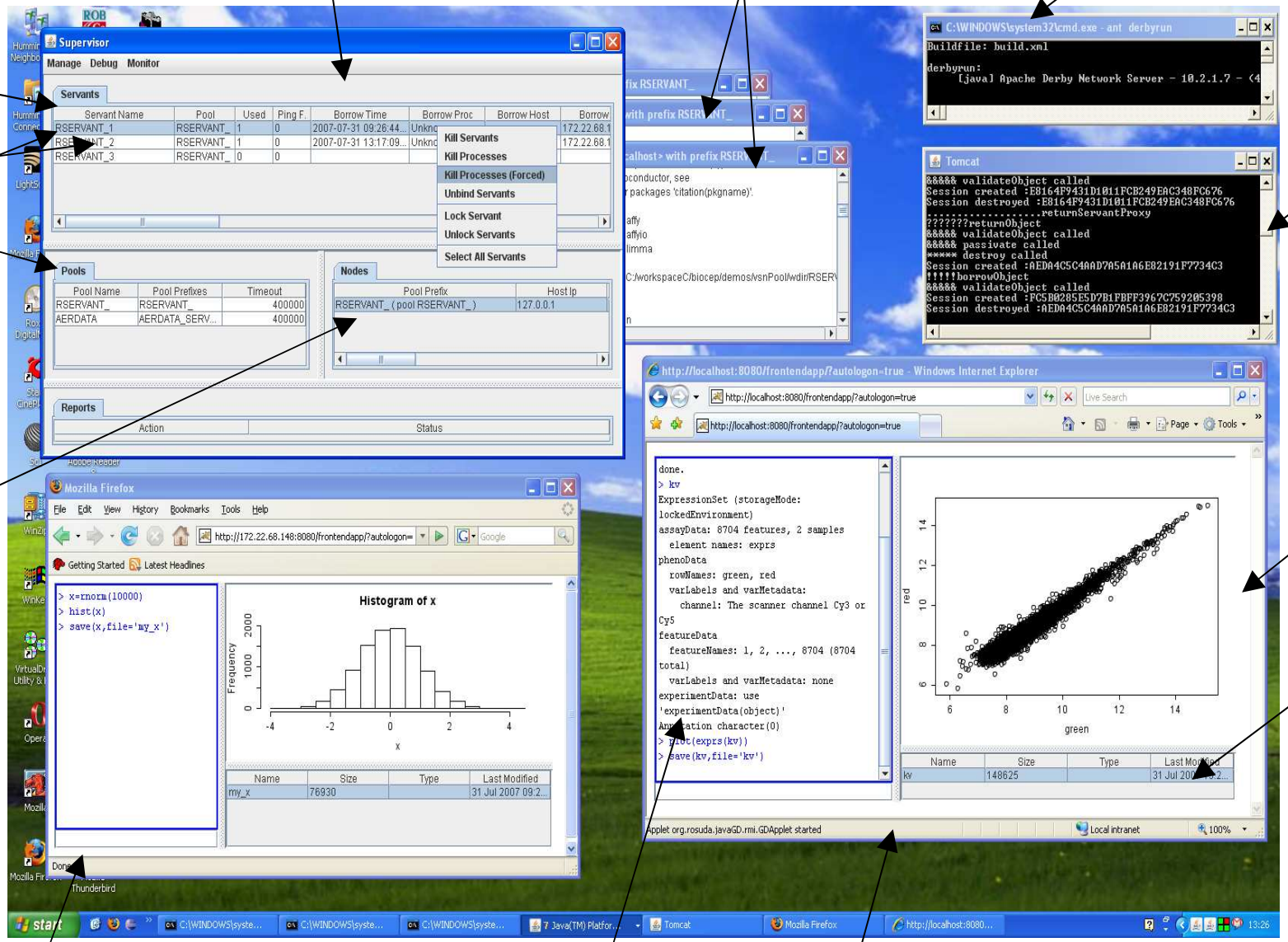
Eclipse Web Service Client Generator



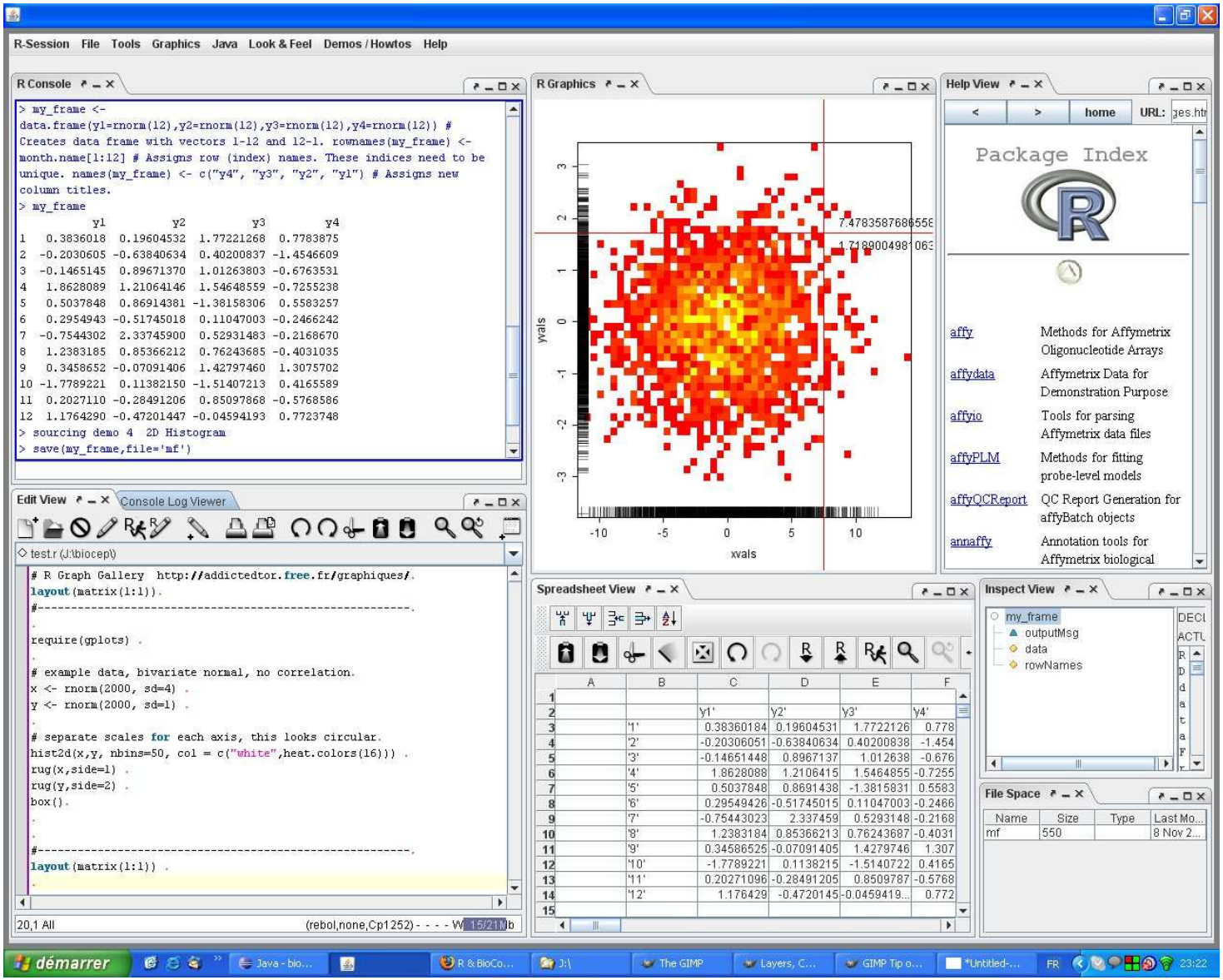
Client artifacts

```
public static void main(String[] args) throws Exception {
   RGlobalEnvFunctionWeb g=new
   RGlobalEnvFunctionWebServiceLocator().getrGlobalEnvFunctionWebPort();
   RNumeric x=new RNumeric(); x.setValue(new Double[]{6.0});
   System.out.println(g.square(x).getValue()[0]);
}
```

Virtualization of R



Virtual R Workbench



Acknowlegments

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R O.O. Programming in a nutshell

- S4 supports : objects / classes / inheritance / polymorhpism

Example

- setClass("Point", representation(x="numeric", y="numeric"))
- setClass("StyledPoint", contains="Point", representation(style="integer"))
- setGeneric("distance", **function**(p1,p2) standardGeneric("distance"))
- setMethod("distance", signature("Point", "Point") ,
  function(p1, p2) { sqrt((p2@x-p1@x)^2 + (p2@y-p1@y)^2) })
- O<-new ("Point", x=12,y=2); P<-new("Point", x=52, y=90)
- distance(O,P)

Introspection functions

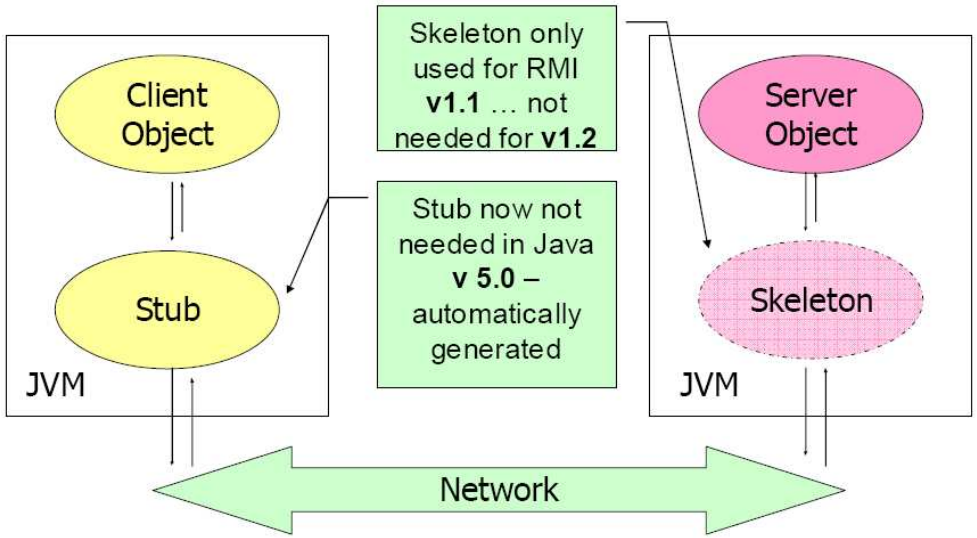
- class(P) / getClass("Point“) / getSlots(“Point“) / ..
- showMethods(class = "Point") / showMethods("distance") / isGeneric ("distance") / ..
- extends("StyledPoint") / ..

Unions

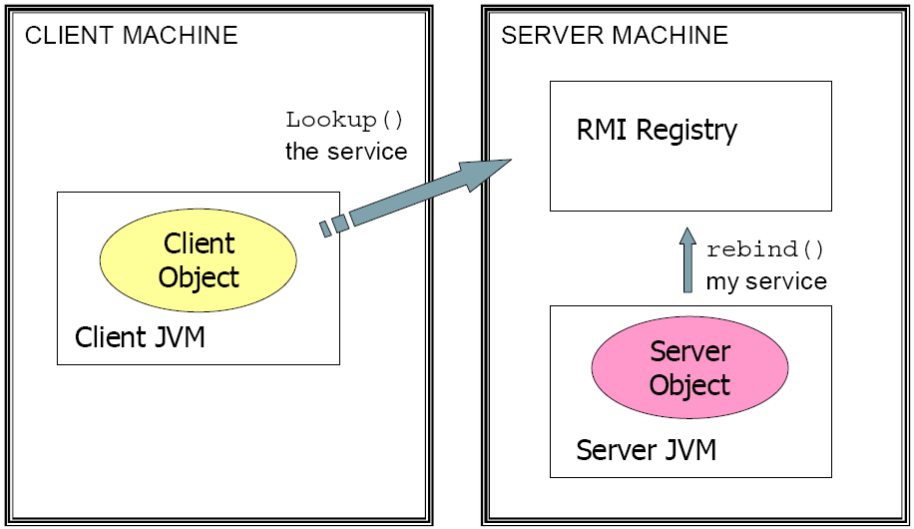
setClass("Egg", representation(color="integer")); setClassUnion("Thing", c("Point","Egg"));

RMI in a nutshell

How does RMI work ? Stubs and Skeletons



RMI Registry



Functions Mapping

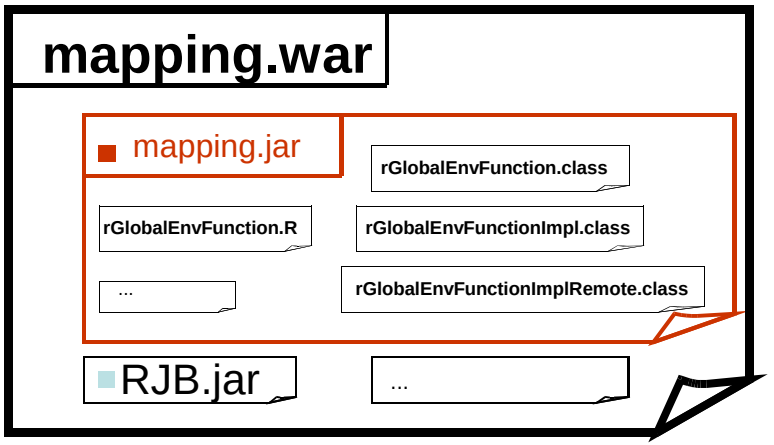
Script / globals.r

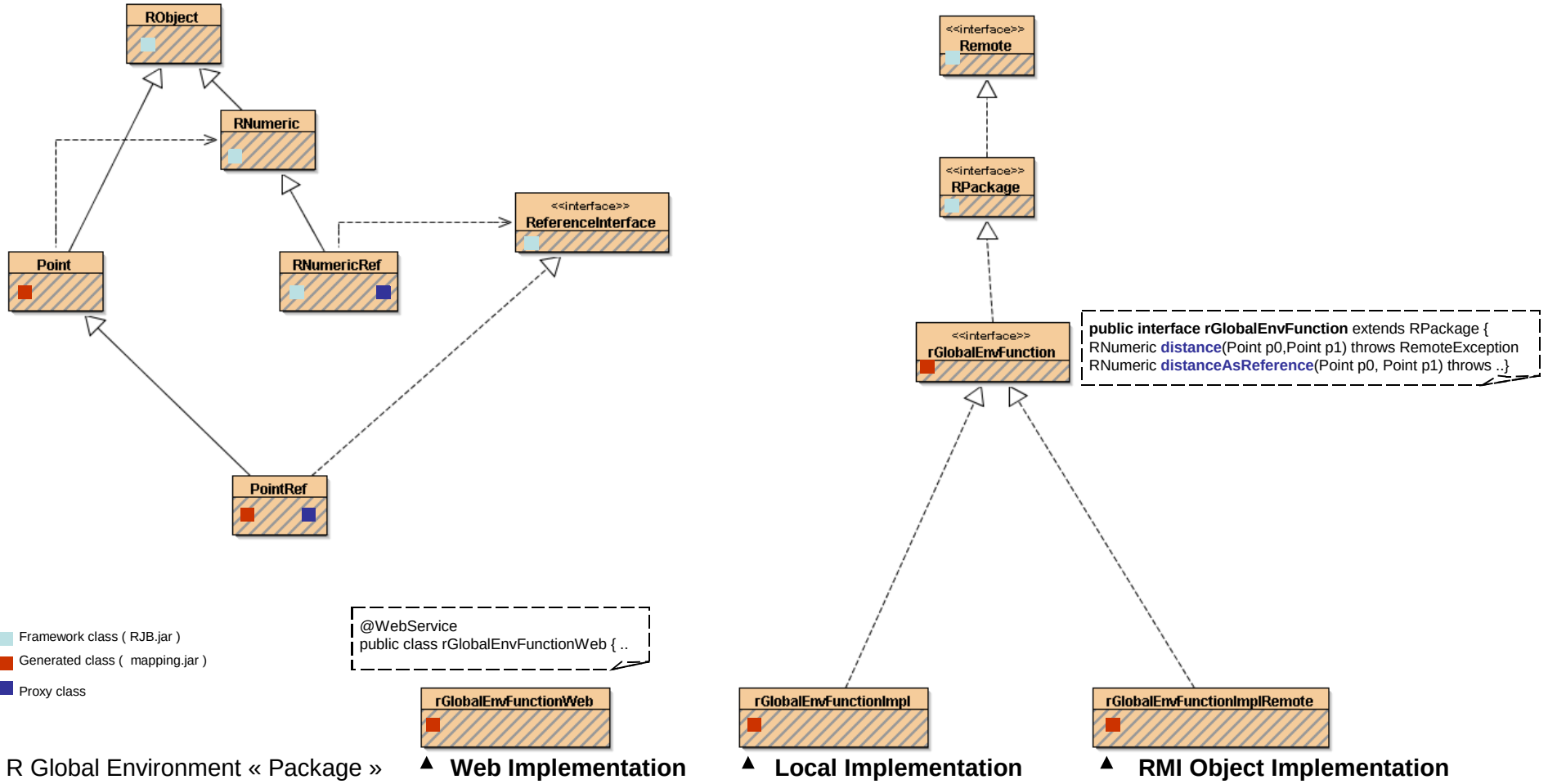
```
setClass("Point", representation(x="numeric", y="numeric"))
setGeneric("distance", function(p1,p2) standardGeneric("distance"))
setMethod("distance", signature("Point", "Point") , function(p1, p2) {
    sqrt( (p2@x-p1@x)^2 + (p2@y-p1@y)^2 )    })
```

Script / rjmap.xml

```
<rj>
 <publish>
  <functions><function name="distance" forWeb="true“ returnType="numeric"/></functions>
 </publish>
 <scripts>  <initScript name="globals.r" embed="true"/> </scripts>
</rj>
```

ant demogen





R Global Environment « Package »

▲ **Web Implementation**

▲ **Local Implementation**

▲ **RMI Object Implementation**

Prerequisites

1. Checkout the **EBI-Biocep** project
   public svn URL : https://svn.ebi.ac.uk/ma/branches/biocep/
   login : ma-guest
   password : CN85JIZ5
   (README.txt contains the instructions to run the demos)

2. **JDK 5 or 6** [Java SE 6 is required for JAX-WS Web Services]
   - JAVA_HOME environment variable set to the installation root folder of the jdk
   - PATH environment variable must include the jdk bin directory

3. **ant >= 1.7.x** installed
   - ANT_HOME environment variable set to the installation root folder of ant
   - PATH environment variable must include the ant bin directory

4. **R >= 2.5.x** installed
   - R_HOME environment variable set to the installation root folder of R
   - Bioconductor packages installed (only vsn & its dependencies for the demos)
   - **TypeInfo** package installed
   - **rJava** package installed
   - **JavaGD** package installed

if you encounter problems installing rJava, check the following :

on Unix like systems : grep JAVA $R_HOME/Makeconf

→ if R is not using the right jdk set JAVA_HOME to the path of the right one

→ "R CMD javareconf"

→ install rJava

5. **apache-tomcat-5.5.x** installed
   - TOMCAT_HOME environment variable set to the installation root folder of tomcat

6. **apache derby 10.x** installed
   - DERBY_HOME environment variable set to the installation root folder of derby

Useful links :

Java SE: http://java.sun.com/javase/downloads/index.jsp
ant: http://ant.apache.org/bindownload.cgi
R: http://cran.r-project.org/
BioConductor : source("http://bioconductor.org/biocLite.R");biocLite()
R packages : biocLite(c('TypeInfo', 'rJava', 'JavaGD'))
tomcat : http://tomcat.apache.org/download-55.cgi
derby : http://db.apache.org/derby/derby_downloads.html

Deployement of a Virtualized R infrastructure

cd biocep/VirtualRWorkbench

ant clean

ant compile

(on windows only) : **ant download.pstools**

ant demogen

ant webcompile

ant demodeploy

ant –Dspawn=true derbyrun

ant demodb

ant tomcat.startup

new terminal (cd biocep/VirtualRWorkbench) **ant demonode**

new terminal (cd biocep/VirtualRWorkbench) **ant demotop**

new browser → type the URL : **http://127.0.0.1/frontendapp/** (applet)

or **http://127.0.0.1/frontendapp/jaws** (Java Web Start)

Logon (click ok, Login Dialog)

In the console part of the R applet :

Create a normal distribution **x<-rnorm(1000)**

Plot it **plot(x)**

Draw the histogram of x **hist(x)**

Save x : **save(x,file='x_data')**

Right-click on the file and save it to your local disk

Use an editor to create an R script on your local disk : 'script.r'

Add any R commands to your script

Right click on the working directory area of the R applet and copy the script you've created there

Source your script : **source('script.r')**

Bring the supervisor window up front to have it simultaniously visible with the applet

Type **logoff**, notice the changes on the supervisor

Type **logon**, (ok) notice the changes on the supervisor

type **data(kidney)**

type **jk<-justvsn(kidney)**

plot the expression of jk

right-click on the console log area and copy the Java Serialization of jk to your disk (jk.ser) [can be used directly by java code]

right-click on the console area and push the Java Serialization (jk.ser) to R, name the

target variable jk2

plot the expression of jk2 **plot(exprs(jk2))**

Project Home:

http://www.ebi.ac.uk/microarray-srv/frontendapp/

R Workbench installation link

http://www.ebi.ac.uk/microarray-srv/frontendapp/rworkbench.jnlp

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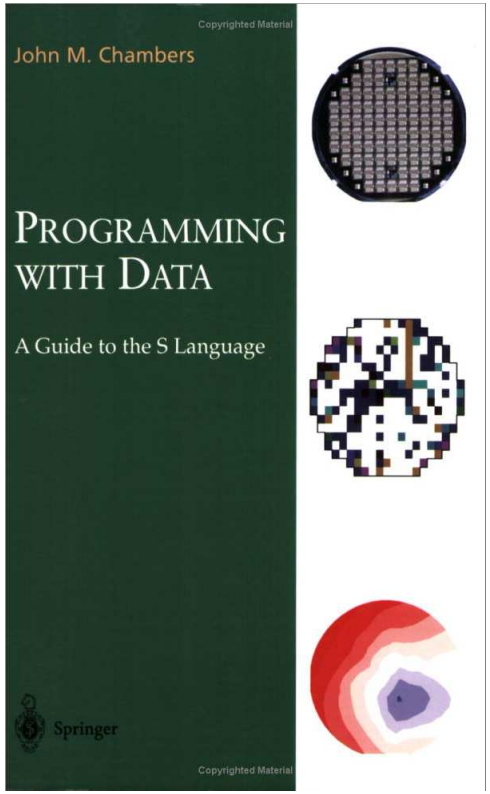
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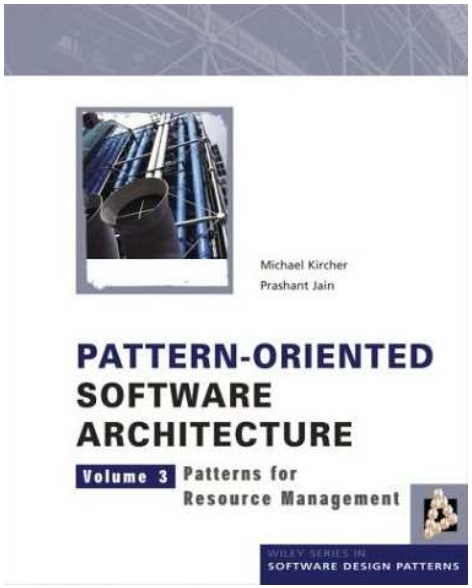
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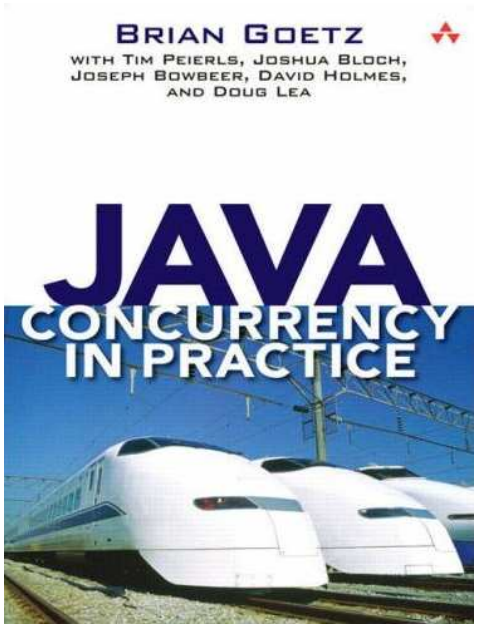
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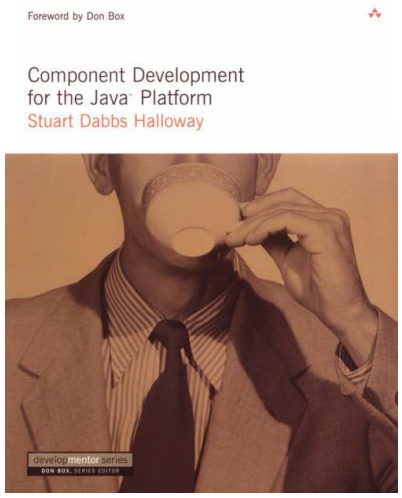
JAVA CONCURRENCY IN PRACTICE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Stuart Dabbs Halloway
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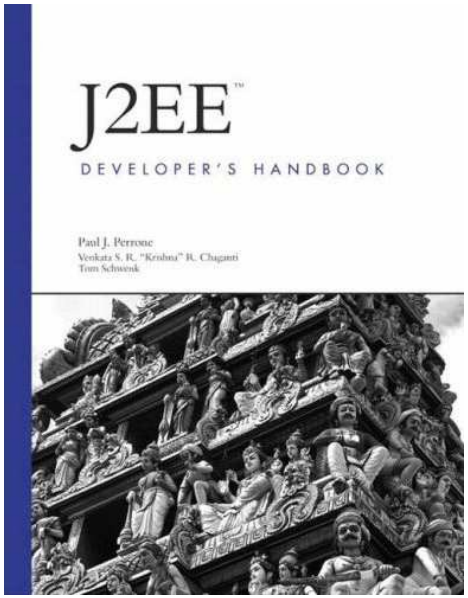
DON BOX, SERIES EDITOR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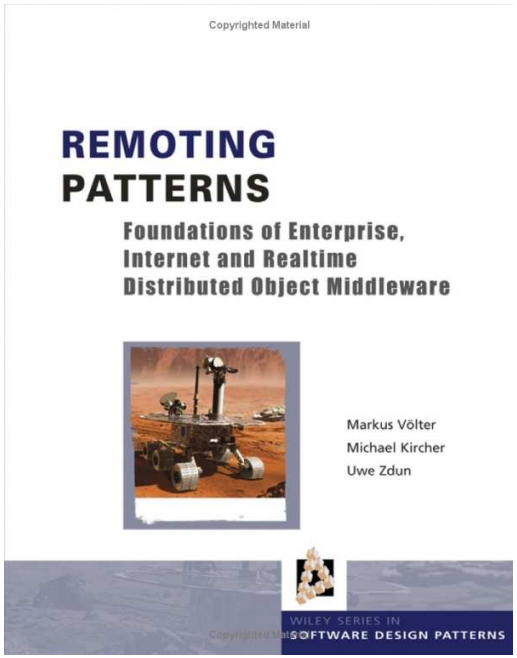
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