aneurIST

Integrated biomedical informatics for the management of cerebral aneurysms

Workflows for Data Mining in integrated multi-modal data on Intracranial Aneurysms using KNIME

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Outline

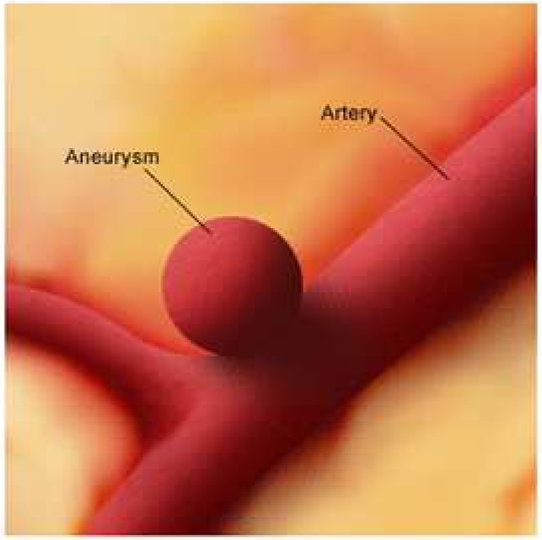
- Introduction
  - Model disease
  - @neurIST project
  - Problem
  - Route to solution
- Introductory to KNIME
- Demonstration KNIME in model disease
- R application in KNIME
- Obtained results – an example

Model disease

- Intracranial Aneurysm (IA): a bulbous expansion of a brain artery
- Prevalence of 2-5% in the EU population
- Risk of rupture leading to severe bleeding: 0.7 % per year
- Better imaging → more asymptomatic IA are detected
- Therapy: surgical procedure or *watchful waiting*
- Aim: predict outcome

- EU project: @neurIST

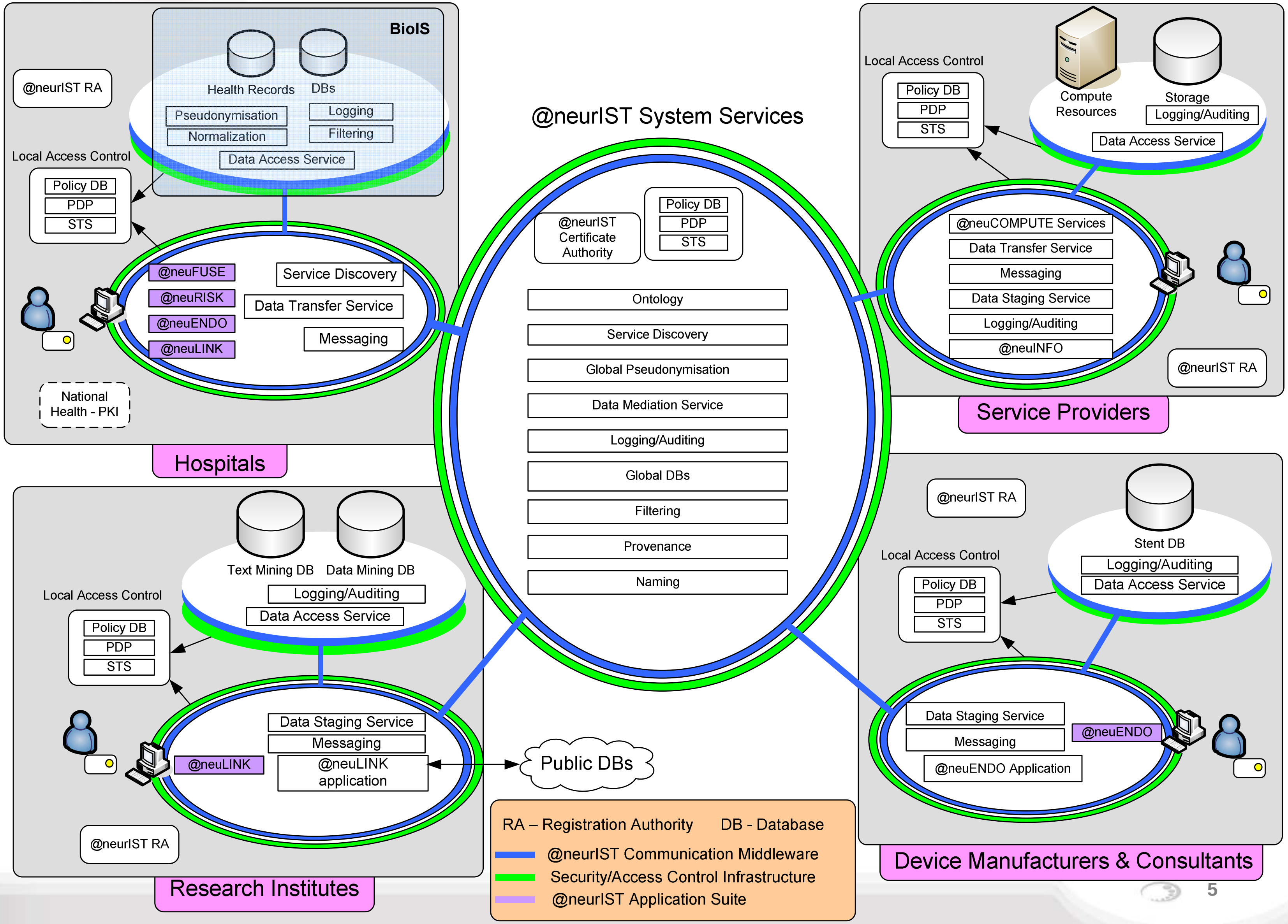
Cerebral Aneurysm



@neurIST

- Development of an integrated healthcare infrastructure to improve decision support for IA
- Integrated European FP6 healthcare GRID Project with 32 partners http://www.aneurist.org
- Objective: predict the risk of rupture of IA for an individual patient
- Multi-modal data
  - Imaging data: morphology, haemodynamic models
  - Clinical data
  - Genetic data (SNP)
  - Epidemiological data
  - Literature data

@neurIST System Services



@neurIST Certificate Authority
Policy DB
PDP
STS
Ontology
Service Discovery
Global Pseudonymisation
Data Mediation Service
Logging/Auditing
Global DBs
Filtering
Provenance
Naming

Hospitals

BioIS
Health Records
DBs
Pseudonymisation
Normalization
Logging
Filtering
Data Access Service
@neurIST RA
Local Access Control
Policy DB
PDP
STS
@neuFUSE
@neuRISK
@neuENDO
@neuLINK
Service Discovery
Data Transfer Service
Messaging
National Health - PKI

Service Providers

Local Access Control
Policy DB
PDP
STS
Compute Resources
Storage
Logging/Auditing
Data Access Service
@neuCOMPUTE Services
Data Transfer Service
Messaging
Data Staging Service
Logging/Auditing
@neuINFO
@neurIST RA

Research Institutes

Text Mining DB
Data Mining DB
Logging/Auditing
Data Access Service
Local Access Control
Policy DB
PDP
STS
Data Staging Service
Messaging
@neuLINK
@neuLINK application
Public DBs
@neurIST RA

Device Manufacturers & Consultants

@neurIST RA
Stent DB
Logging/Auditing
Data Access Service
Local Access Control
Policy DB
PDP
STS
Data Staging Service
Messaging
@neuENDO
@neuENDO Application

RA – Registration Authority DB - Database
🟦 @neurIST Communication Middleware
🟩 Security/Access Control Infrastructure
🟪 @neurIST Application Suite

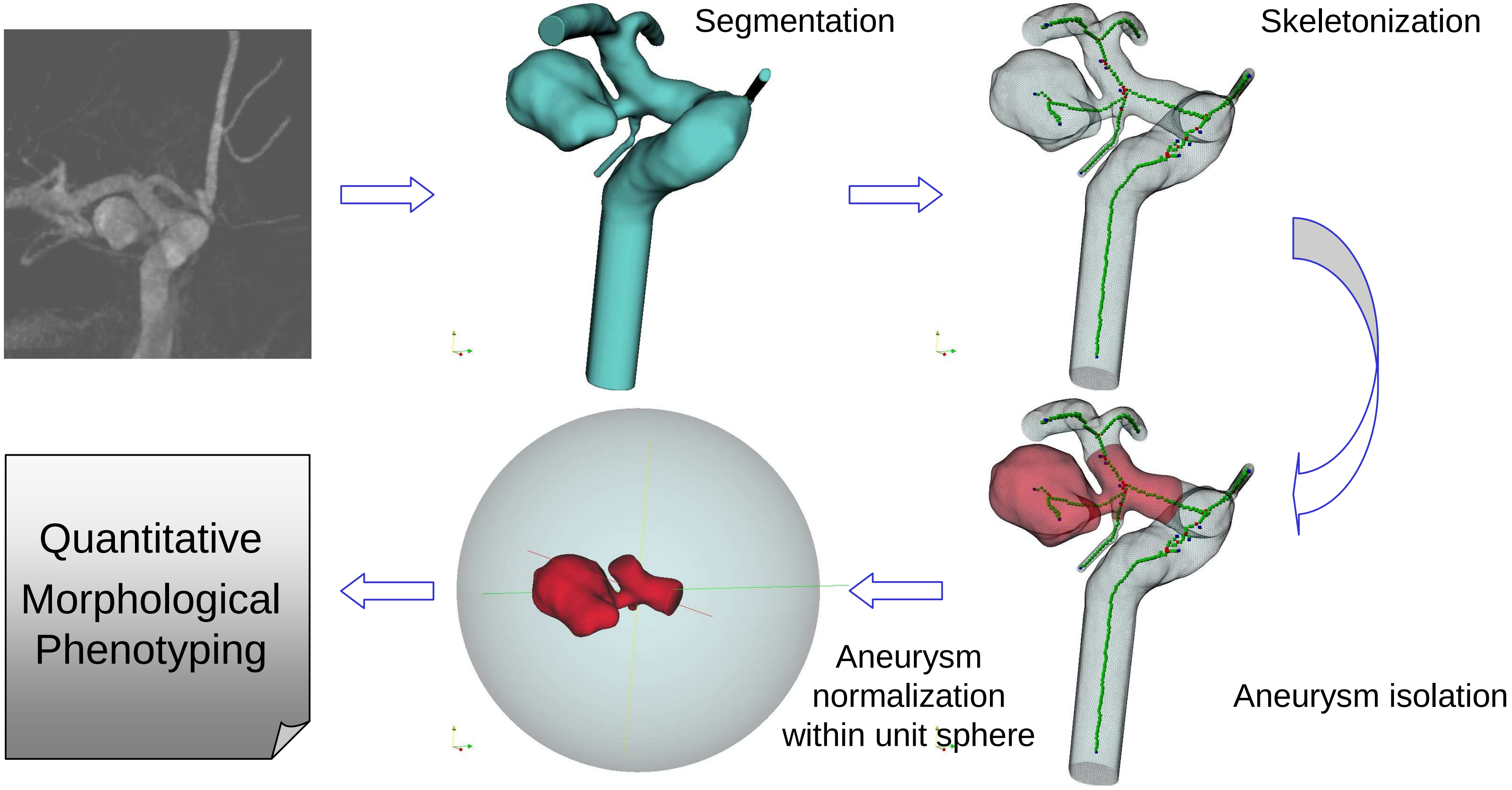
Clinical issue

Since aneurysm shape is likely to be dependent on the balance between haemodynamic forces and the aneurysmal surrounding environment, an appropriate morphological 3-D characterization is likely to provide a practical surrogate to quickly evaluate the risk of rupture.

Modeling this morphological characterization of all individuals in a large study population.

Compare morphological characterizations

Morphological phenotyping - global shape descriptor



Segmentation

Skeletonization

Aneurysm isolation

Aneurysm normalization within unit sphere

Quantitative Morphological Phenotyping

Calculation of similarity

- Segmentation of the intracranial aneurysm
- Use of 3D Zernike moments
  - compressed representation of shape
  - yields a numerical vector
- Additionally add nominal information, e.g. location and side
- Distance based on Gower-metric, allowing nominals and numerics

Problem

Use of ‘monolithic mining scripts’ leads to difficulties with:

- maintenance
- re-use of mining strategies
- user presentation of data flows
- use by non R users
- presentation of results to non R users

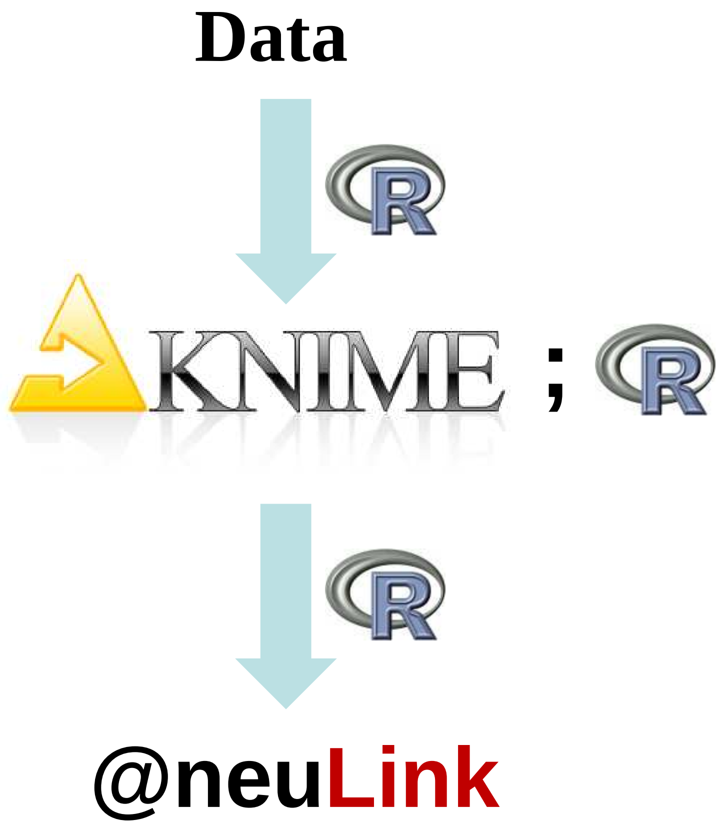
Roadmap to a solution

Considering that in the GRID context workflows like Taverna (http://taverna.sourceforge.net/) have shown great success (HealthGrid 2009, Medline publications);

Make use of a workflow engine:

- KNIME, exploration platform for multi-modal data:
  - R scripts
  - Weka
  - Java/Python
  - …
  - …

Overall workflow



Data

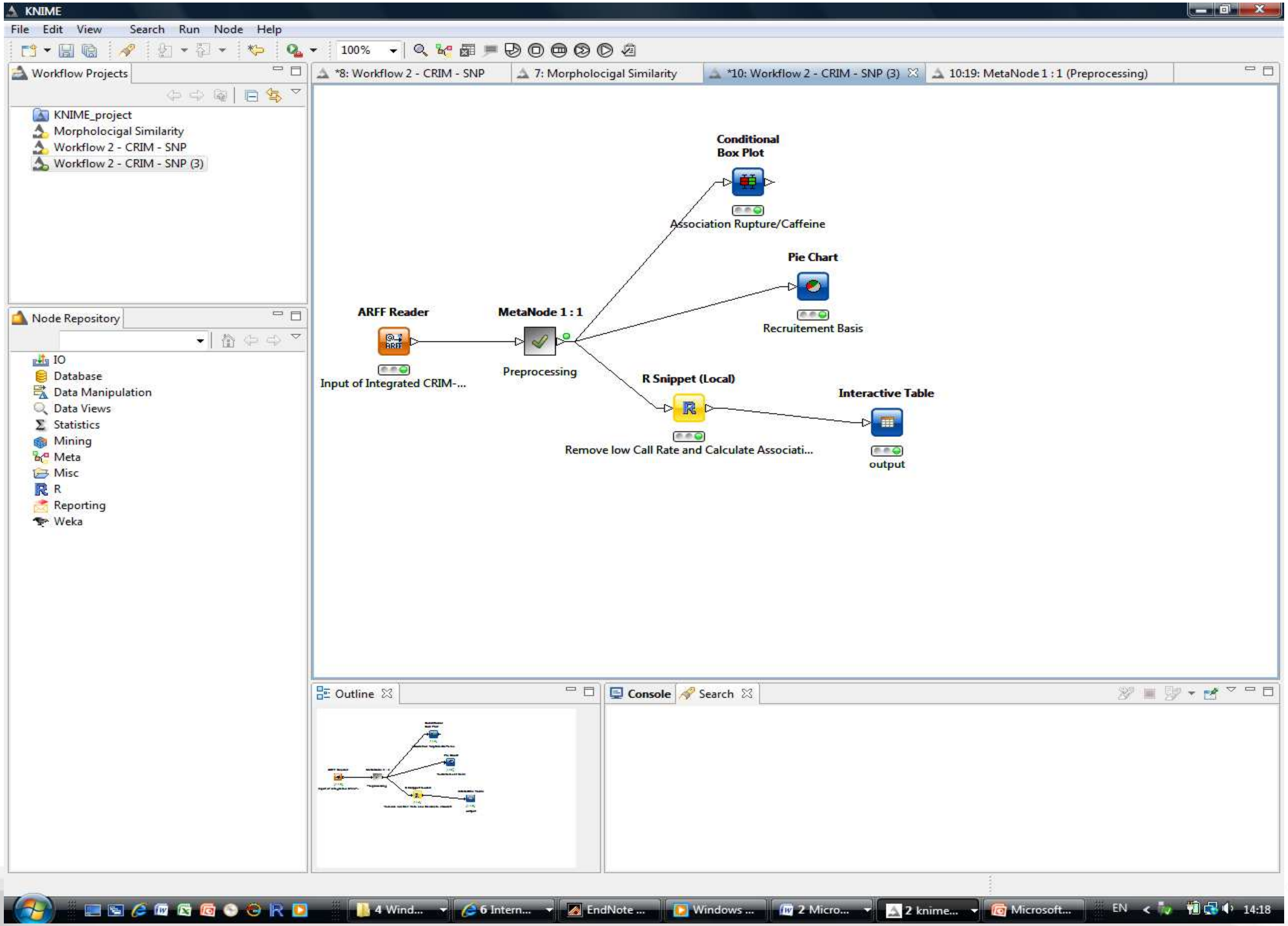
KNIME ; R

@neuLink

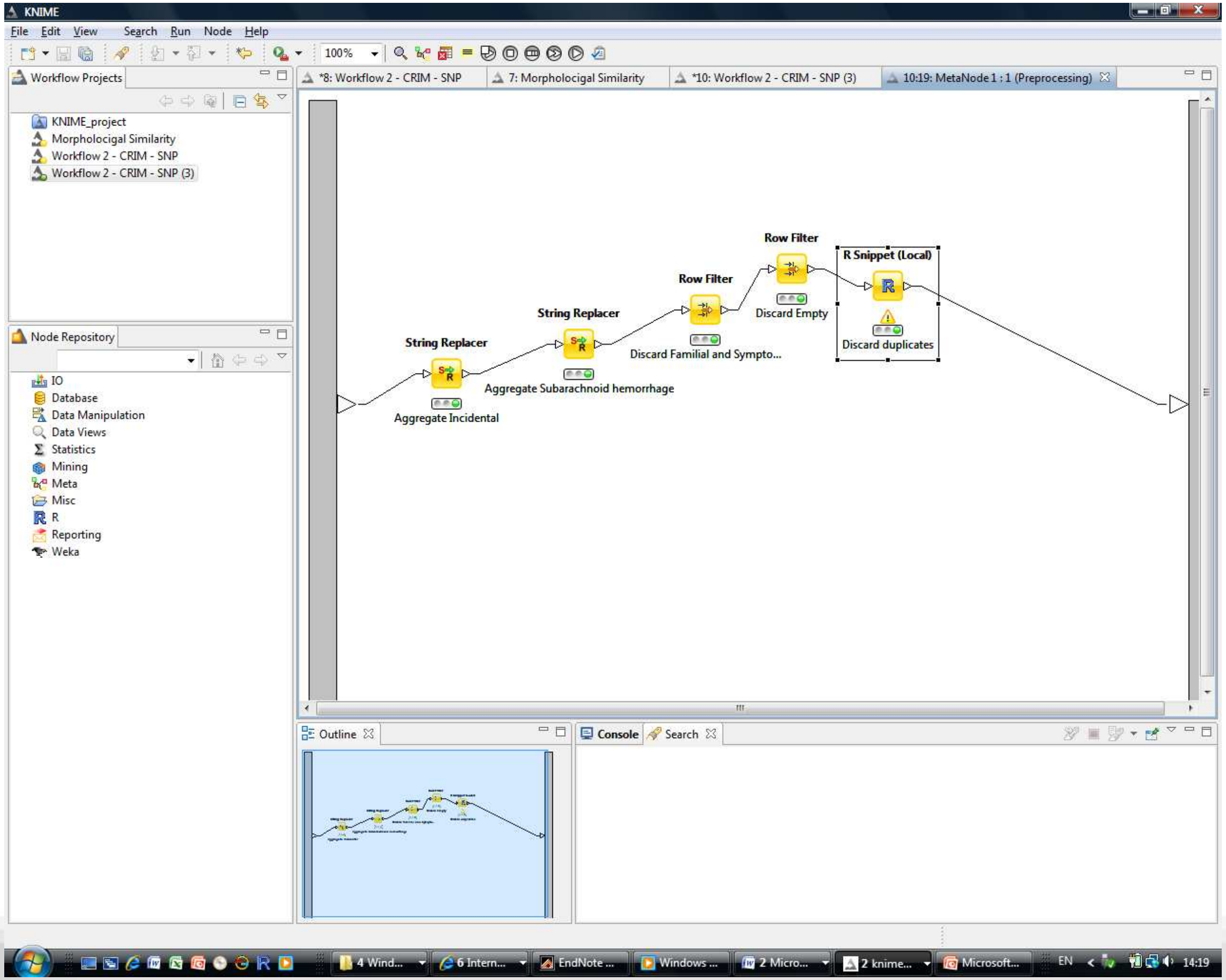
KNIME (http://www.knime.org)

- Konstanz Information Miner
- Workflow based Knowledge Discovery Tool
- Easy to use and Open Source
- Based on Eclipse
- Supports sub-workflows and evaluation workflows
- Includes ao R, Weka, and Java/Python
- Includes simple Graphics capabilities
- Workflows can be saved and run as a Batch

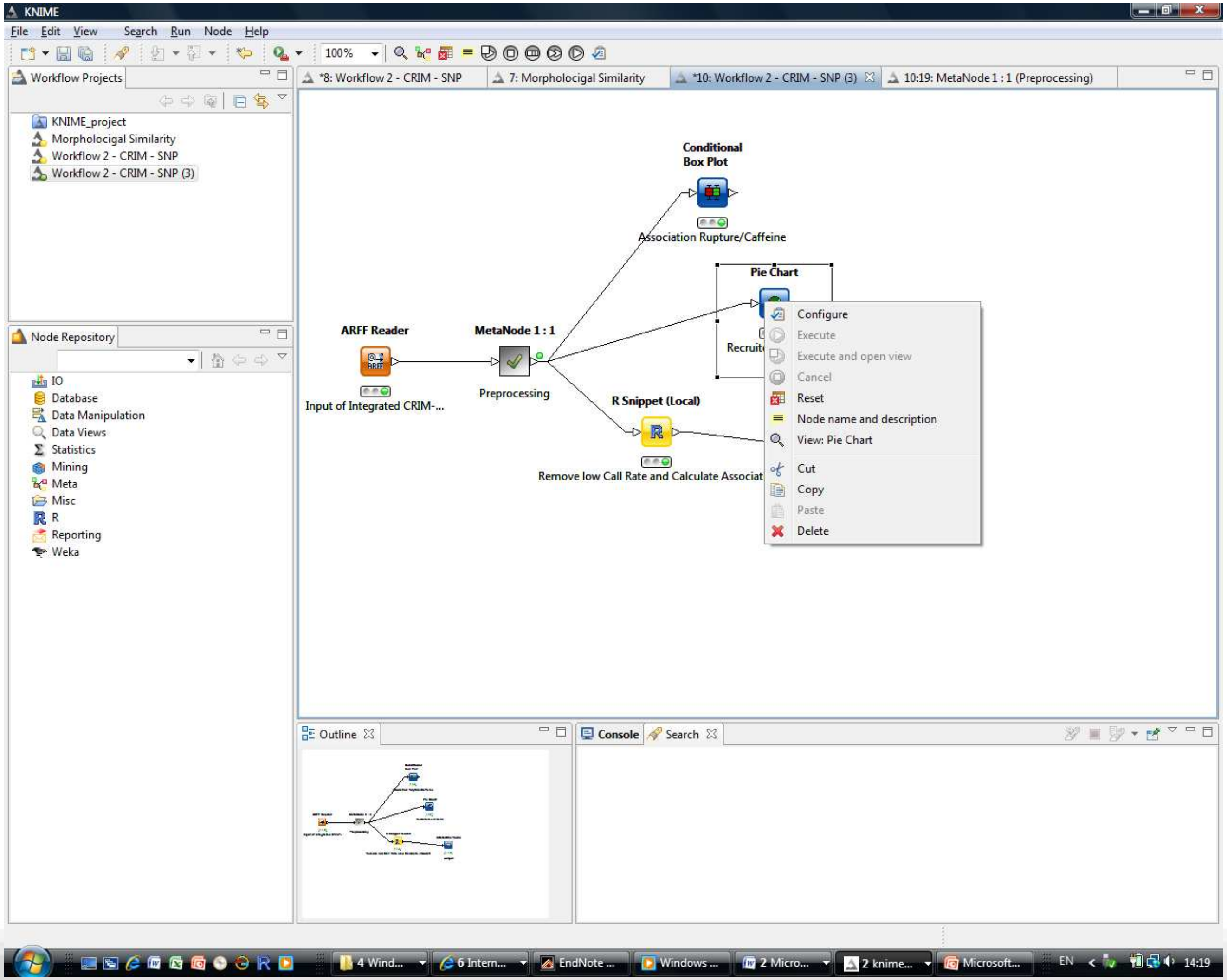
KNIME – Workflow overview



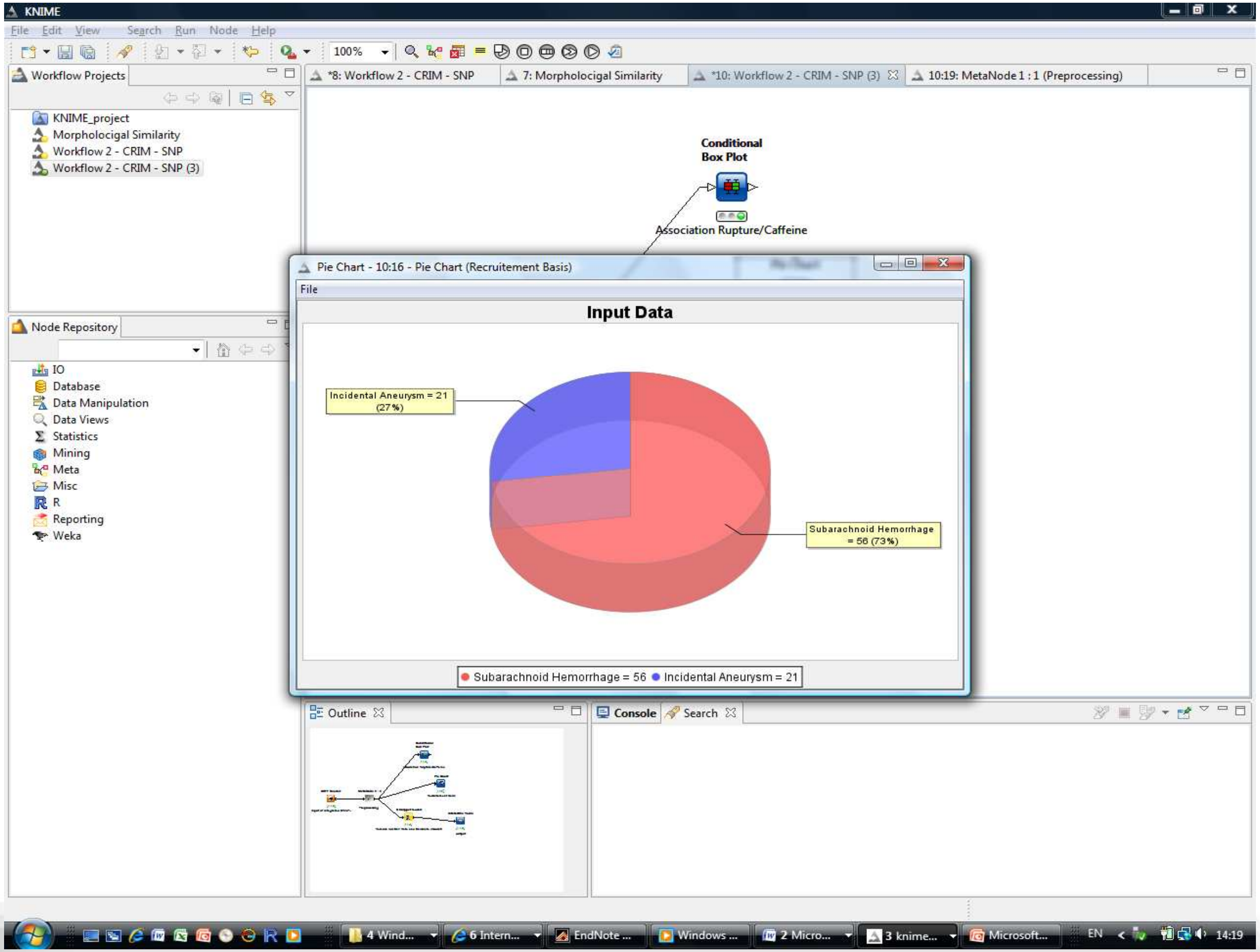
Meta node


KNIME
File Edit View Search Run Node Help
100%
Workflow Projects
KNIME_project
Morphological Similarity
Workflow 2 - CRIM - SNP
Workflow 2 - CRIM - SNP (3)
*8: Workflow 2 - CRIM - SNP
7: Morphological Similarity
*10: Workflow 2 - CRIM - SNP (3)
10:19: MetaNode 1 : 1 (Preprocessing)
String Replacer
Aggregate Incidental
String Replacer
Aggregate Subarachnoid hemorrhage
Row Filter
Discard Familial and Sympto...
Row Filter
Discard Empty
R Snippet (Local)
Discard duplicates
Node Repository
IO
Database
Data Manipulation
Data Views
Statistics
Mining
Meta
Misc
R
Reporting
Weka
Outline
Console
Search
4 Wind...
6 Intern...
EndNote ...
Windows ...
2 Micro...
2 knime...
Microsoft...
EN
14:19

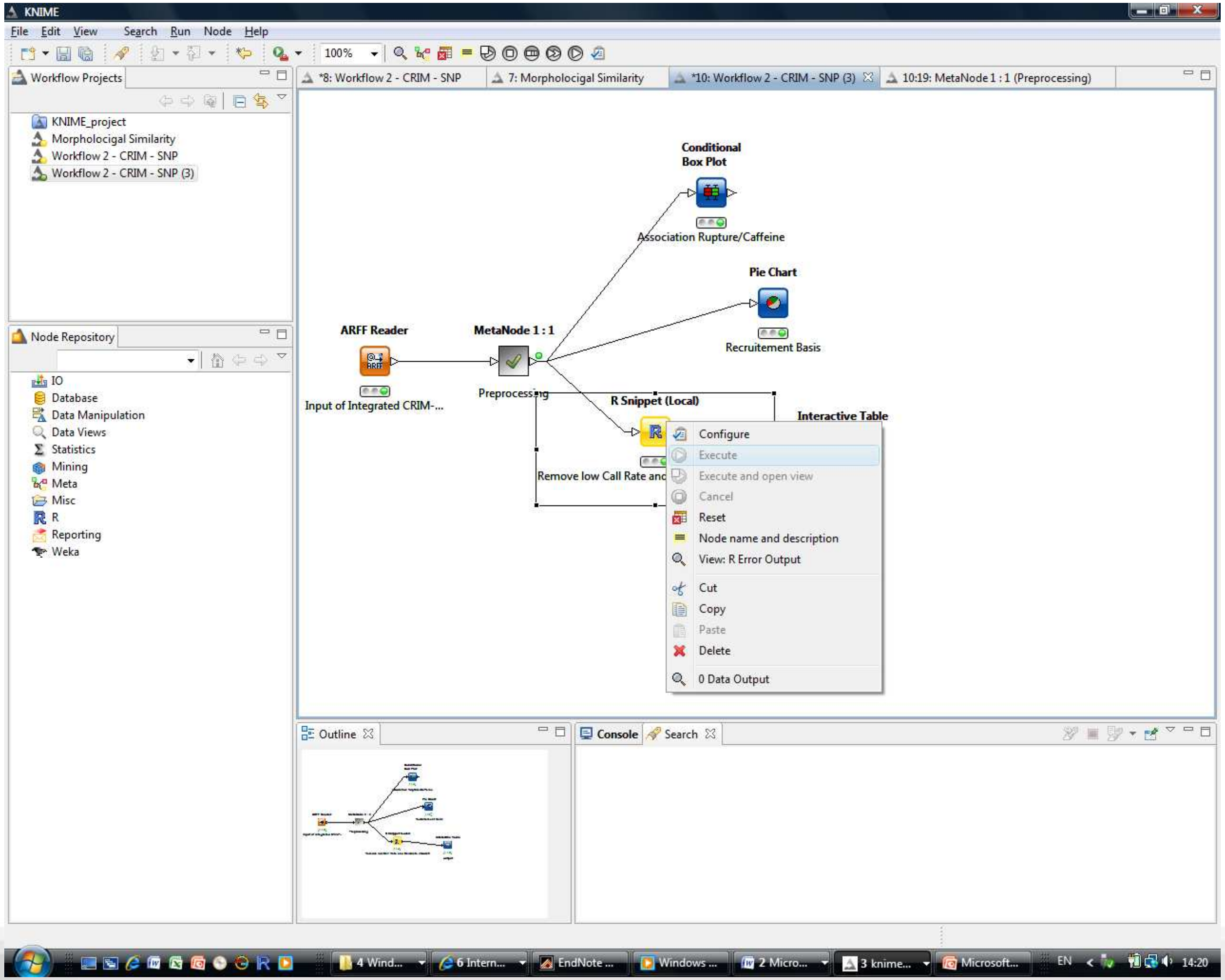
Click node to view Pie chart



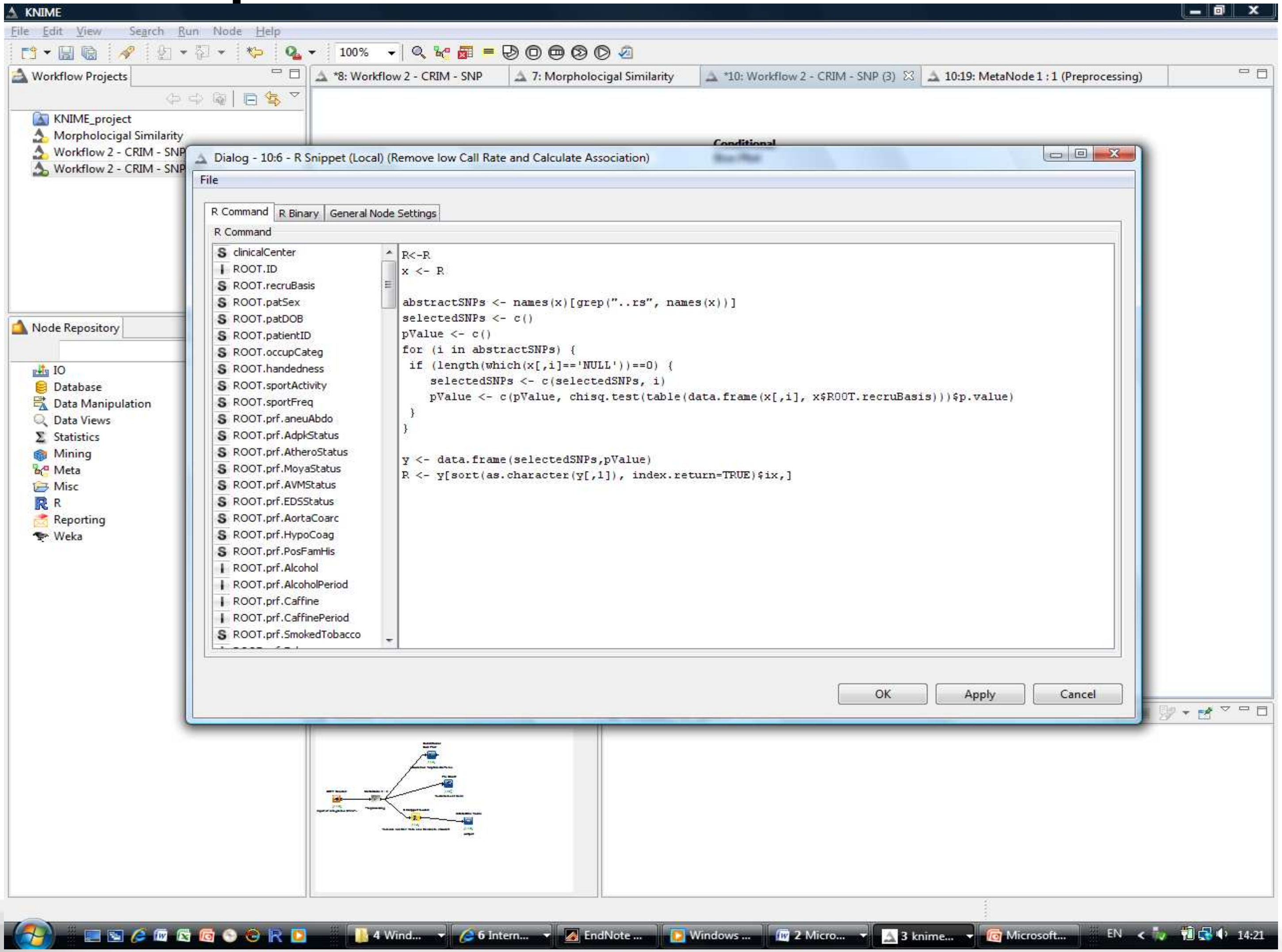
Pie chart


KNIME
File Edit View Search Run Node Help
100%
Workflow Projects
KNIME_project
Morpholocigal Similarity
Workflow 2 - CRIM - SNP
Workflow 2 - CRIM - SNP (3)
*8: Workflow 2 - CRIM - SNP
7: Morpholocigal Similarity
*10: Workflow 2 - CRIM - SNP (3)
10:19: MetaNode 1 : 1 (Preprocessing)
Conditional Box Plot
Association Rupture/Caffeine
Node Repository
IO
Database
Data Manipulation
Data Views
Statistics
Mining
Meta
Misc
R
Reporting
Weka
Pie Chart - 10:16 - Pie Chart (Recruitement Basis)
File
Input Data
Incidental Aneurysm = 21 (27%)
Subarachnoid Hemorrhage = 56 (73%)
Subarachnoid Hemorrhage = 56
Incidental Aneurysm = 21
Outline
Console
Search
4 Wind...
6 Intern...
EndNote ...
Windows ...
2 Micro...
3 knime...
Microsoft...
EN
14:19

Click R node to view script



R-script

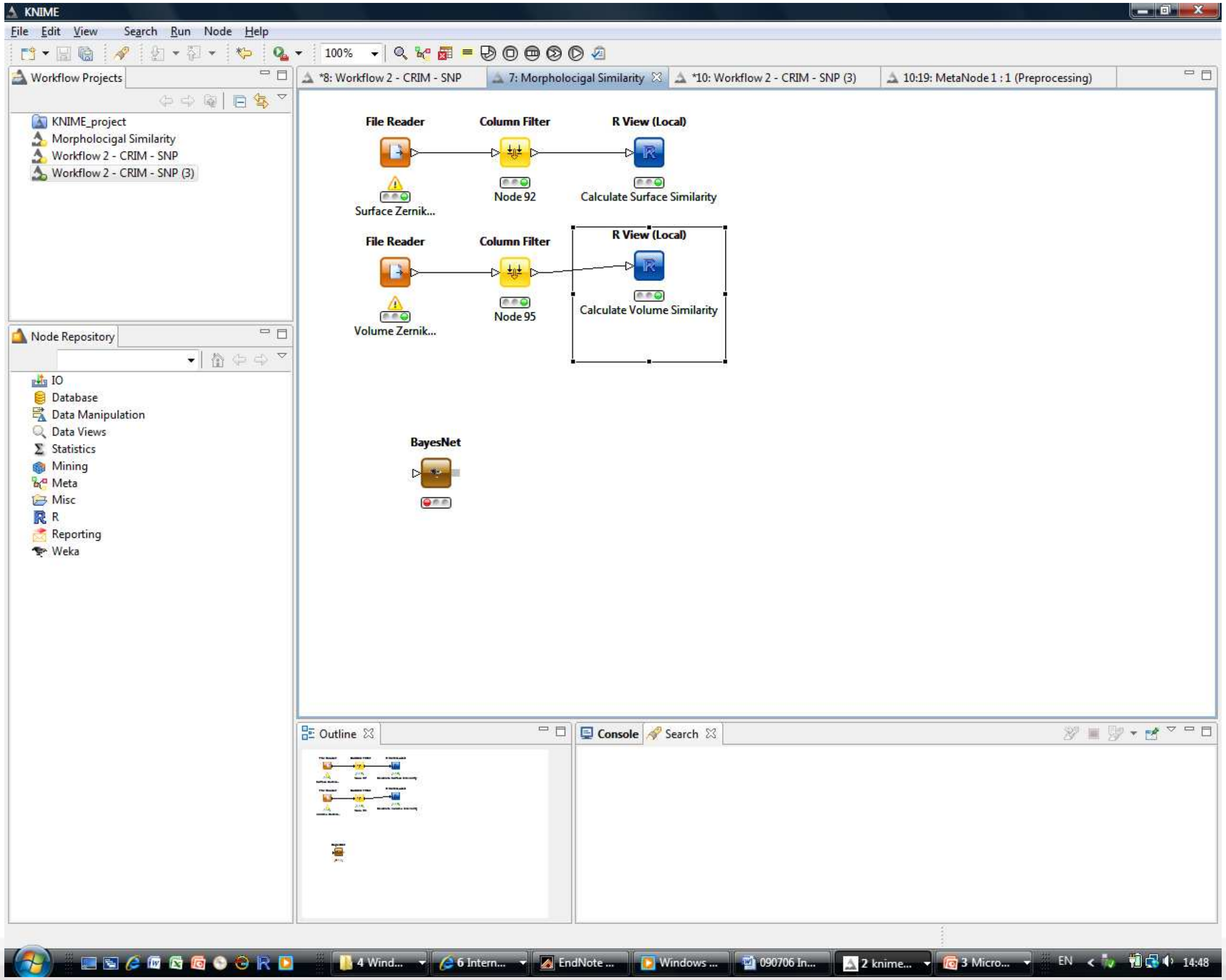


```
R<-R
x <- R

abstractSNPs <- names(x)[grep("..rs", names(x))]
selectedSNPs <- c()
pValue <- c()
for (i in abstractSNPs) {
 if (length(which(x[,i]=='NULL'))==0) {
    selectedSNPs <- c(selectedSNPs, i)
    pValue <- c(pValue, chisq.test(table(data.frame(x[,i], x$ROOT.recruBasis)))$p.value)
 }
}

y <- data.frame(selectedSNPs,pValue)
R <- y[sort(as.character(y[,1]), index.return=TRUE)$ix,]
```

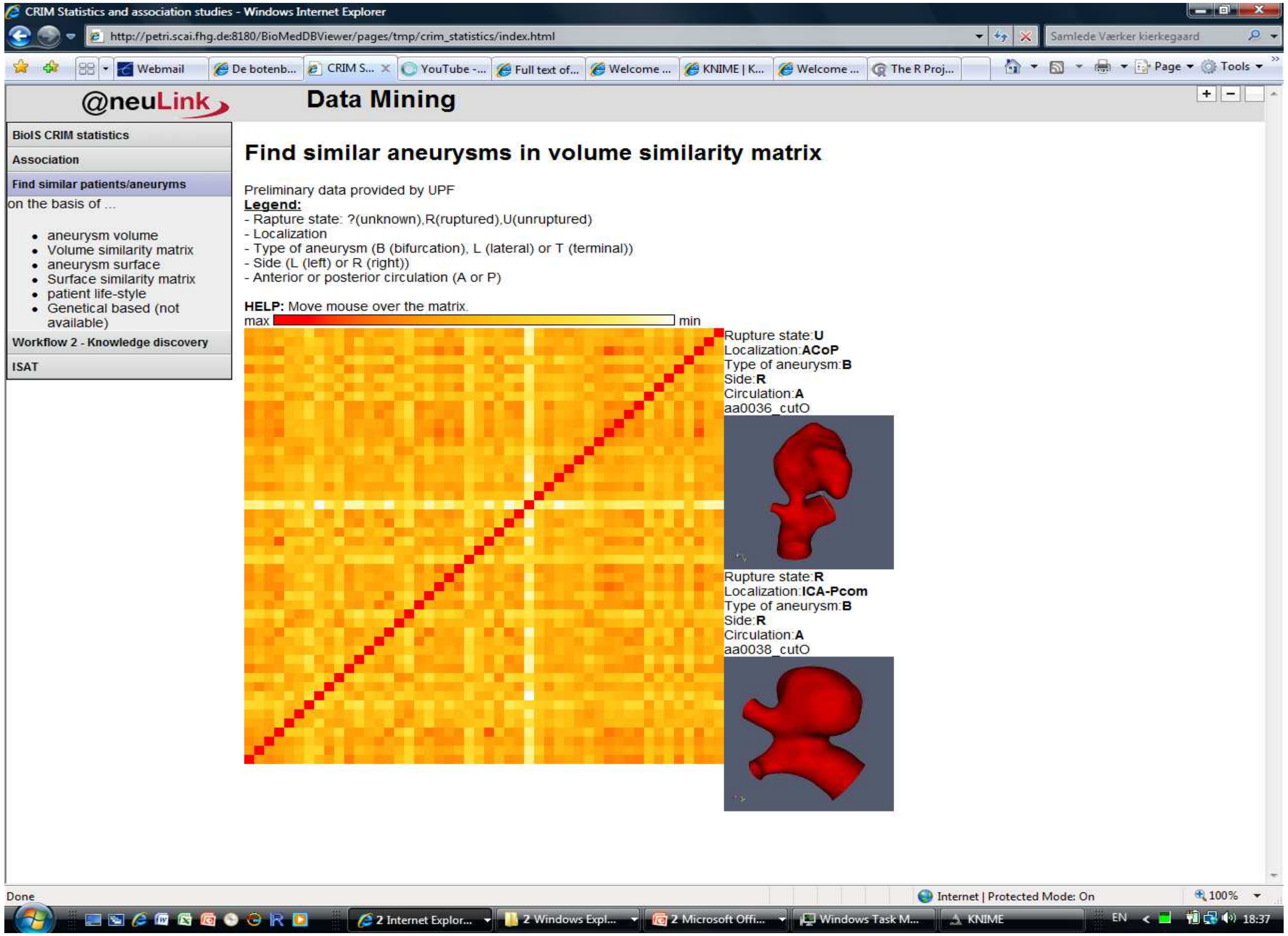
Volume based symmetry workflow



R script

```
for (i in 1:length(blo.dis)) {
   inter <-  as.character(blo.dis[sort(dis.matrix[i,], index.return=TRUE)$ix[1:10]])
   distan <- dis.matrix[i,sort(dis.matrix[i,], index.return=TRUE)$ix[1:10]]
   inter <- as.vector(rbind(inter, distan))
   blo.res <- rbind(blo.res, inter)  }
write.table(blo.res, paste("similarAneurysmsId",modeName,".txt", sep=""), quote=FALSE,
       row.names=FALSE, sep="\t", col.names=FALSE)
write.table(dis.matrix, paste("similarityMatrix",modeName,".txt", sep=""), quote=FALSE,
       row.names=FALSE, sep="\t", col.names=FALSE)
png("similarAneurysmsClusterSurface.png")
 image(1:nrow(dis.matrix), 1:nrow(dis.matrix), dis.matrix, main=paste(modeName," based
       Similarity", sep=""))
dev.off()
x.res <- biclust(dis.matrix, method=BCCC(), number=2)
drawHeatmap(dis.matrix,x.res,1)
image(1:nrow(dis.matrix), 1:nrow(dis.matrix), dis.matrix, main=paste(modeName," based
       Similarity", sep=""))
setwd(savedWd)
```

Outcome of similarity to @neuLink



on the basis of ...

- aneurysm volume
- Volume similarity matrix
- aneurysm surface
- Surface similarity matrix
- patient life-style
- Genetical based (not available)

Find similar aneurysms in volume similarity matrix

Preliminary data provided by UPF

Legend:
- Rapture state: ?(unknown),R(ruptured),U(unruptured)
- Localization
- Type of aneurysm (B (bifurcation), L (lateral) or T (terminal))
- Side (L (left) or R (right))
- Anterior or posterior circulation (A or P)

HELP: Move mouse over the matrix.

Rupture state:**U**
Localization:**ACoP**
Type of aneurysm:**B**
Side:**R**
Circulation:**A**
aa0036_cutO

Rupture state:**R**
Localization:**ICA-Pcom**
Type of aneurysm:**B**
Side:**R**
Circulation:**A**
aa0038_cutO

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