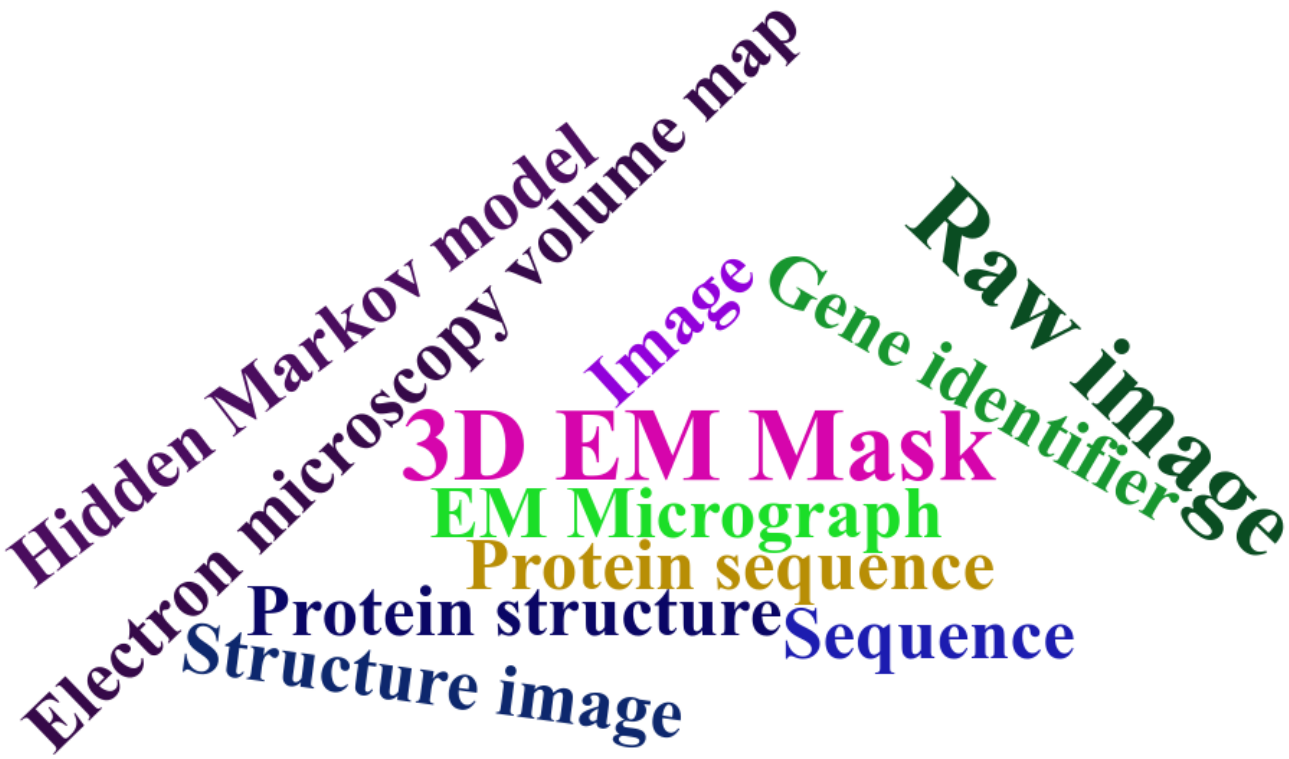

Hidden Markov model
Electron microscopy volume map
Image
Gene identifier
Raw image
3D EM Mask
EM Micrograph
Protein sequence
Protein structure
Sequence
Structure image

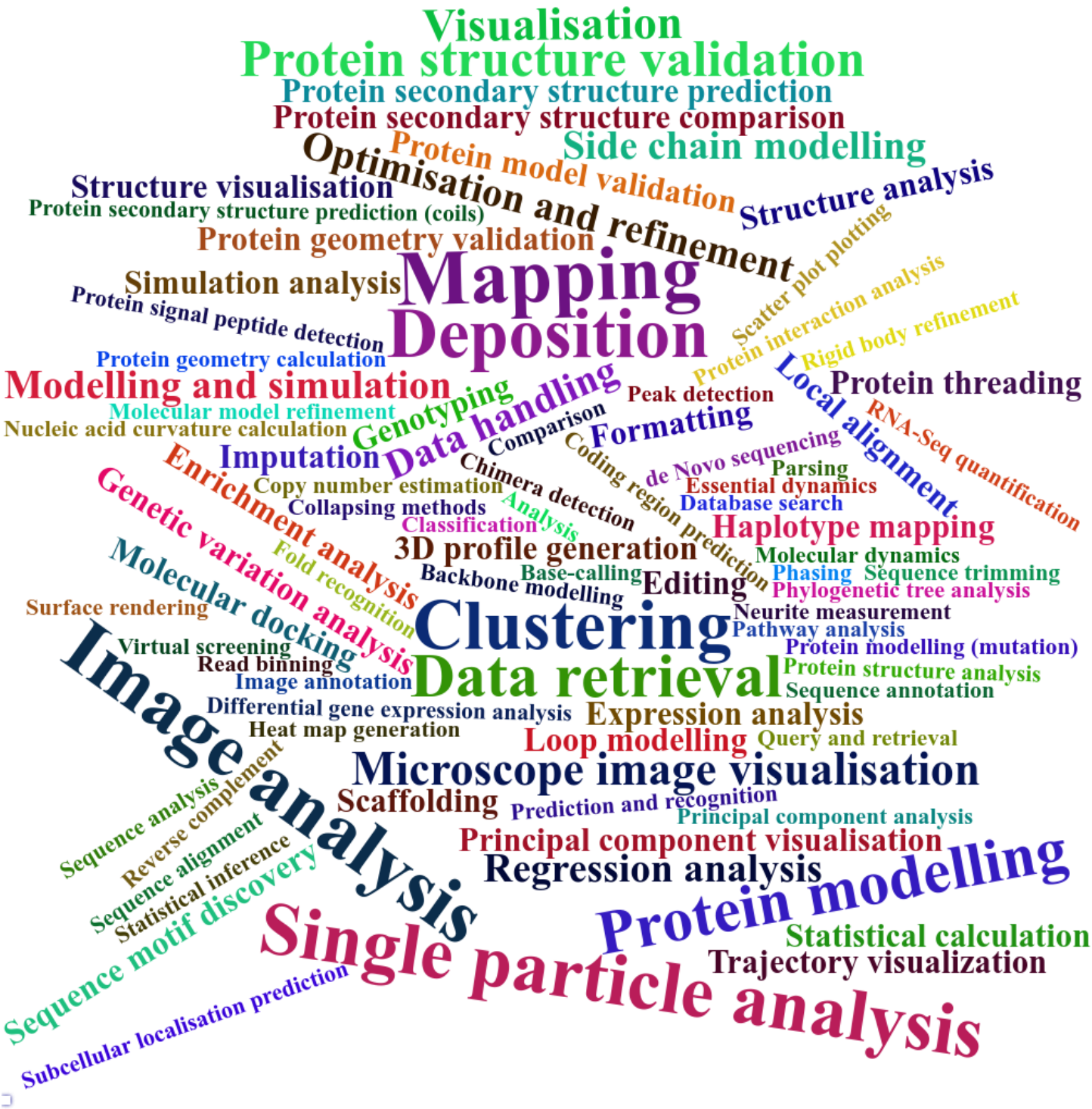
Image format

FASTA

PDB

LGPL-3.0
Freeware
MIT
BSD-2-Clause
Artistic-2.0
BSD-3-Clause
AGPL-3.0
Other
Apache-2.0
GPL-2.0
GPL-3.0

Mac
Linux
Windows


Visualisation
Protein structure validation
Protein secondary structure prediction
Protein secondary structure comparison
Side chain modelling
Protein model validation
Optimisation and refinement
Structure visualisation
Structure analysis
Protein secondary structure prediction (coils)
Protein geometry validation
Scatter plot plotting
Simulation analysis
Mapping
Protein interaction analysis
Protein signal peptide detection
Deposition
Rigid body refinement
Protein geometry calculation
Modelling and simulation
Protein threading
Genotyping
Data handling
Peak detection
Local alignment
Molecular model refinement
Comparison
Formatting
RNA-Seq quantification
Nucleic acid curvature calculation
Imputation
Coding region prediction
de Novo sequencing
Parsing
Chimera detection
Copy number estimation
Essential dynamics
Enrichment analysis
Collapsing methods
Analysis
Database search
Genetic variation analysis
Classification
Haplotype mapping
3D profile generation
Molecular dynamics
Fold recognition
Molecular docking
Backbone modelling
Base-calling
Editing
Phasing
Sequence trimming
Phylogenetic tree analysis
Surface rendering
Clustering
Neurite measurement
Pathway analysis
Virtual screening
Protein modelling (mutation)
Image analysis
Read binning
Data retrieval
Protein structure analysis
Image annotation
Sequence annotation
Differential gene expression analysis
Expression analysis
Heat map generation
Loop modelling
Query and retrieval
Microscope image visualisation
Sequence analysis
Reverse complement
Scaffolding
Prediction and recognition
Principal component analysis
Sequence alignment
Principal component visualisation
Statistical inference
Regression analysis
Protein modelling
Sequence motif discovery
Statistical calculation
Trajectory visualization
Single particle analysis
Subcellular localisation prediction

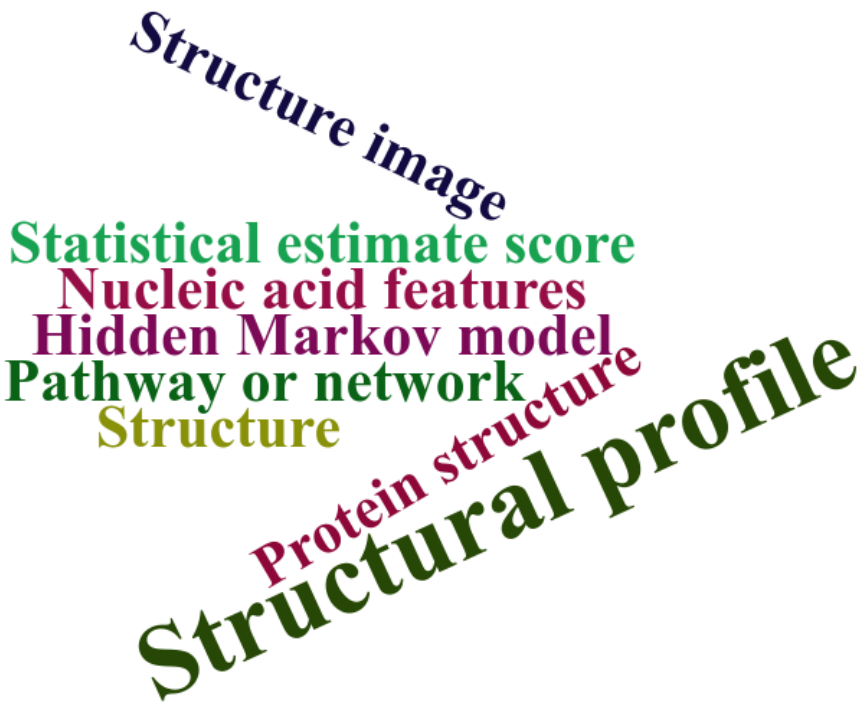
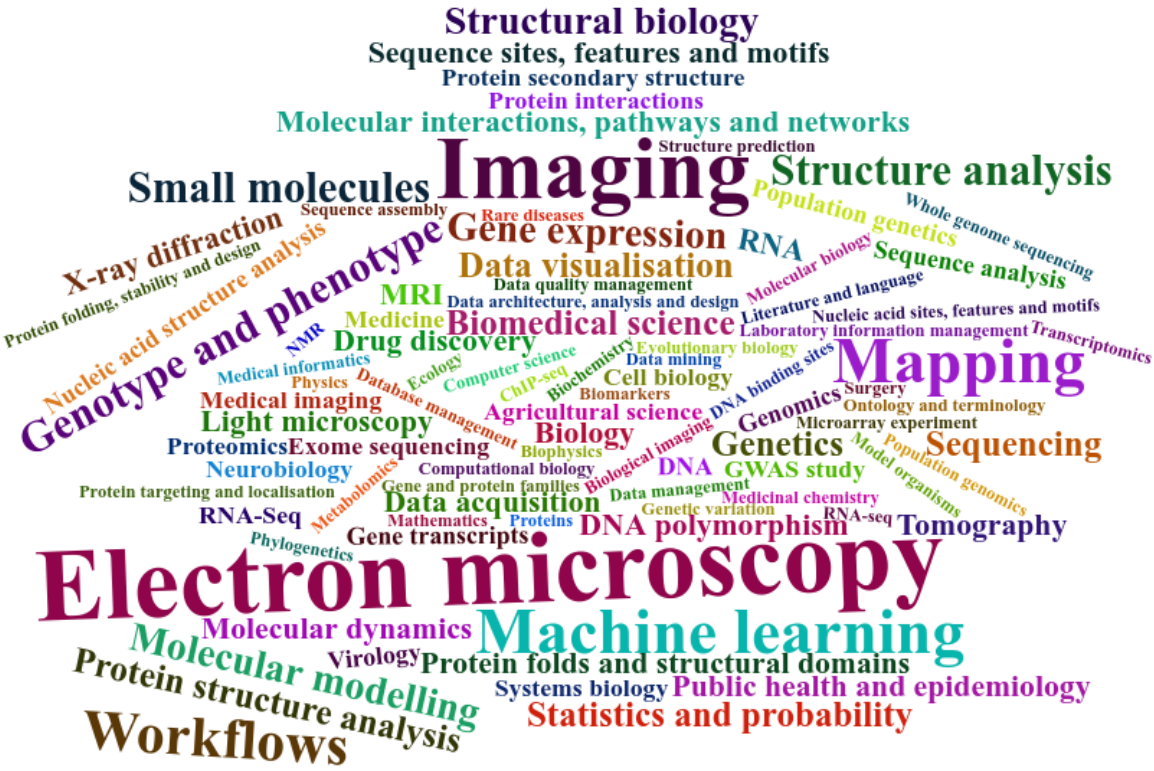
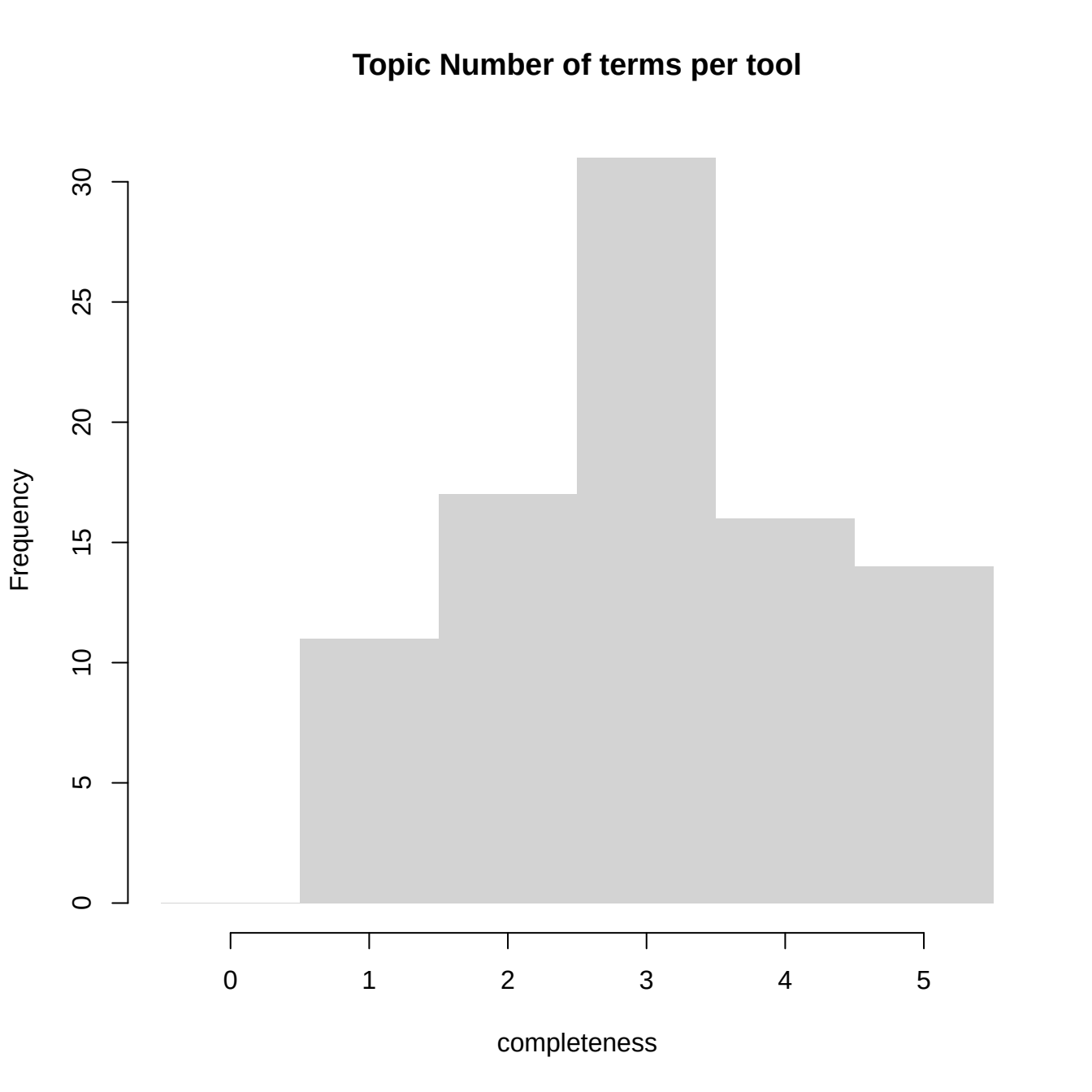

Structure image
Statistical estimate score
Nucleic acid features
Hidden Markov model
Pathway or network
Structure
Protein structure
Structural profile

Image format
Workflow format

Database portal
Workflow
Script
Web application
Plug-in
Ontology
Suite
Command-line tool
Desktop application
Library
Workbench


Structural biology
Sequence sites, features and motifs
Protein secondary structure
Protein interactions
Molecular interactions, pathways and networks
Structure prediction
Small molecules
Imaging
Structure analysis
Population genetics
Whole genome sequencing
X-ray diffraction
Sequence assembly
Rare diseases
Protein folding, stability and design
Nucleic acid structure analysis
Genotype and phenotype
Gene expression
RNA
Molecular biology
Sequence analysis
Data visualisation
Data quality management
MRI
Data architecture, analysis and design
Literature and language
Nucleic acid sites, features and motifs
Medicine
Biomedical science
Laboratory information management
Transcriptomics
NMR
Drug discovery
Evolutionary biology
Data mining
Medical informatics
Physics
Ecology
Computer science
ChIP-seq
Biochemistry
DNA binding sites
Mapping
Cell biology
Biomarkers
Surgery
Medical imaging
Database management
Agricultural science
Genomics
Ontology and terminology
Light microscopy
Microarray experiment
Biology
Proteomics
Exome sequencing
Biophysics
Genetics
Sequencing
Biological imaging
Population genomics
Neurobiology
Computational biology
DNA
GWAS study
Model organisms
Protein targeting and localisation
Gene and protein families
Metabolomics
Data management
Medicinal chemistry
Data acquisition
Genetic variation
RNA-seq
RNA-Seq
Mathematics
Proteins
DNA polymorphism
Tomography
Gene transcripts
Phylogenetics
Electron microscopy
Molecular dynamics
Machine learning
Virology
Protein folds and structural domains
Molecular modelling
Systems biology
Public health and epidemiology
Protein structure analysis
Statistics and probability
Workflows


Topic Number of terms per tool
Frequency
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15
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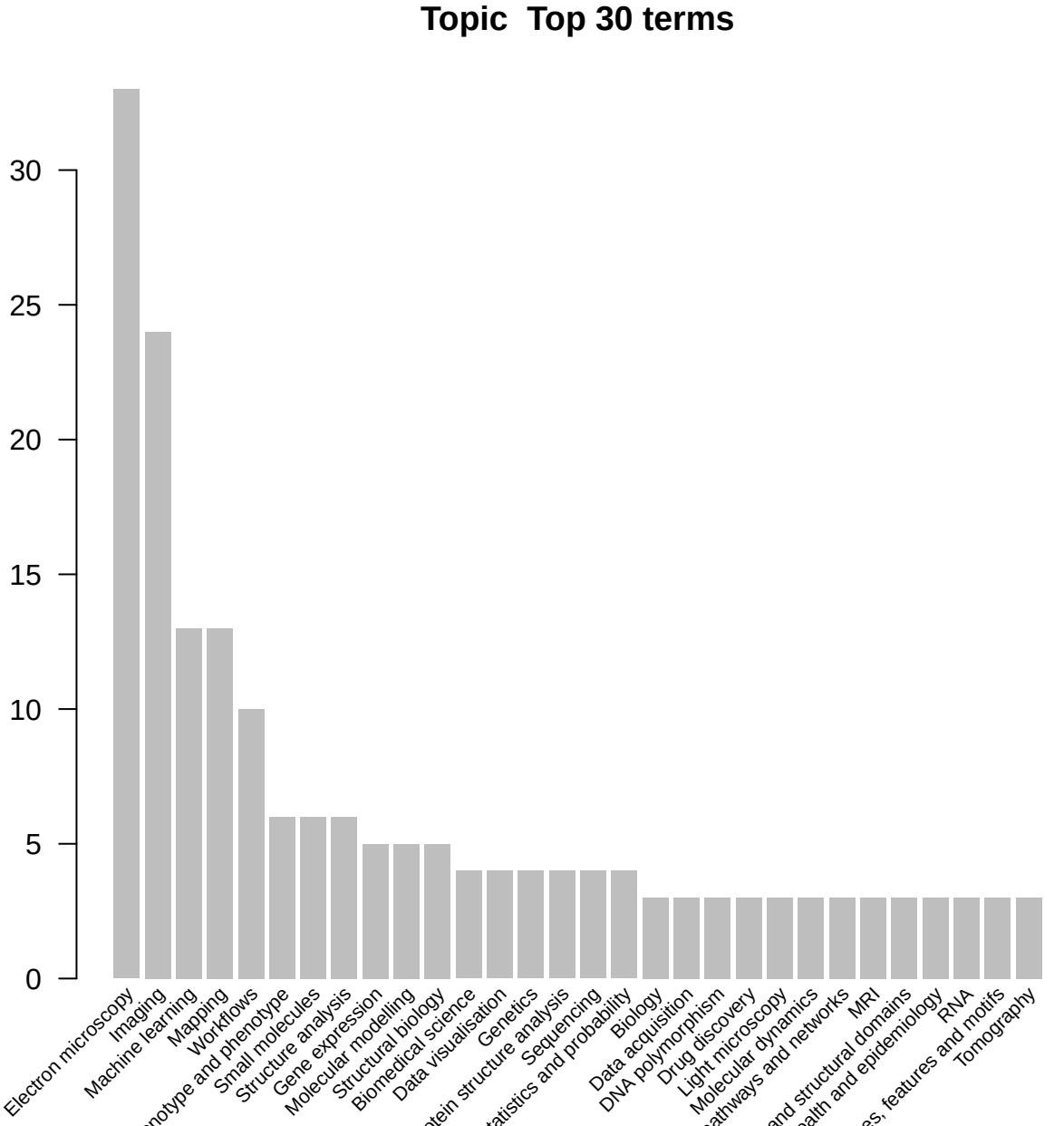
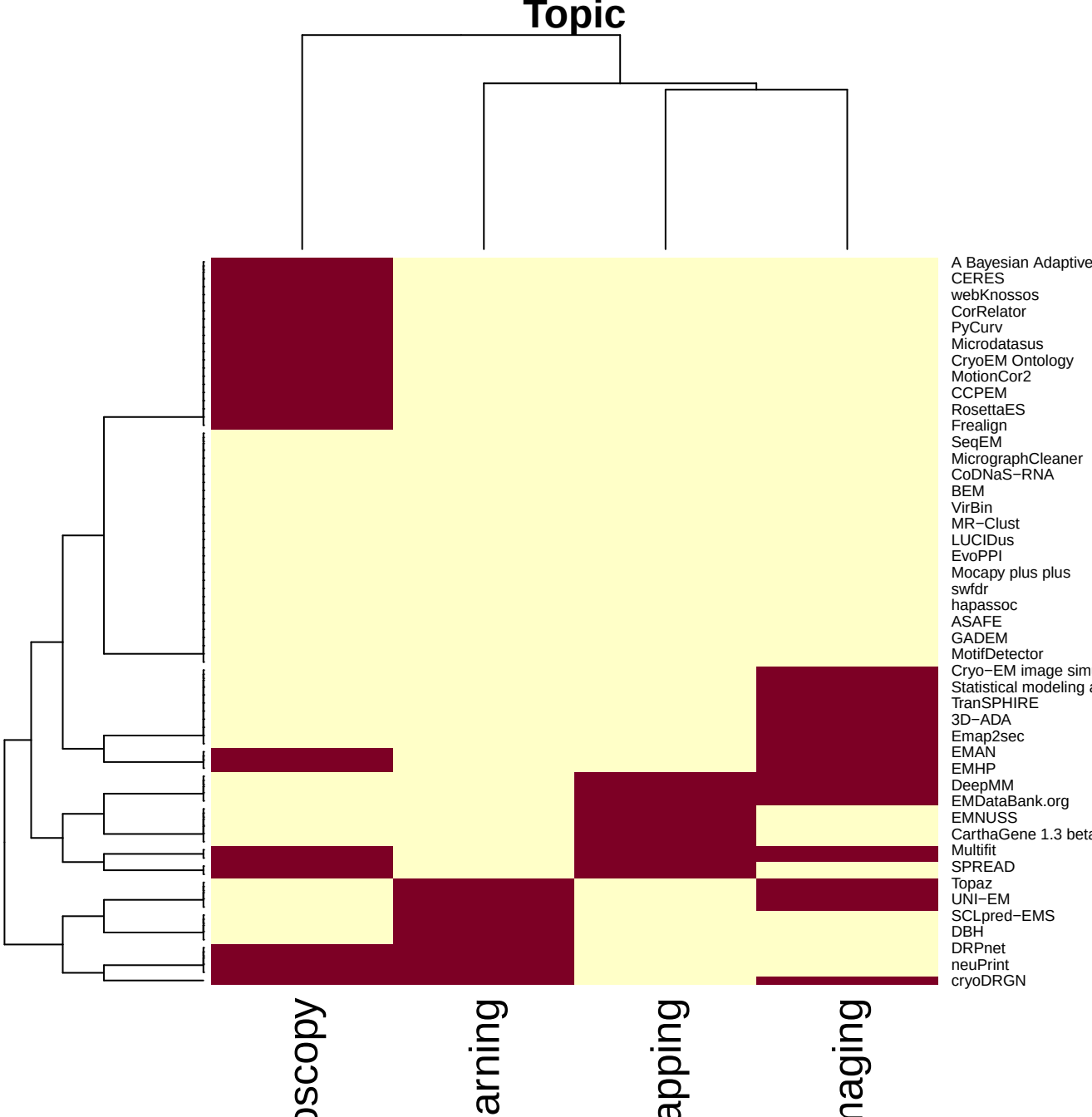
25
30
0
1
2
3
4
5
completeness


Topic Top 30 terms
30
25
20
15
10
5
0
Electron microscopy
Imaging
Machine learning
Mapping
Workflows
Genotype and phenotype
Small molecules
Structure analysis
Gene expression
Molecular modelling
Structural biology
Biomedical science
Data visualisation
Genetics
Protein structure analysis
Sequencing
Statistics and probability
Biology
Data acquisition
DNA polymorphism
Drug discovery
Light microscopy
Molecular dynamics
Molecular networks
MRI
folds and structural domains
ions, pathways and networks
blic health and epidemiology
RNA
nce sites, features and motifs
Tomography


Topic
A Bayesian Adaptive
CERES
webKnossos
CorRelator
PyCurv
Microdatasus
CryoEM Ontology
MotionCor2
CCPEM
RosettaES
Frealign
SeqEM
MicrographCleaner
CoDNaS−RNA
BEM
VirBin
MR−Clust
LUCIDus
EvoPPI
Mocapy plus plus
swfdr
hapassoc
ASAFE
GADEM
MotifDetector
Cryo−EM image sim
Statistical modeling
TranSPHIRE
3D−ADA
Emap2sec
EMAN
EMHP
DeepMM
EMDataBank.org
EMNUSS
CarthaGene 1.3 beta
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SPREAD
Topaz
UNI−EM
SCLpred−EMS
DBH
DRPnet
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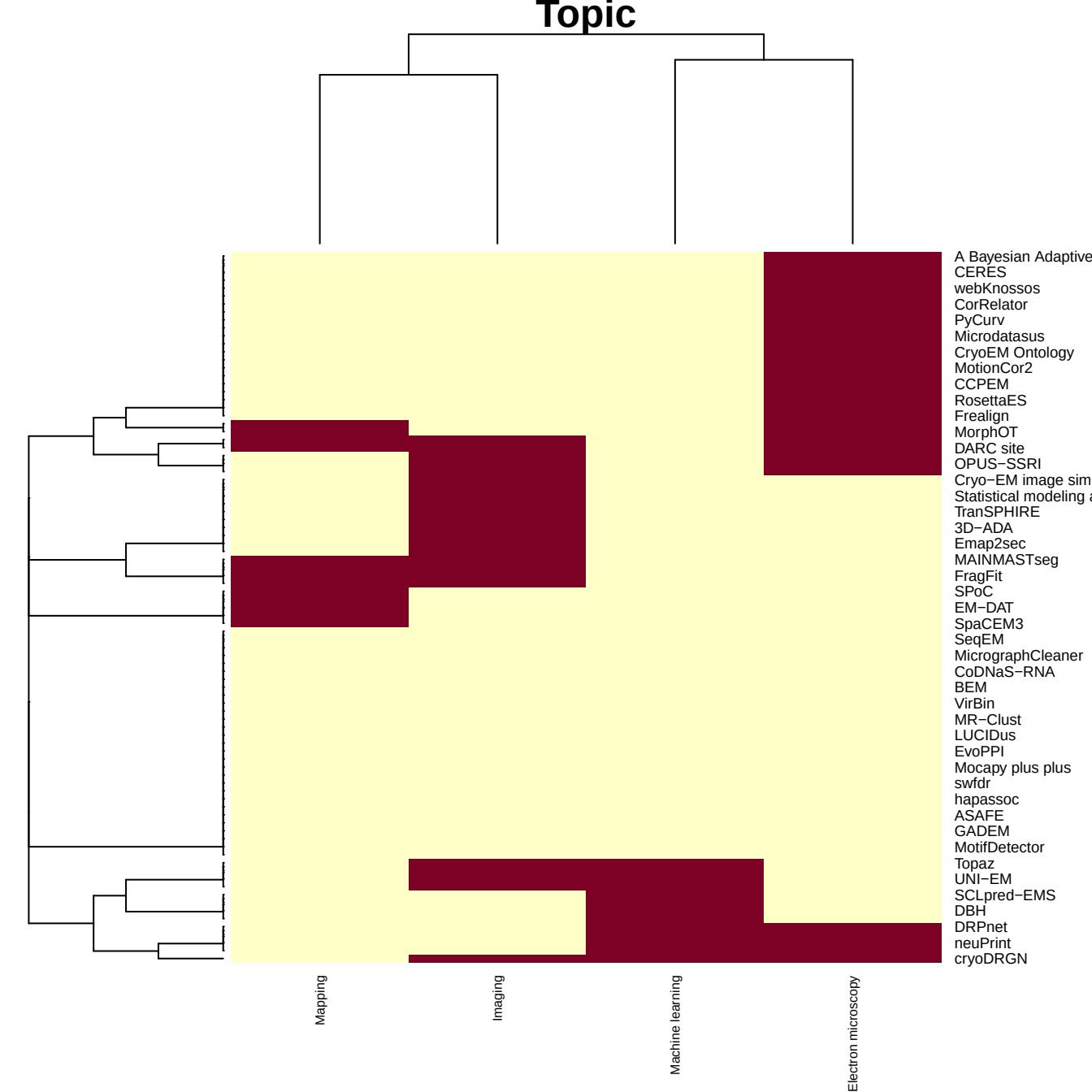
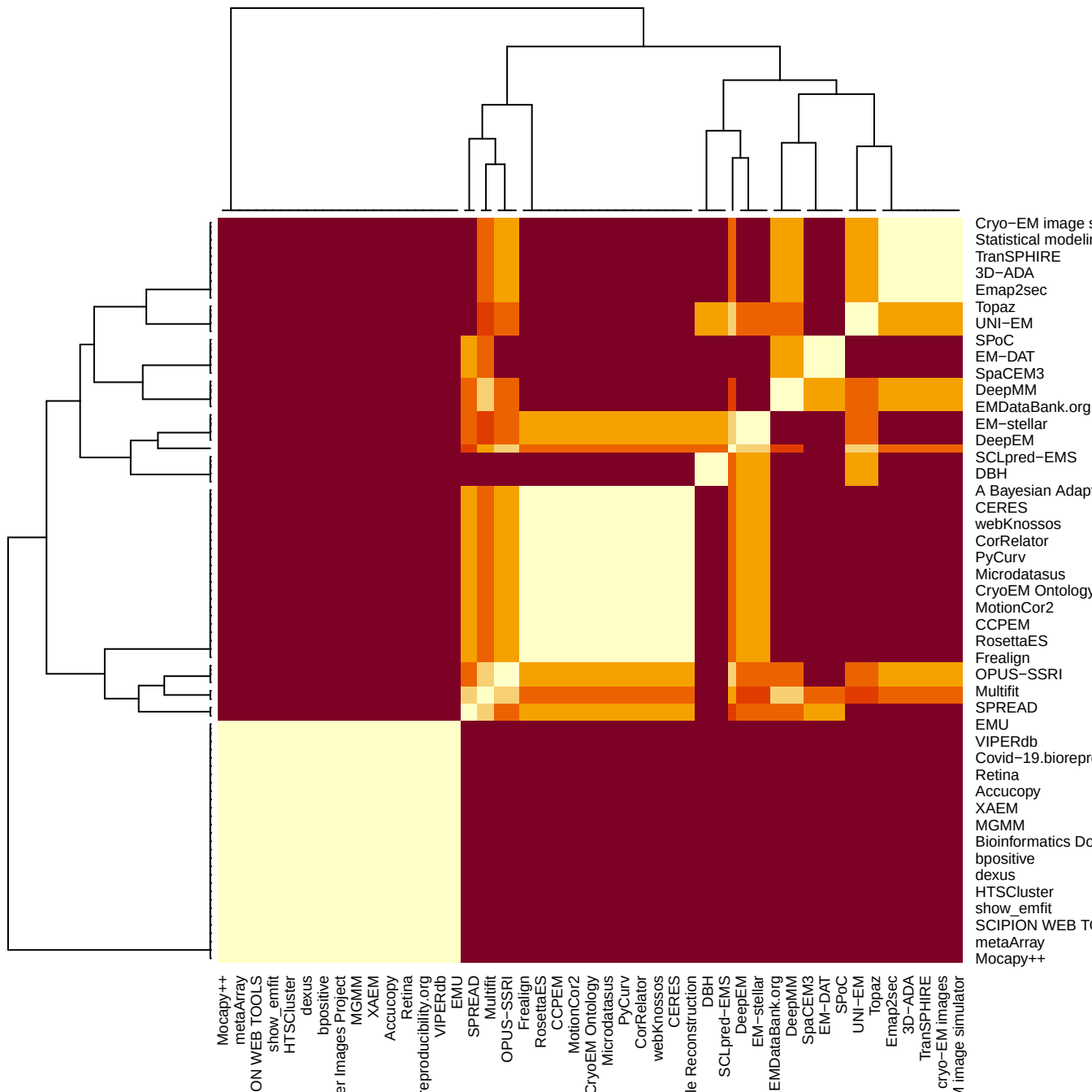

Topic
A Bayesian Adaptive
CERES
webKnossos
CorRelator
PyCurv
Microdatasus
CryoEM Ontology
MotionCor2
CCPEM
RosettaES
Frealign
MorphOT
DARC site
OPUS−SSRI
Cryo−EM image sim
Statistical modeling a
TranSPHIRE
3D−ADA
Emap2sec
MAINMASTseg
FragFit
SPoC
EM−DAT
SpaCEM3
SeqEM
MicrographCleaner
CoDNaS−RNA
BEM
VirBin
MR−Clust
LUCIDus
EvoPPI
Mocapy plus plus
swfdr
hapassoc
ASAFE
GADEM
MotifDetector
Topaz
UNI−EM
SCLpred−EMS
DBH
DRPnet
neuPrint
cryoDRGN
Mapping
Imaging
Machine learning
Electron microscopy


Cryo−EM image s
Statistical modelin
TranSPHIRE
3D−ADA
Emap2sec
Topaz
UNI−EM
SPoC
EM−DAT
SpaCEM3
DeepMM
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EM−stellar
DeepEM
SCLpred−EMS
DBH
A Bayesian Adapt
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webKnossos
CorRelator
PyCurv
Microdatasus
CryoEM Ontology
MotionCor2
CCPEM
RosettaES
Frealign
OPUS−SSRI
Multifit
SPREAD
EMU
VIPERdb
Covid−19.biorepr
Retina
Accucopy
XAEM
MGMM
Bioinformatics Do
bpositive
dexus
HTSCluster
show_emfit
SCIPION WEB TO
metaArray
Mocapy++
Mocapy++
metaArray
ON WEB TOOLS
show_emfit
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bpositive
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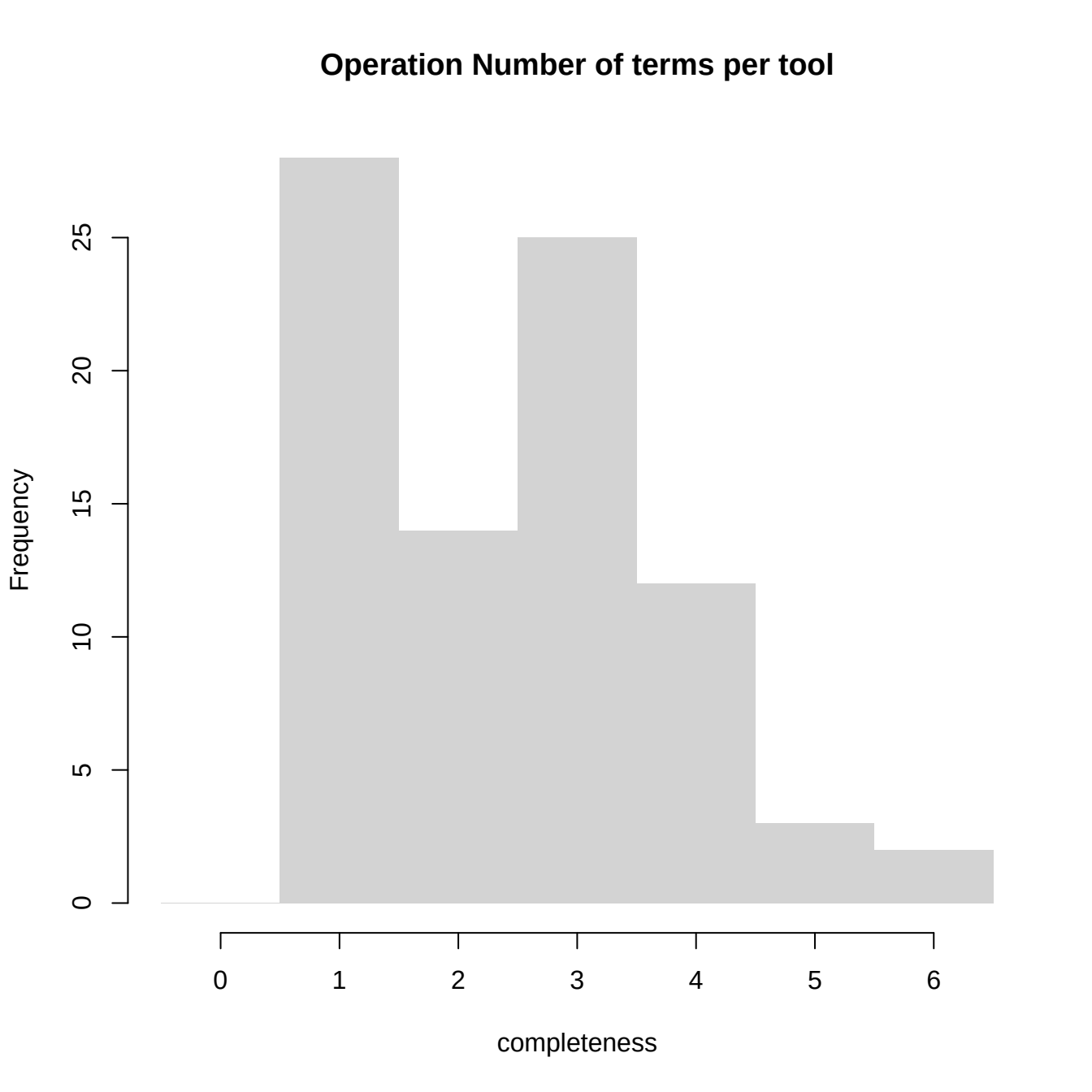
MGMM
XAEM
Accucopy
Retina
eproducibility.org
VIPERdb
EMU
SPREAD
Multifit
OPUS−SSRI
Frealign
RosettaES
CCPEM
MotionCor2
CryoEM Ontology
Microdatasus
PyCurv
CorRelator
webKnossos
CERES
e Reconstruction
DBH
SCLpred−EMS
DeepEM
EM−stellar
EMDataBank.org
DeepMM
SpaCEM3
EM−DAT
SPoC
UNI−EM
Topaz
Emap2sec
3D−ADA
TranSPHIRE
cryo−EM images
image simulator


Operation Number of terms per tool
Frequency
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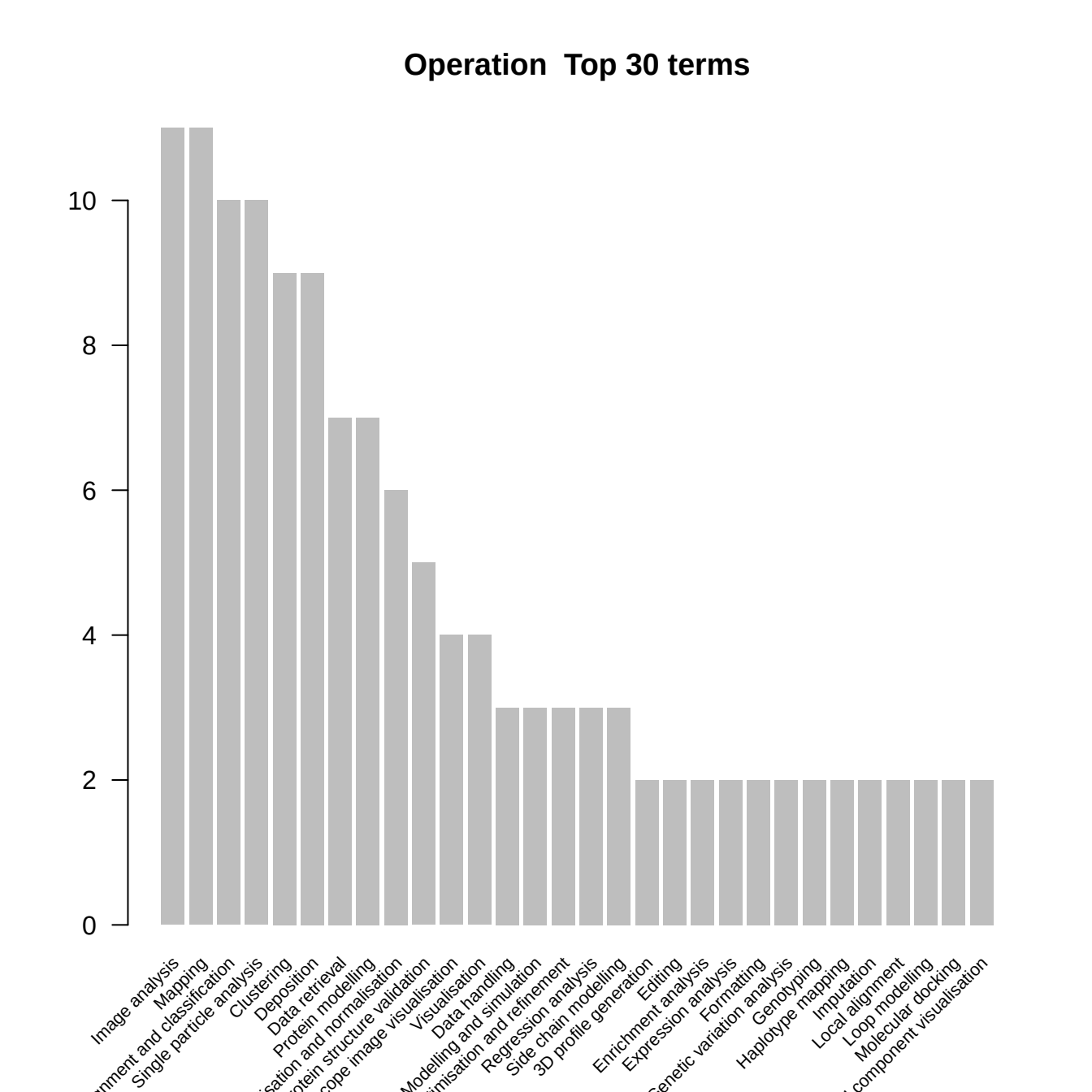
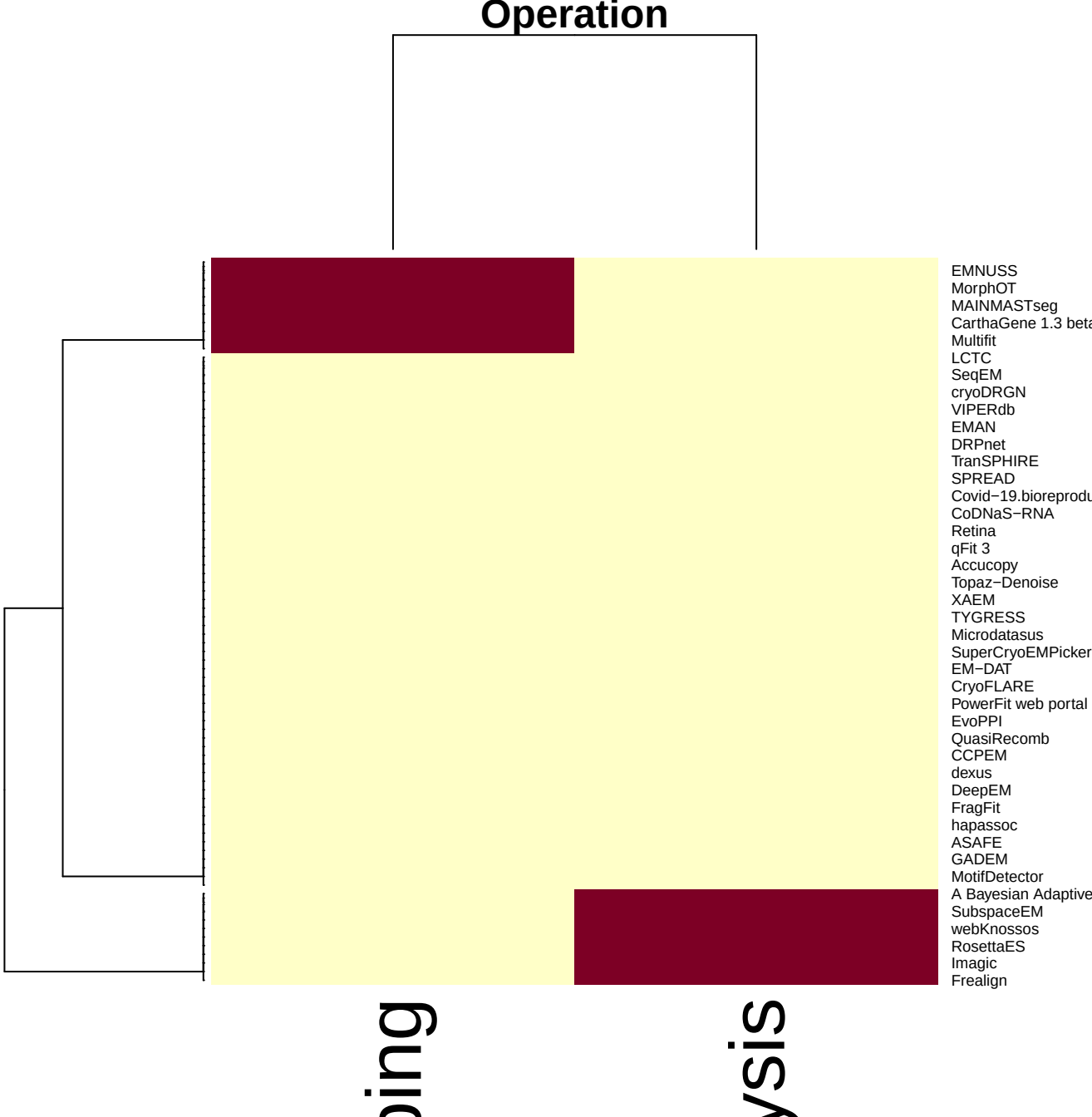
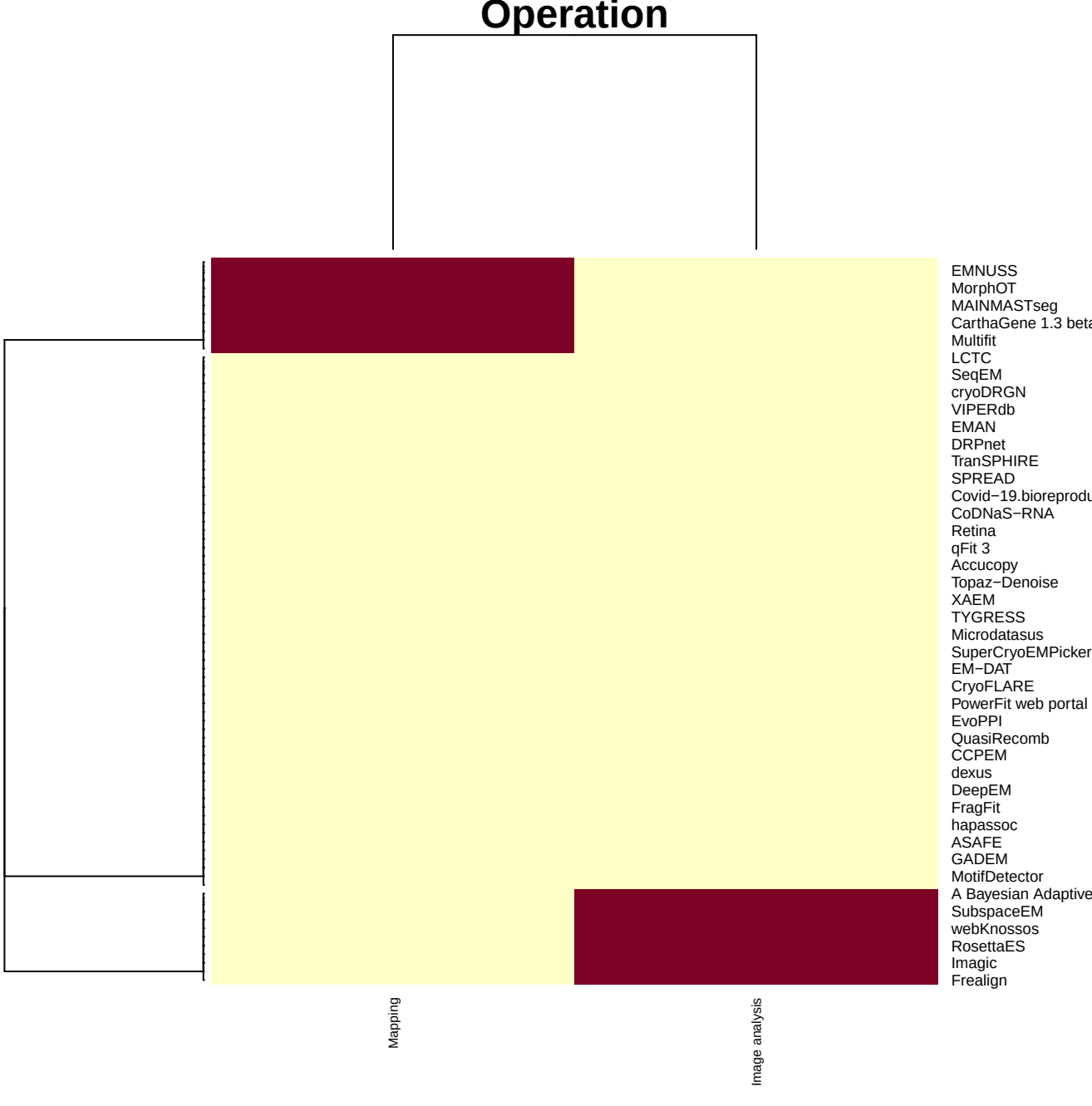
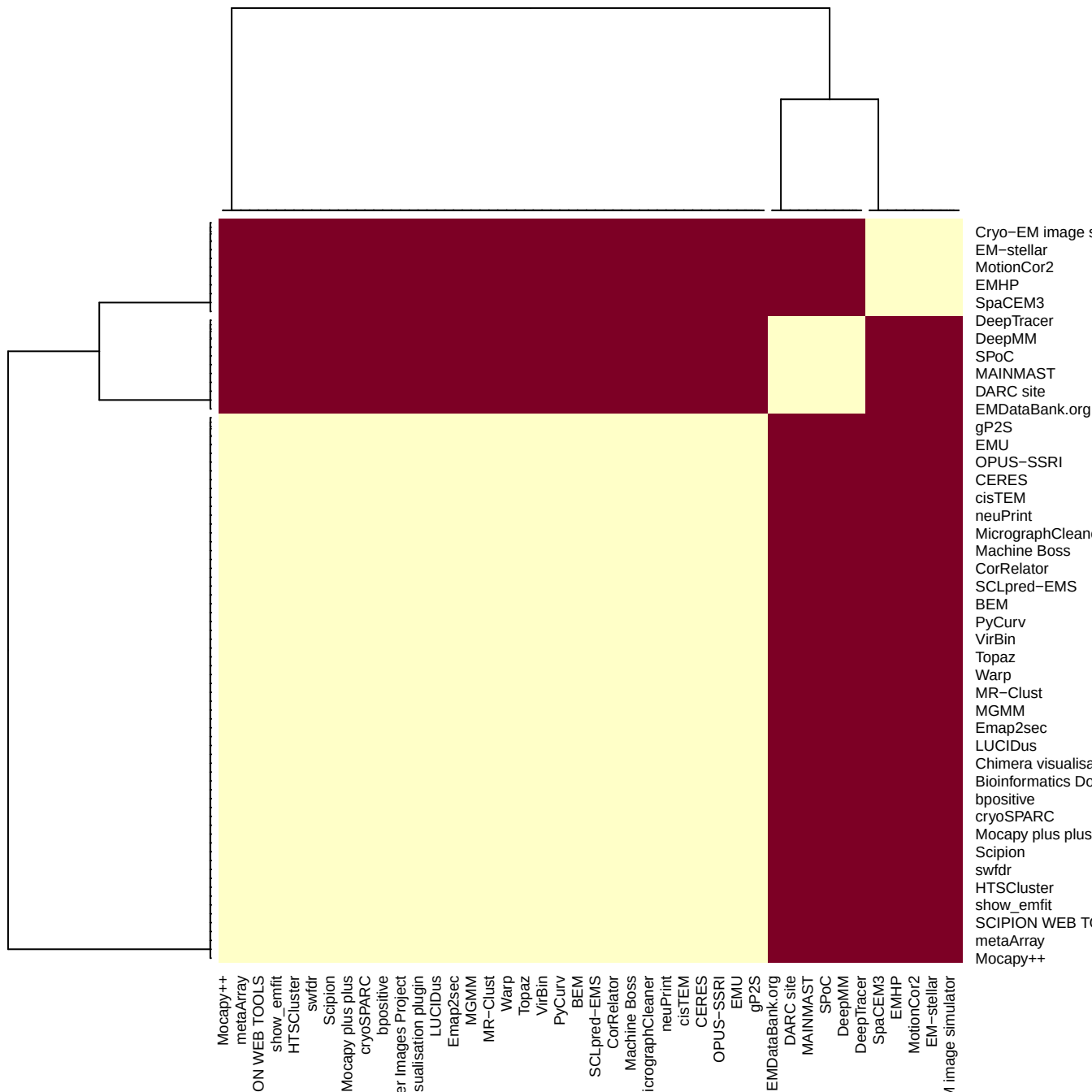
15
20
25
0
1
2
3
4
5
6
completeness


Operation Top 30 terms
0
2
4
6
8
10
Image analysis
Mapping
nment and classification
Single particle analysis
Clustering
Deposition
Data retrieval
Protein modelling
sation and normalisation
otein structure validation
cope image visualisation
Visualisation
Data handling
Modelling and simulation
imisation and refinement
Regression analysis
Side chain modelling
3D profile generation
Editing
Enrichment analysis
Expression analysis
Formatting
enetic variation analysis
Genotyping
Haplotype mapping
Imputation
Local alignment
Loop modelling
Molecular docking
component visualisation


Operation
EMNUSS
MorphOT
MAINMASTseg
CarthaGene 1.3 beta
Multifit
LCTC
SeqEM
cryoDRGN
VIPERdb
EMAN
DRPnet
TranSPHIRE
SPREAD
Covid−19.bioreprodu
CoDNaS−RNA
Retina
qFit 3
Accucopy
Topaz−Denoise
XAEM
TYGRESS
Microdatasus
SuperCryoEMPicker
EM−DAT
CryoFLARE
PowerFit web portal
EvoPPI
QuasiRecomb
CCPEM
dexus
DeepEM
FragFit
hapassoc
ASAFE
GADEM
MotifDetector
A Bayesian Adaptive
SubspaceEM
webKnossos
RosettaES
Imagic
Frealign
ing
ysis


Operation
EMNUSS
MorphOT
MAINMASTseg
CarthaGene 1.3 beta
Multifit
LCTC
SeqEM
cryoDRGN
VIPERdb
EMAN
DRPnet
TranSPHIRE
SPREAD
Covid−19.bioreprodu
CoDNaS−RNA
Retina
qFit 3
Accucopy
Topaz−Denoise
XAEM
TYGRESS
Microdatasus
SuperCryoEMPicker
EM−DAT
CryoFLARE
PowerFit web portal
EvoPPI
QuasiRecomb
CCPEM
dexus
DeepEM
FragFit
hapassoc
ASAFE
GADEM
MotifDetector
A Bayesian Adaptive
SubspaceEM
webKnossos
RosettaES
Imagic
Frealign
Mapping
Image analysis


Cryo−EM image s
EM−stellar
MotionCor2
EMHP
SpaCEM3
DeepTracer
DeepMM
SPoC
MAINMAST
DARC site
EMDataBank.org
gP2S
EMU
OPUS−SSRI
CERES
cisTEM
neuPrint
MicrographClean
Machine Boss
CorRelator
SCLpred−EMS
BEM
PyCurv
VirBin
Topaz
Warp
MR−Clust
MGMM
Emap2sec
LUCIDus
Chimera visualisa
Bioinformatics Do
bpositive
cryoSPARC
Mocapy plus plus
Scipion
swfdr
HTSCluster
show_emfit
SCIPION WEB TO
metaArray
Mocapy++
Mocapy++
metaArray
ON WEB TOOLS
show_emfit
HTSCluster
swfdr
Scipion
Mocapy plus plus
cryoSPARC
bpositive
er Images Project
sualisation plugin
LUCIDus
Emap2sec
MGMM
MR−Clust
Warp
Topaz
VirBin
PyCurv
BEM
SCLpred−EMS
CorRelator
Machine Boss
icrographCleaner
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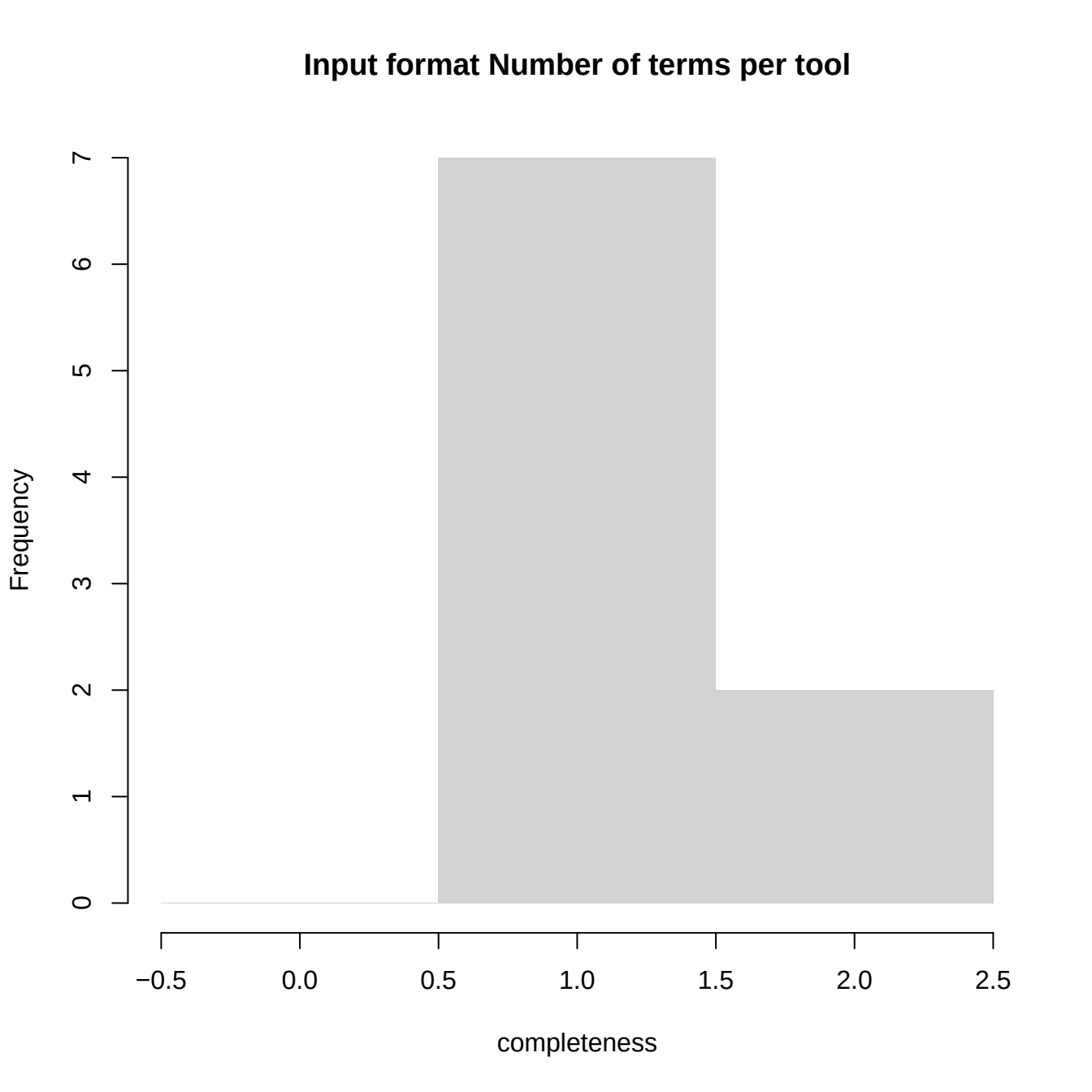
cisTEM
CERES
OPUS−SSRI
EMU
gP2S
EMDataBank.org
DARC site
MAINMAST
SPoC
DeepMM
DeepTracer
SpaCEM3
EMHP
MotionCor2
EM−stellar
M image simulator


Input format Number of terms per tool
Frequency
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5
6
7
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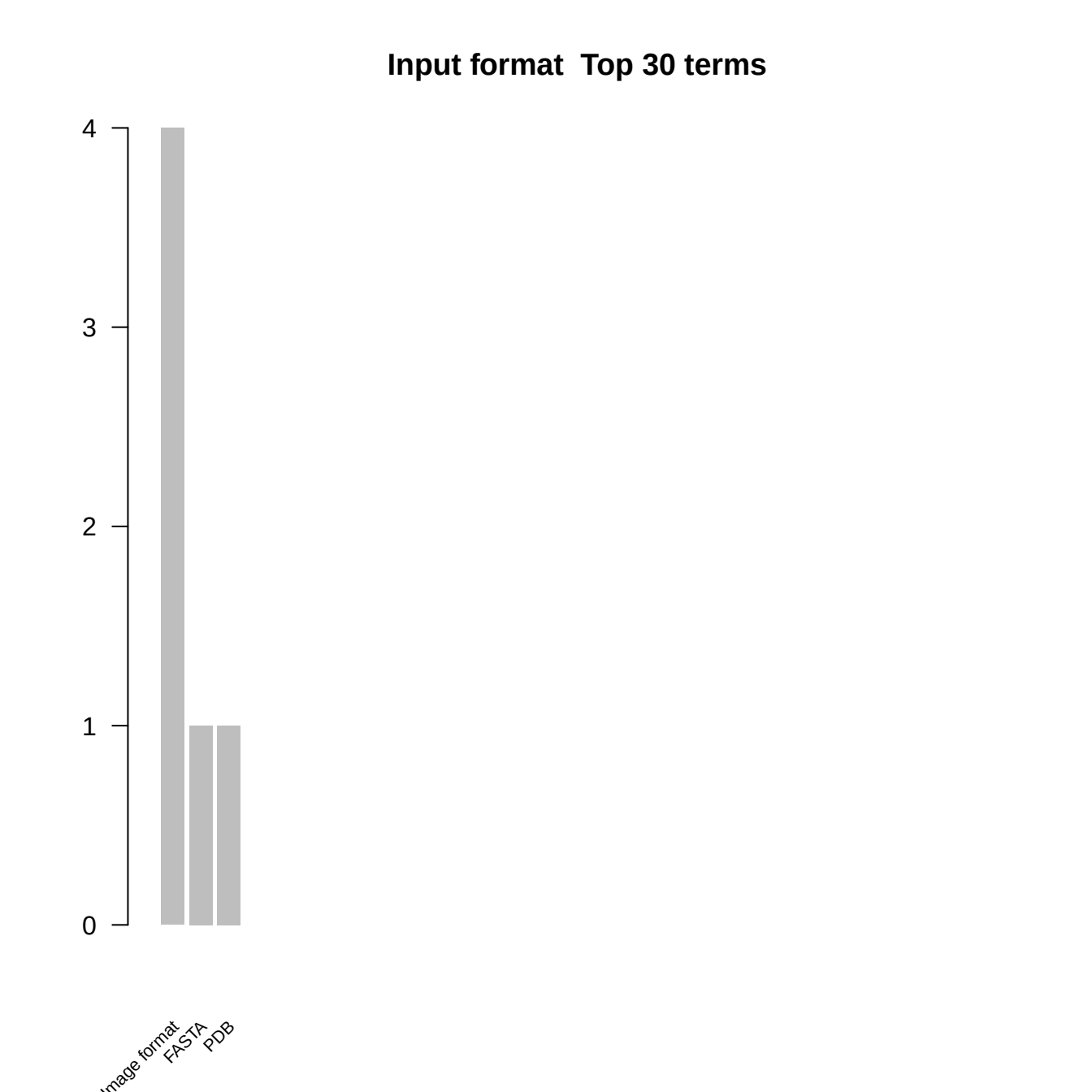
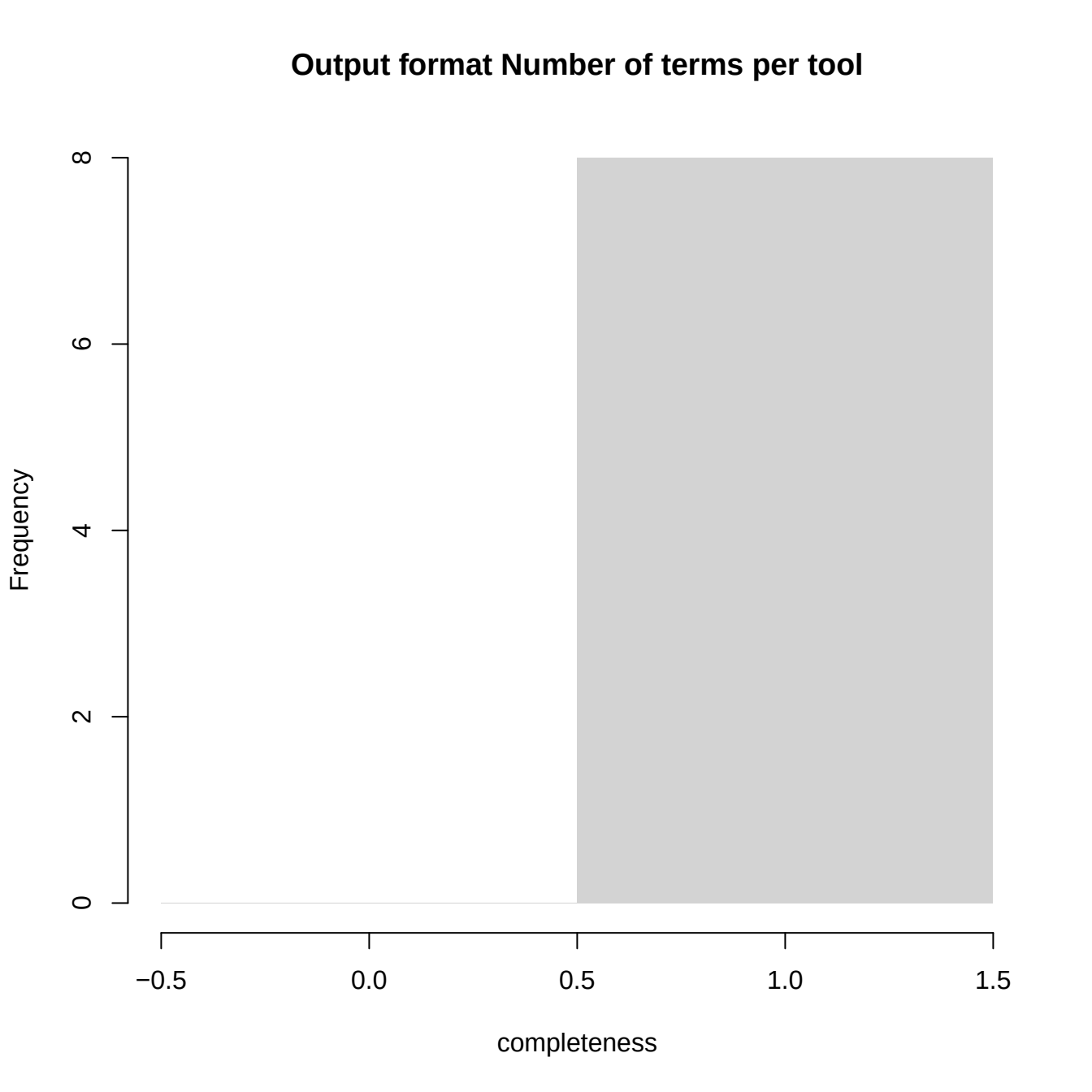
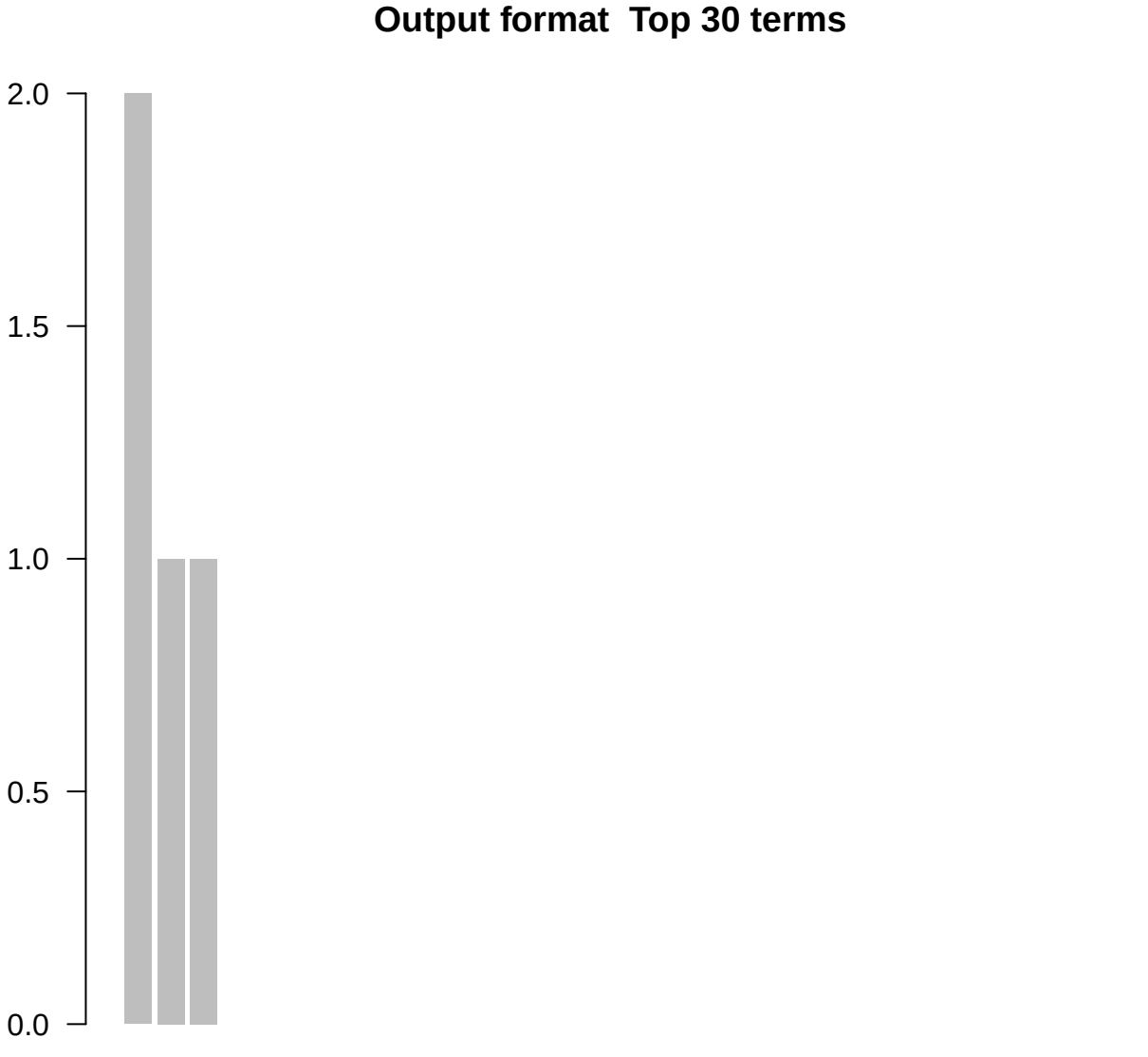
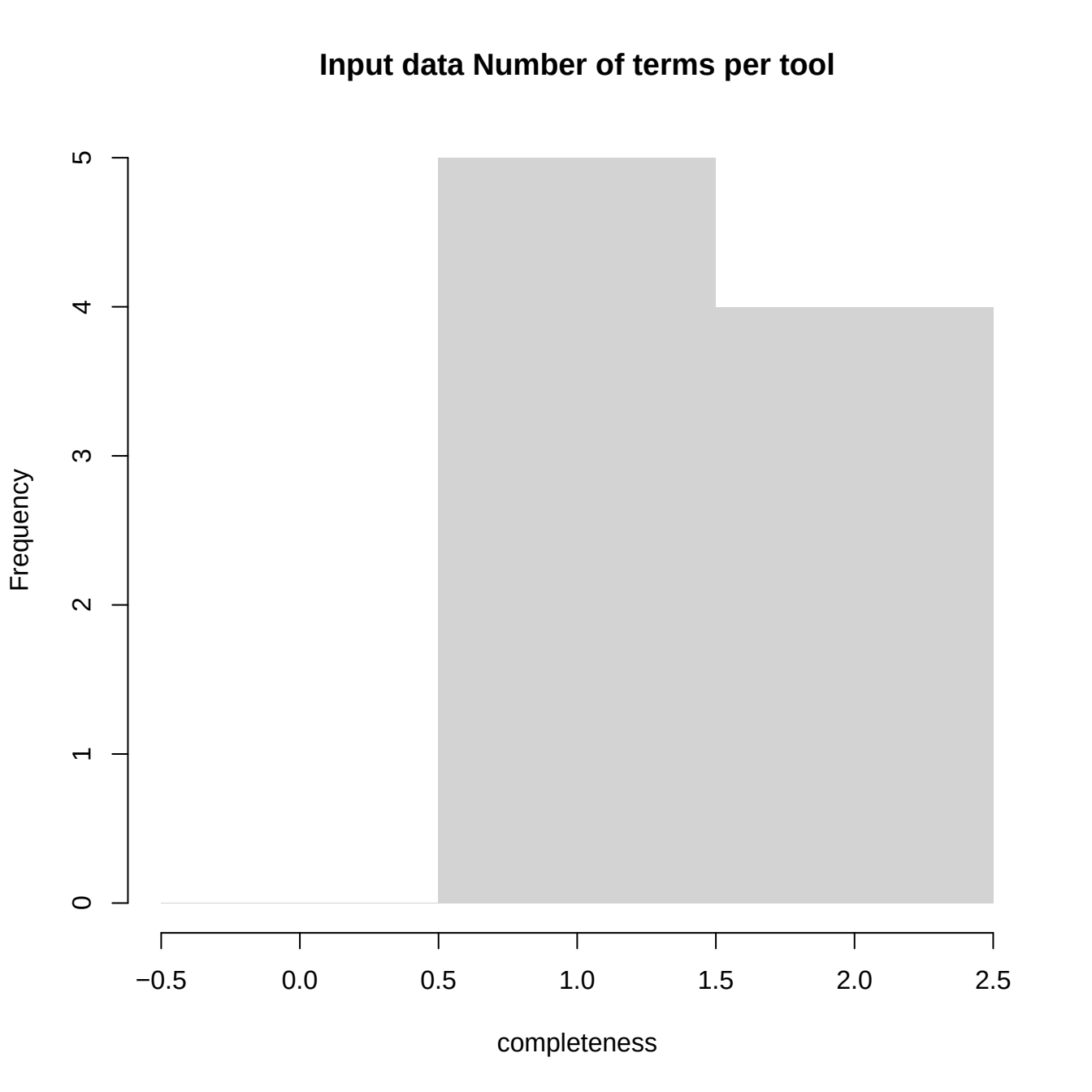
0.0
0.5
1.0
1.5
2.0
2.5
completeness


Input format Top 30 terms
4
3
2
1
0
Image format
FASTA
PDB


Output format Number of terms per tool
Frequency
0
2
4
6
8
−0.5
0.0
0.5
1.0
1.5
completeness


Output format Top 30 terms
2.0
1.5
1.0
0.5
0.0


Input data Number of terms per tool
Frequency
0
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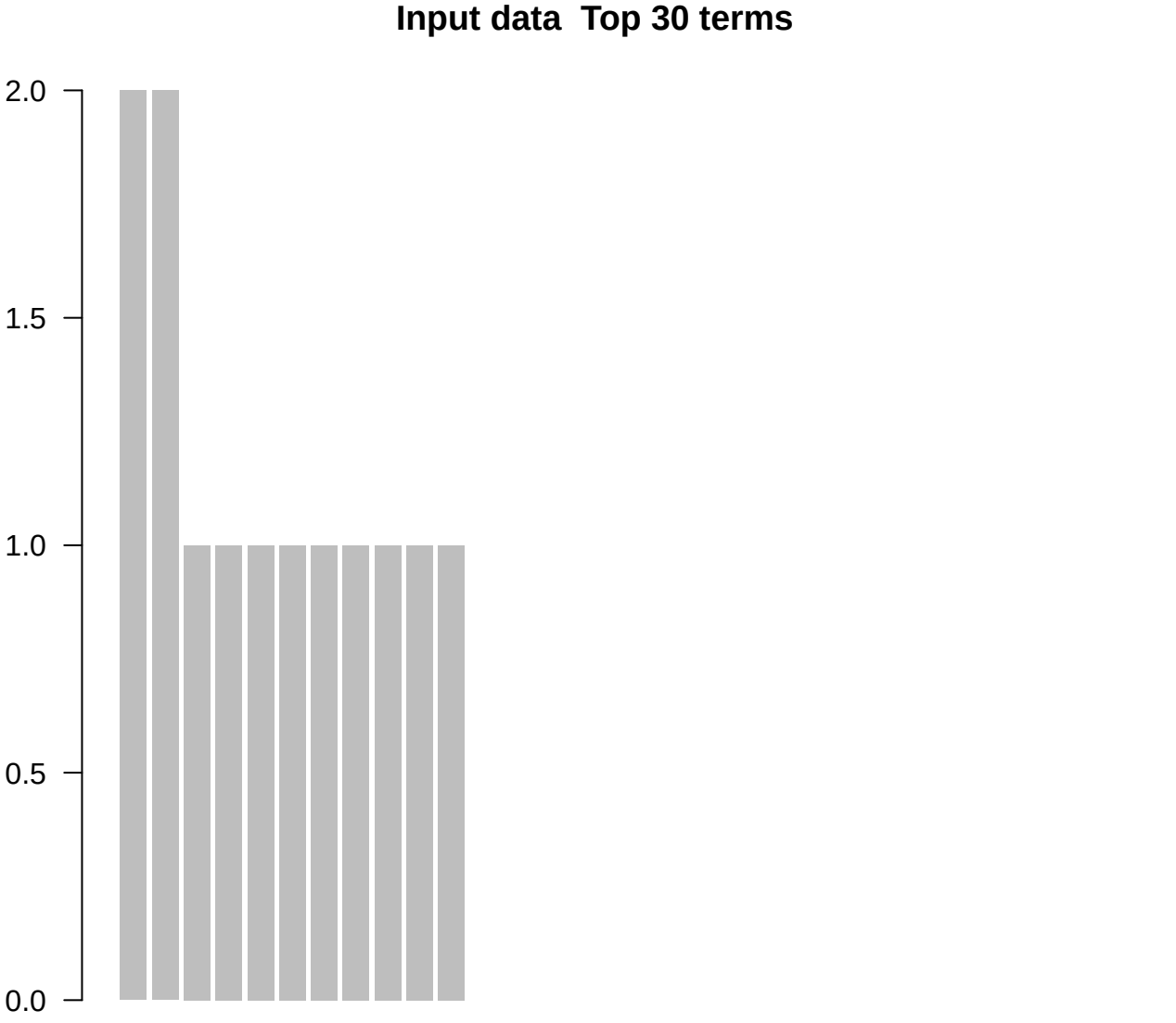
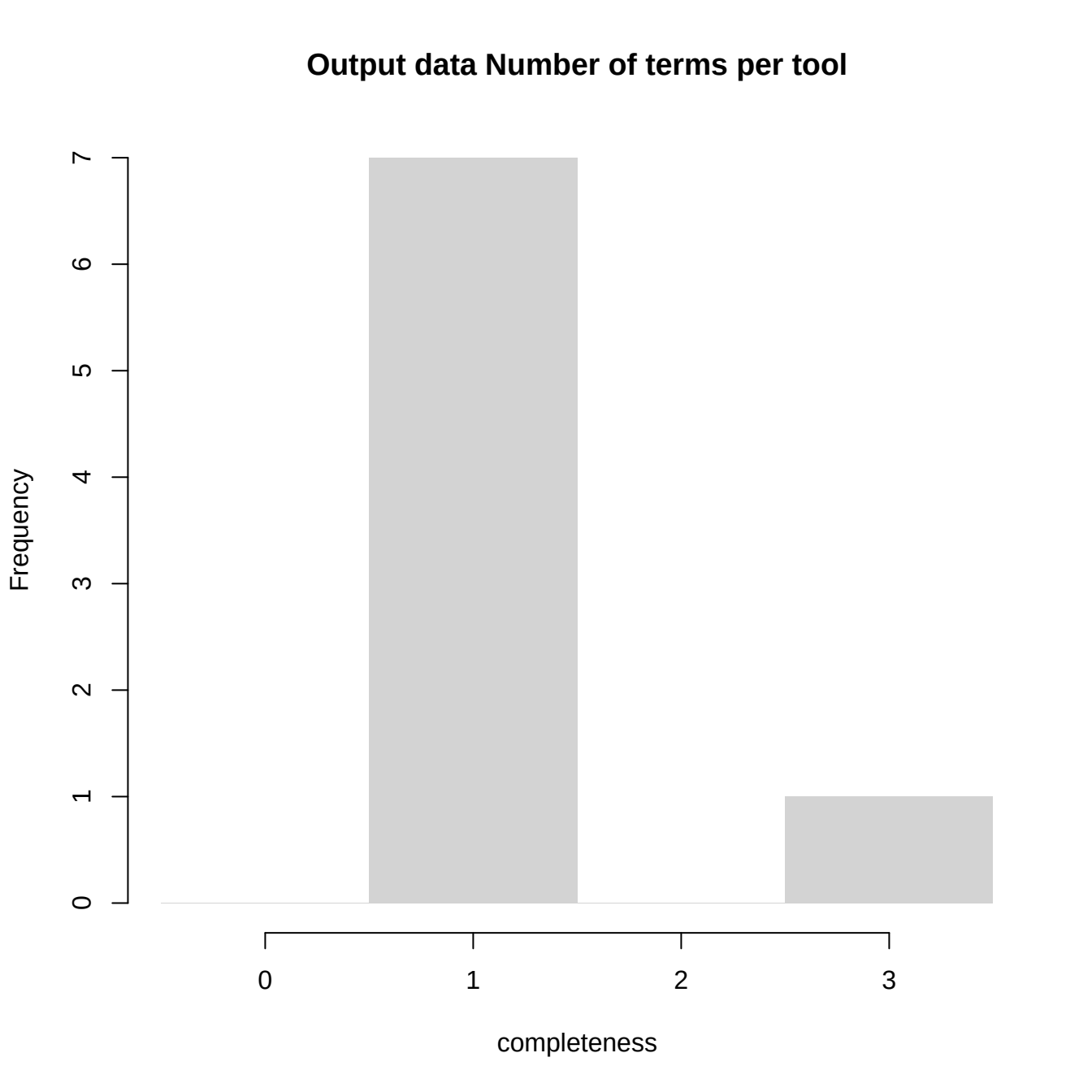
2
3
4
5
−0.5
0.0
0.5
1.0
1.5
2.0
2.5
completeness


Input data Top 30 terms
2.0
1.5
1.0
0.5
0.0


Output data Number of terms per tool
Frequency
0
1
2
3
4
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6
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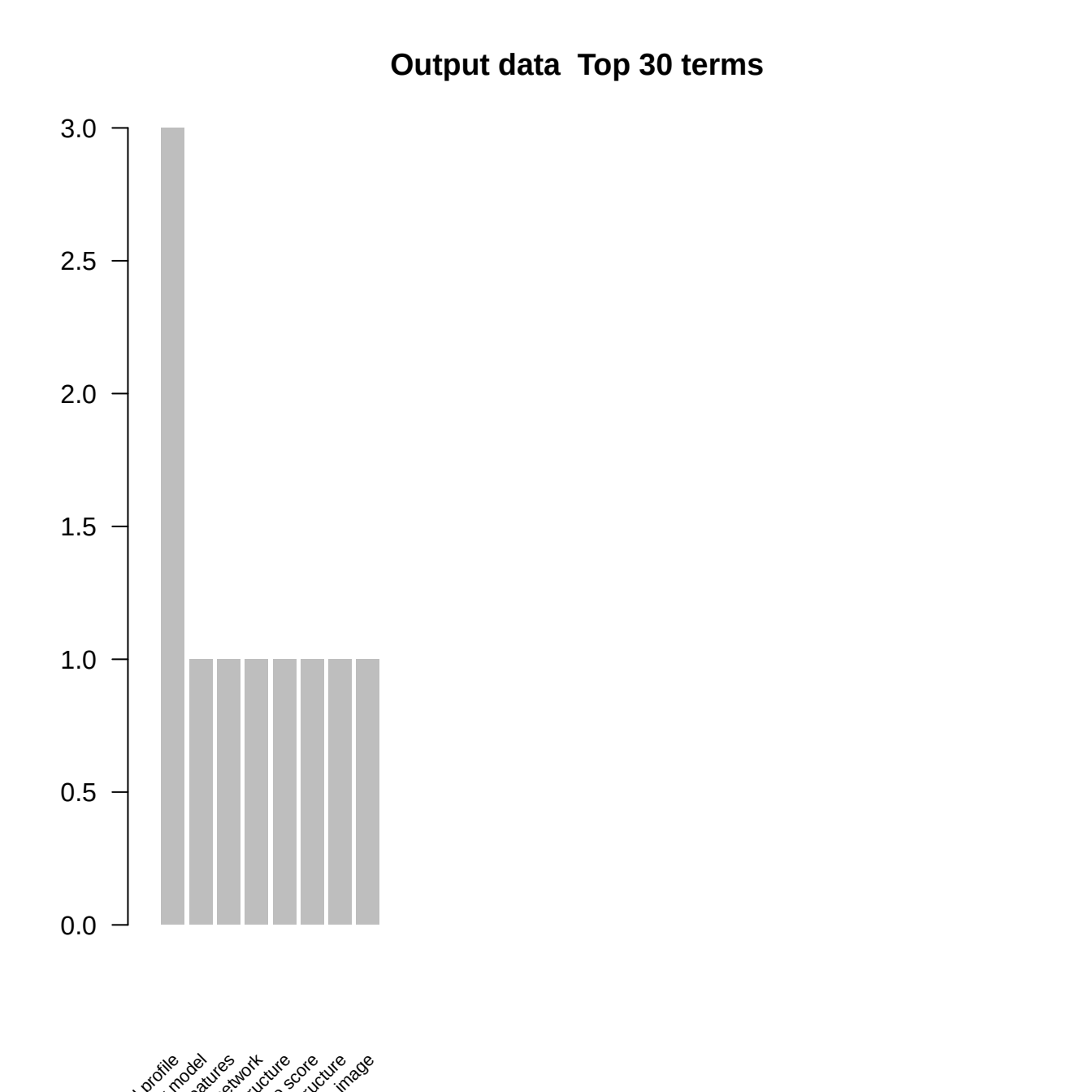
0
1
2
3
completeness


Output data Top 30 terms
3.0
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2.0
1.5
1.0
0.5
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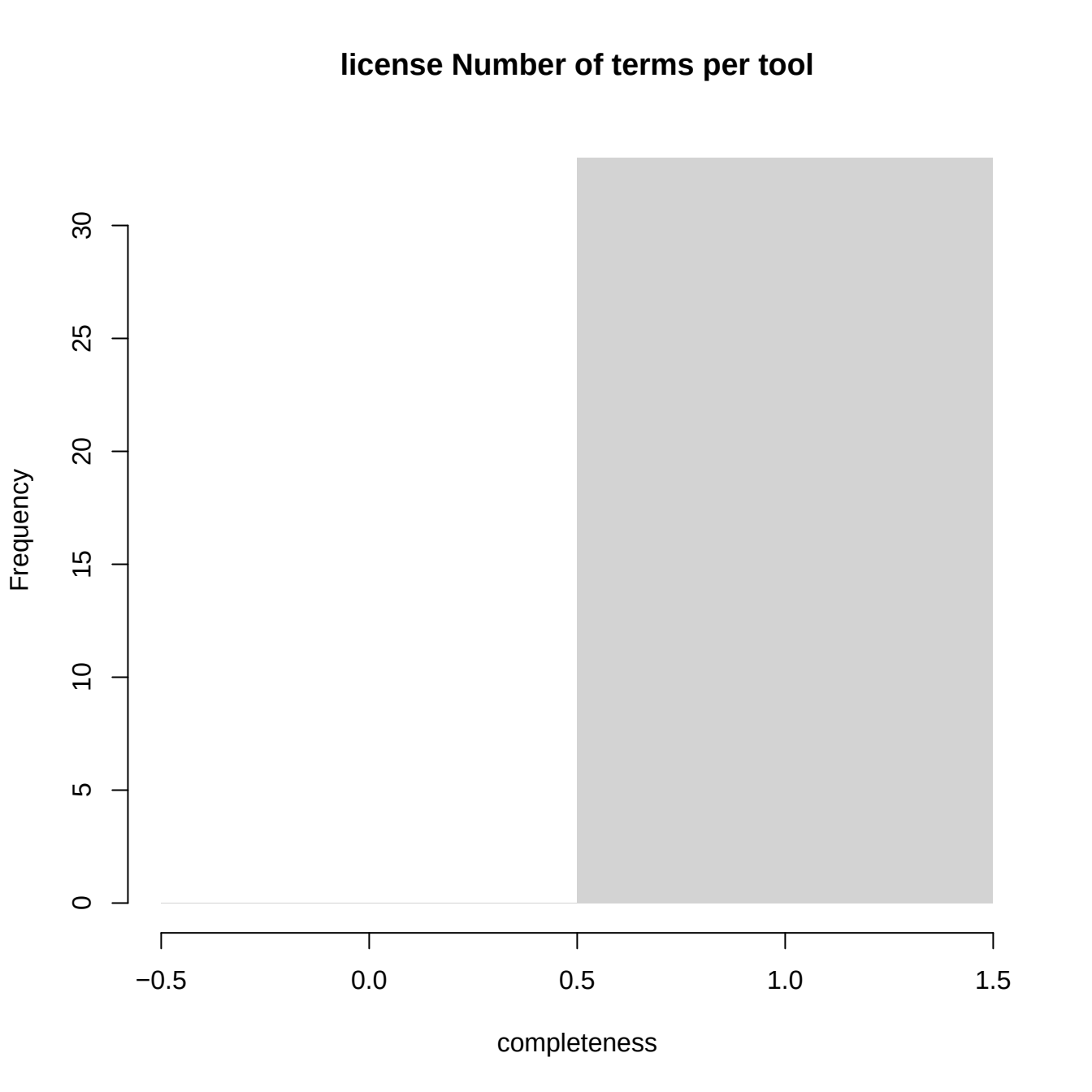
profile
model
atures
etwork
ucture
score
ucture
image


license Number of terms per tool
Frequency
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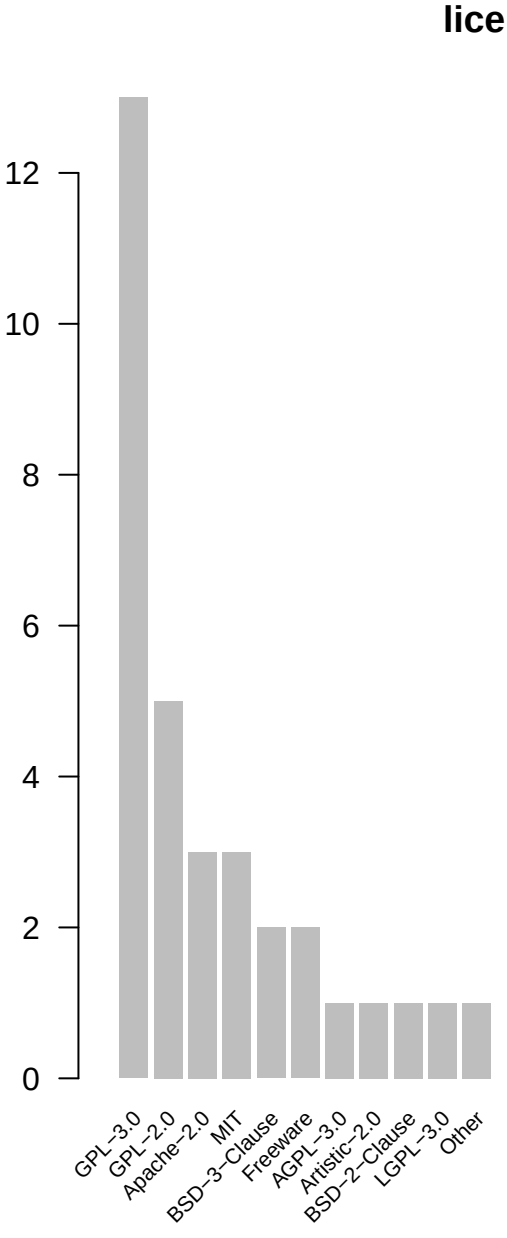
10
15
20
25
30
−0.5
0.0
0.5
1.0
1.5
completeness


license Top 30 terms
12
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8
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4
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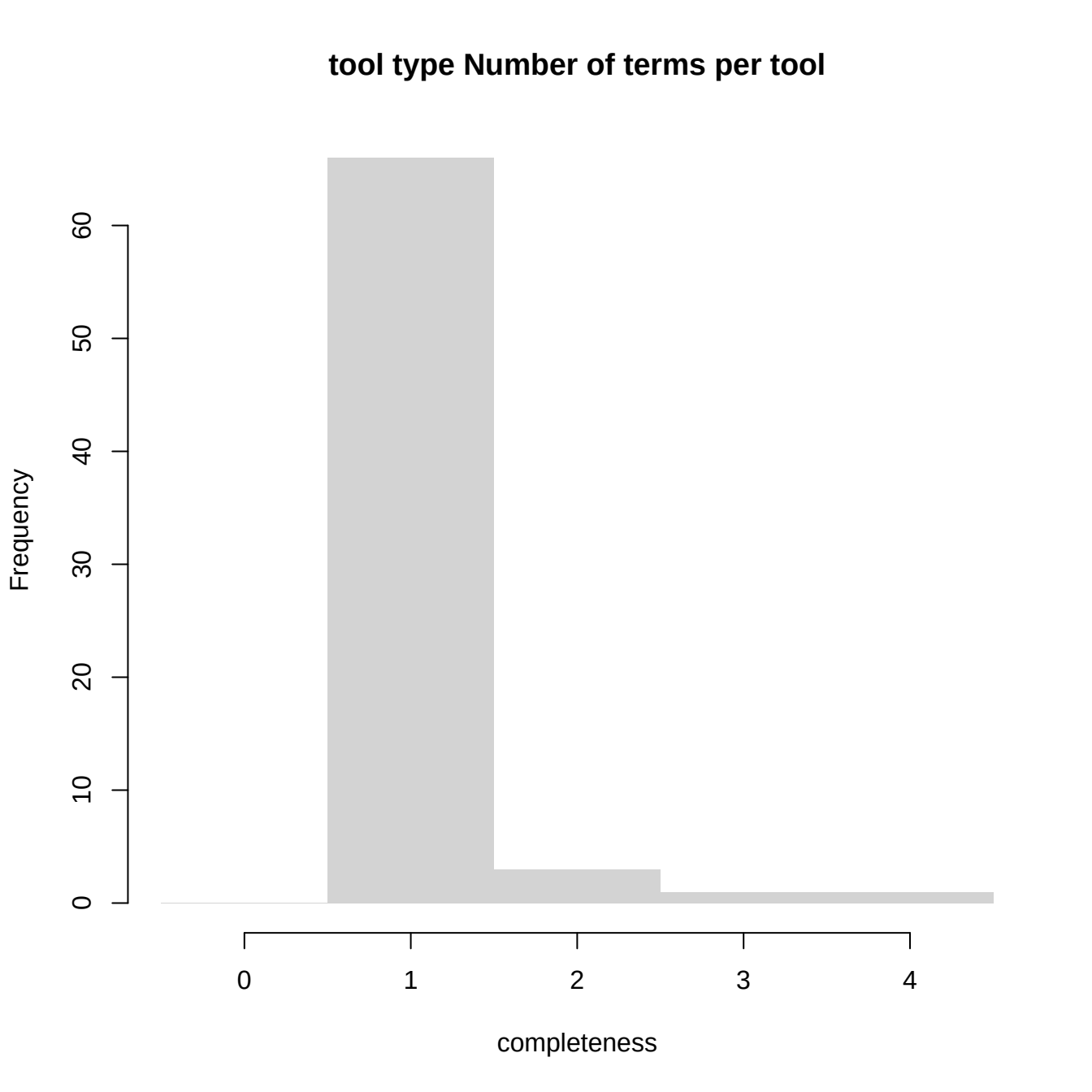
GPL−3.0
GPL−2.0
Apache−2.0
MIT
BSD−3−Clause
Freeware
AGPL−3.0
Artistic−2.0
BSD−2−Clause
LGPL−3.0
Other


tool type Number of terms per tool
Frequency
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50
60
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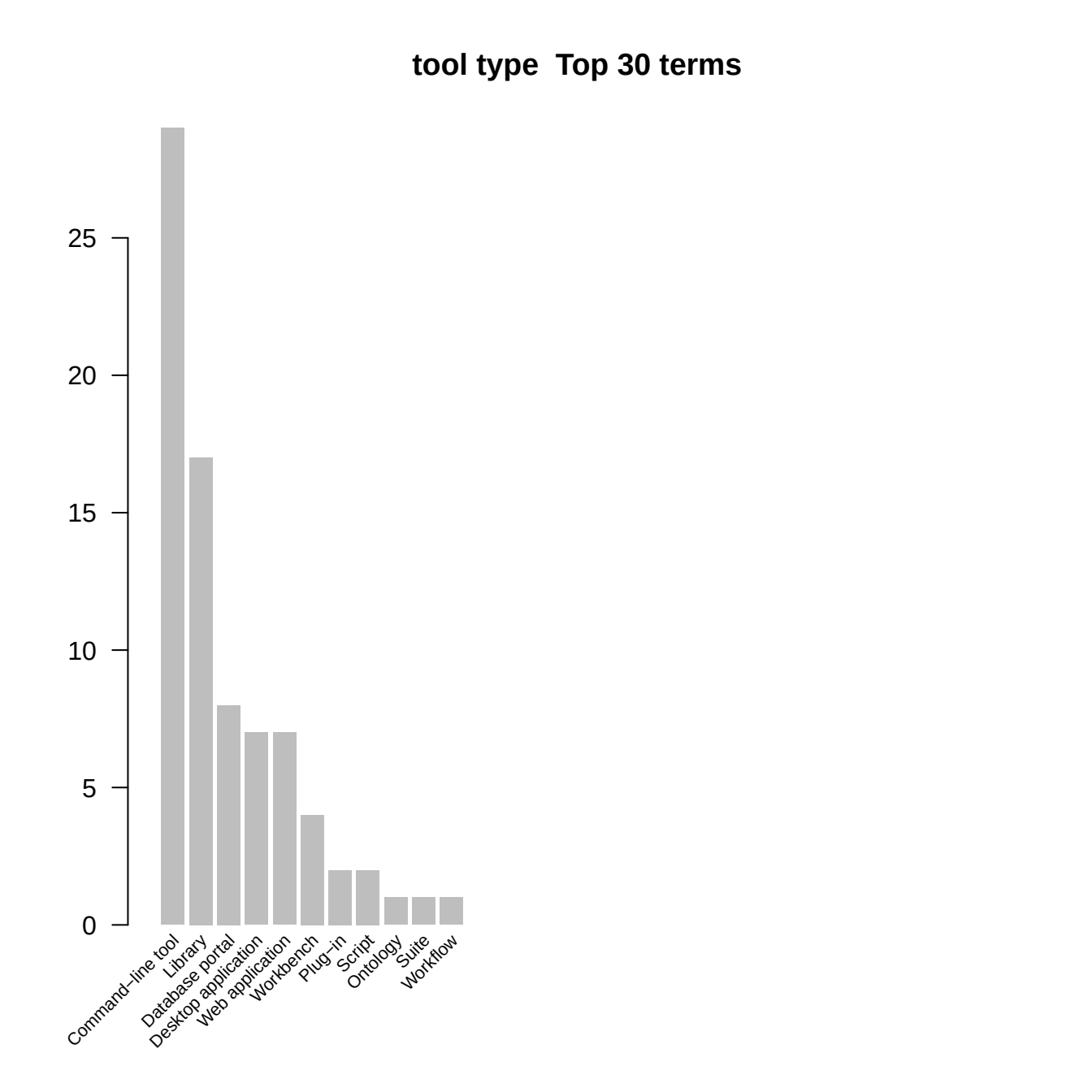
1
2
3
4
completeness


tool type Top 30 terms
25
20
15
10
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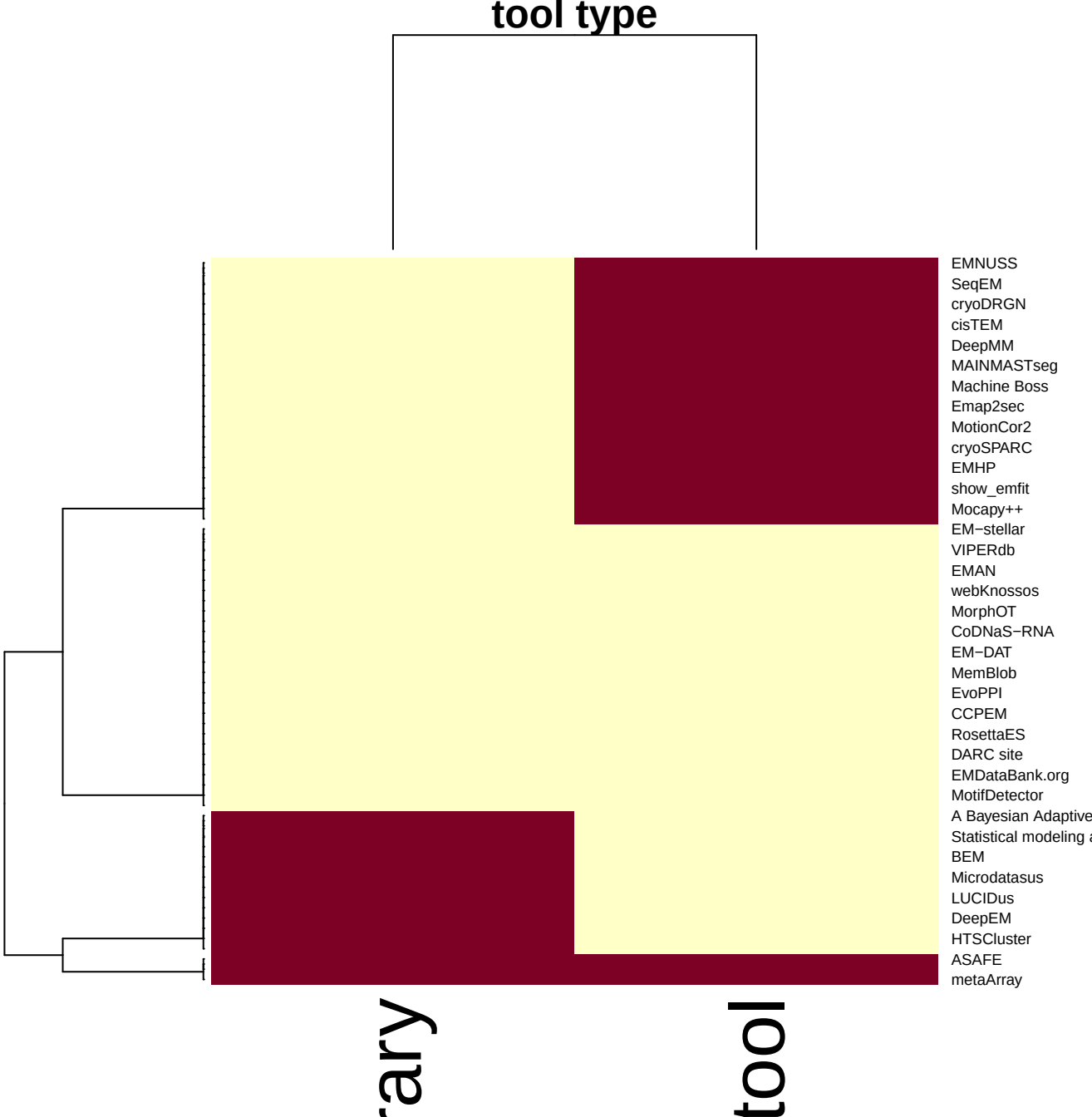
Command−line tool
Library
Database portal
Desktop application
Web application
Workbench
Plug−in
Script
Ontology
Suite
Workflow


tool type
EMNUSS
SeqEM
cryoDRGN
cisTEM
DeepMM
MAINMASTseg
Machine Boss
Emap2sec
MotionCor2
cryoSPARC
EMHP
show_emfit
Mocapy++
EM−stellar
VIPERdb
EMAN
webKnossos
MorphOT
CoDNaS−RNA
EM−DAT
MemBlob
EvoPPI
CCPEM
RosettaES
DARC site
EMDataBank.org
MotifDetector
A Bayesian Adaptive
Statistical modeling a
BEM
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LUCIDus
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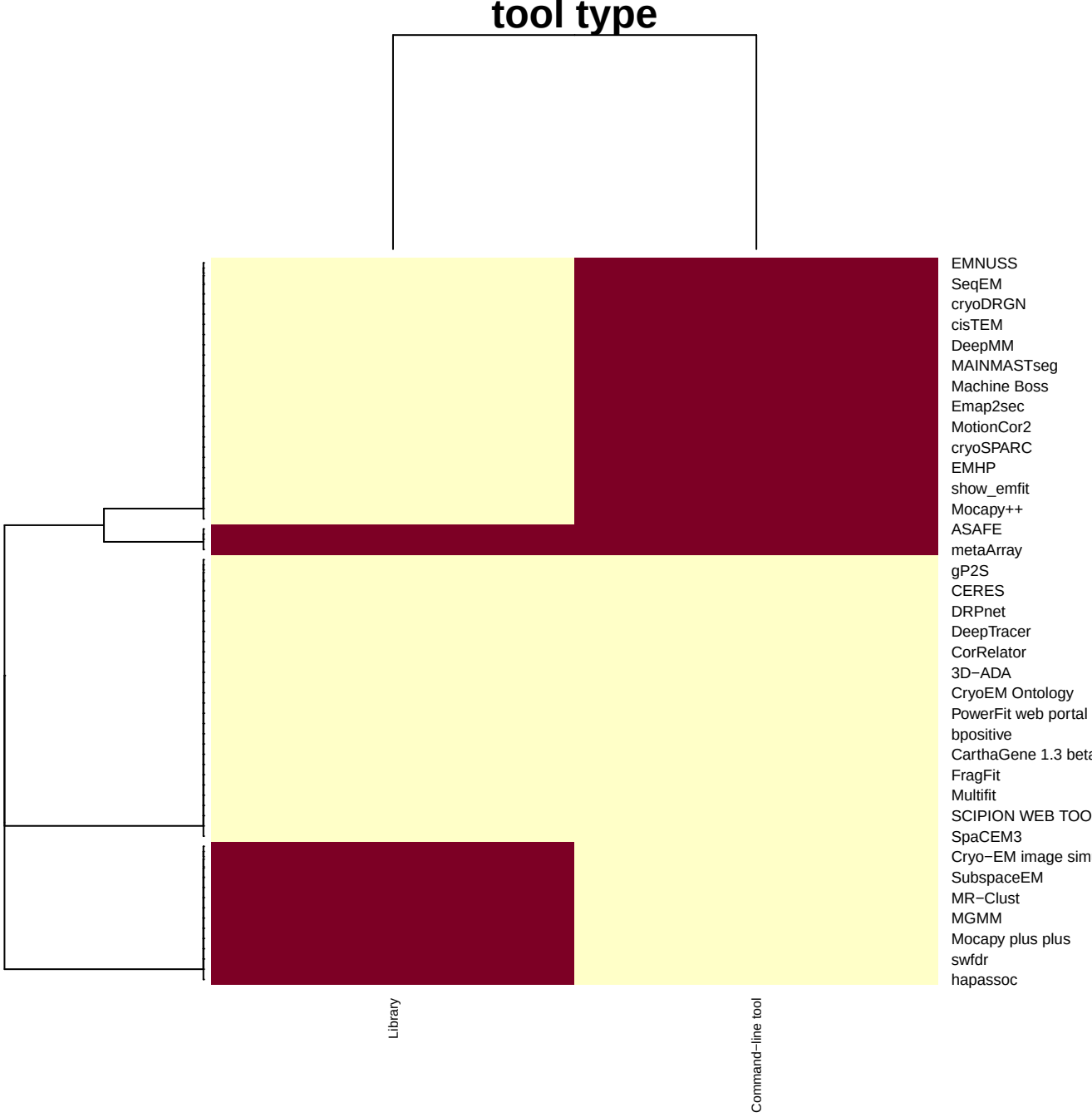
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Machine Boss
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MotionCor2
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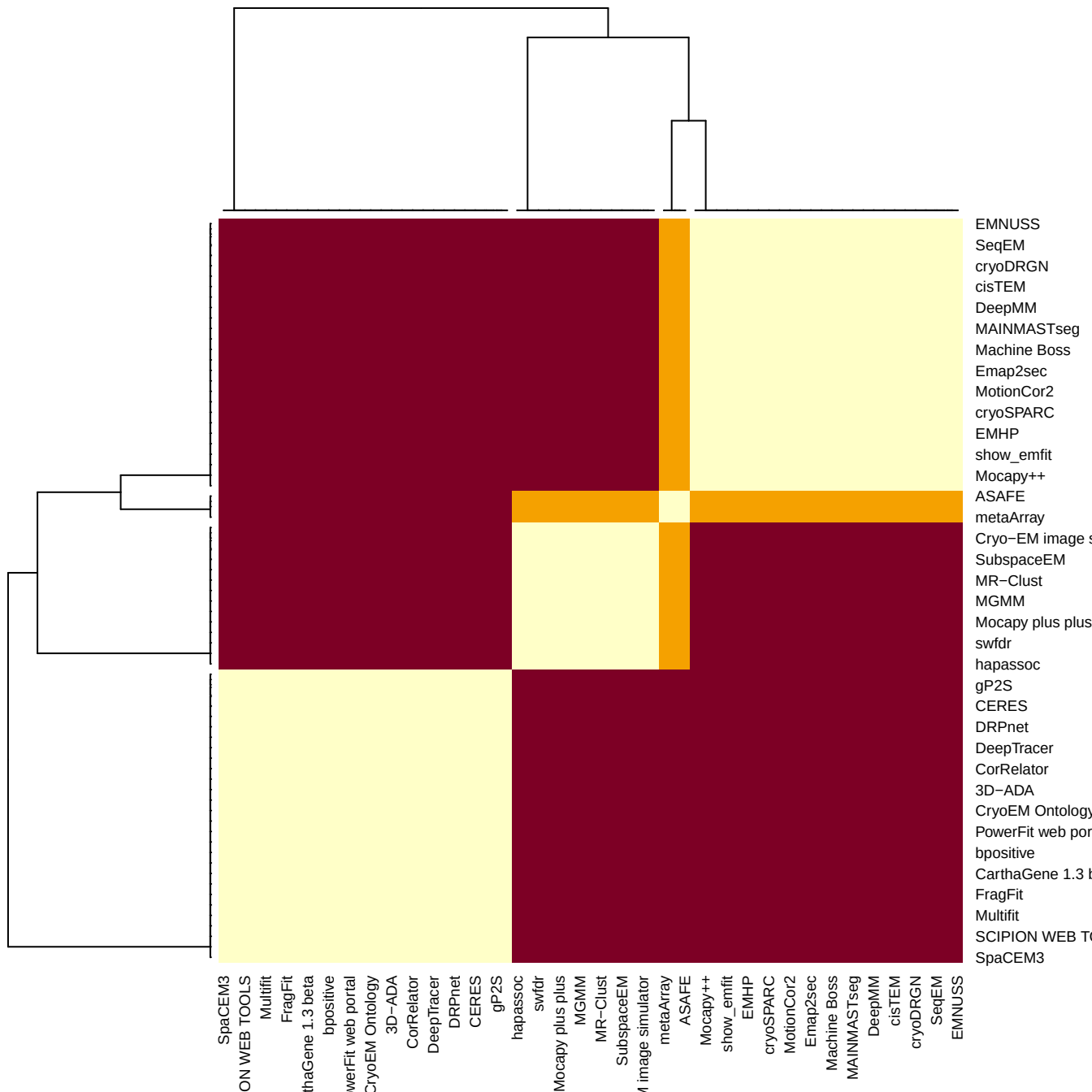
Mocapy++
ASAFE
metaArray
gP2S
CERES
DRPnet
DeepTracer
CorRelator
3D−ADA
CryoEM Ontology
PowerFit web portal
bpositive
CarthaGene 1.3 beta
FragFit
Multifit
SCIPION WEB TOO
SpaCEM3
Cryo−EM image sim
SubspaceEM
MR−Clust
MGMM
Mocapy plus plus
swfdr
hapassoc
Library
Command−line tool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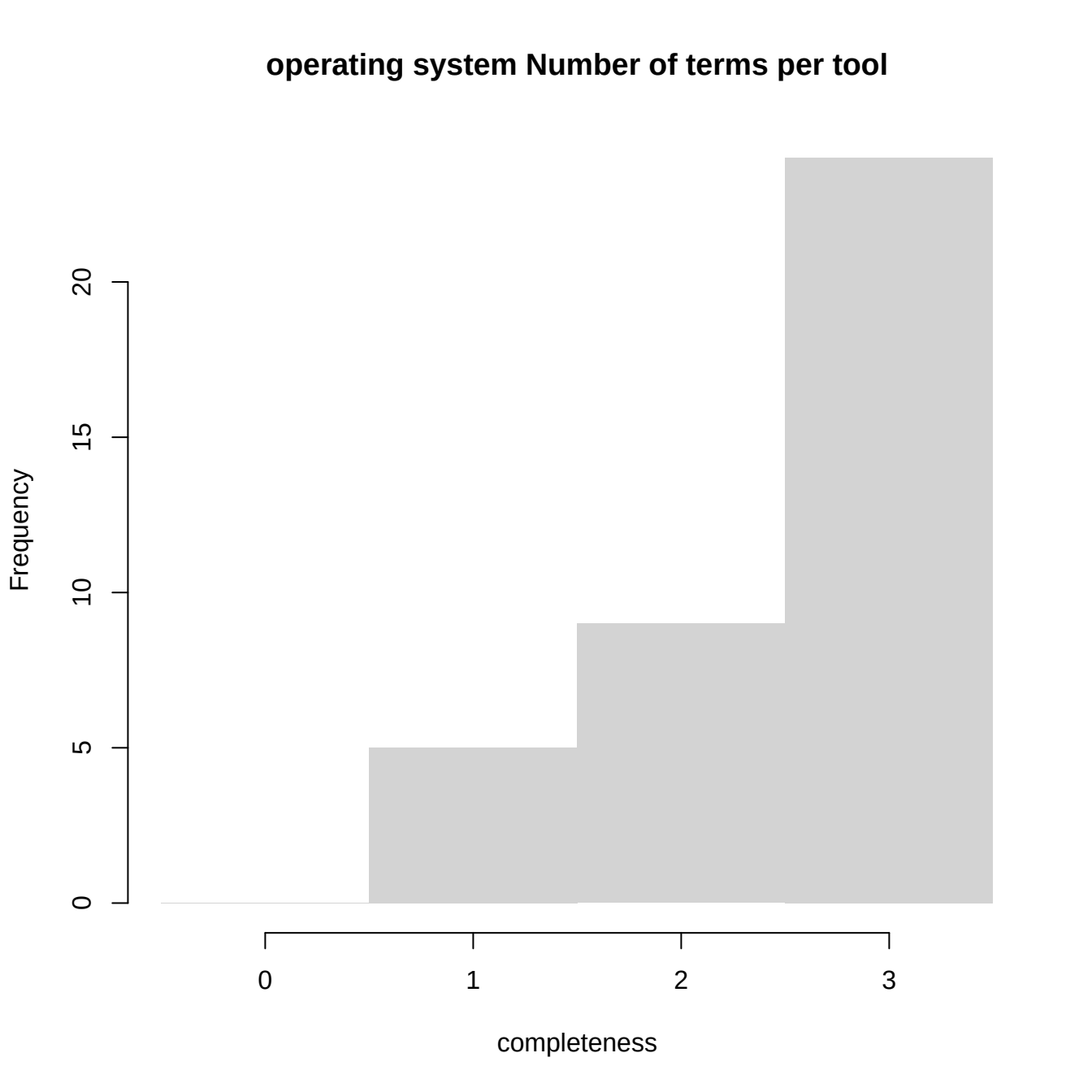
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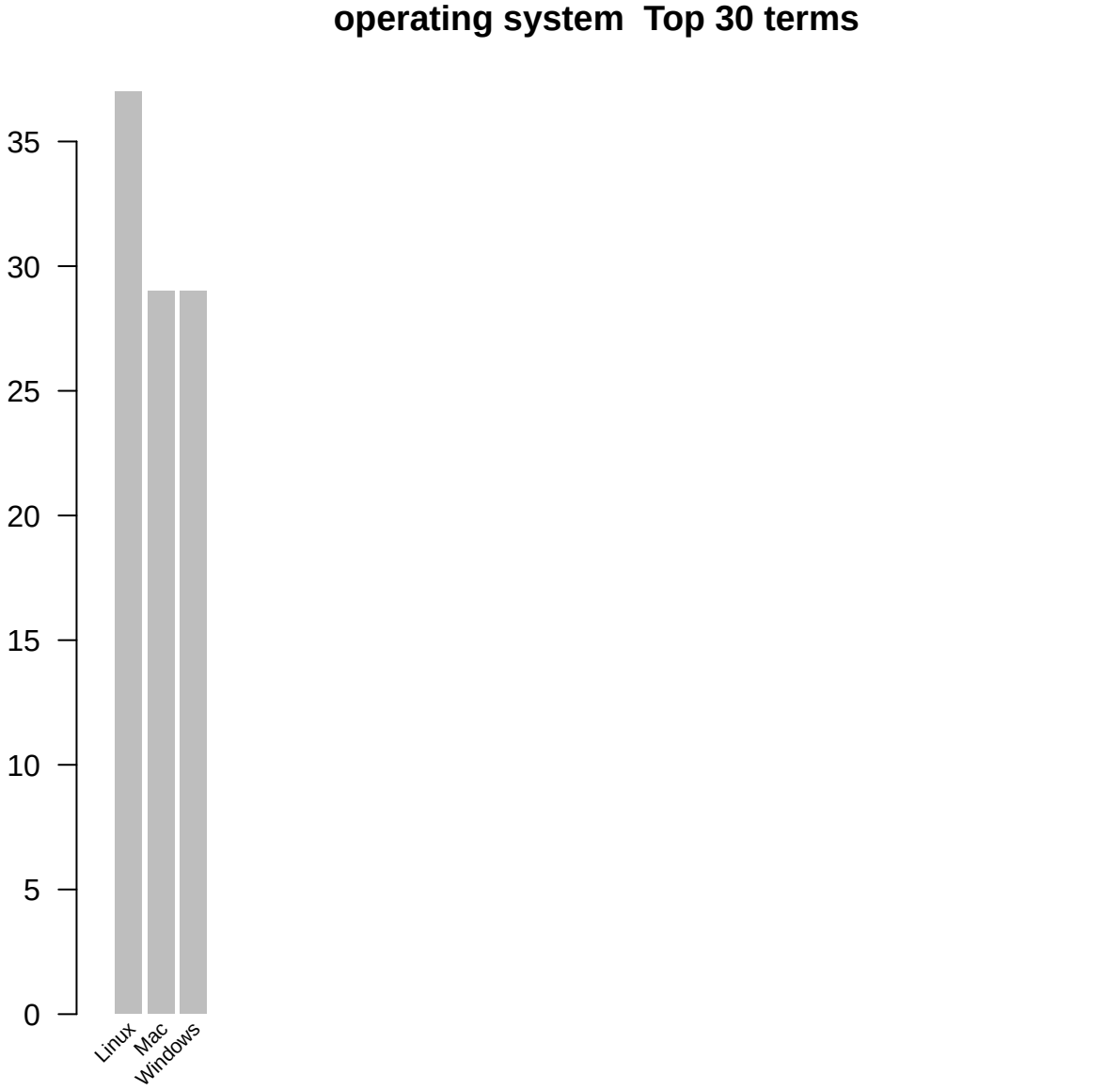
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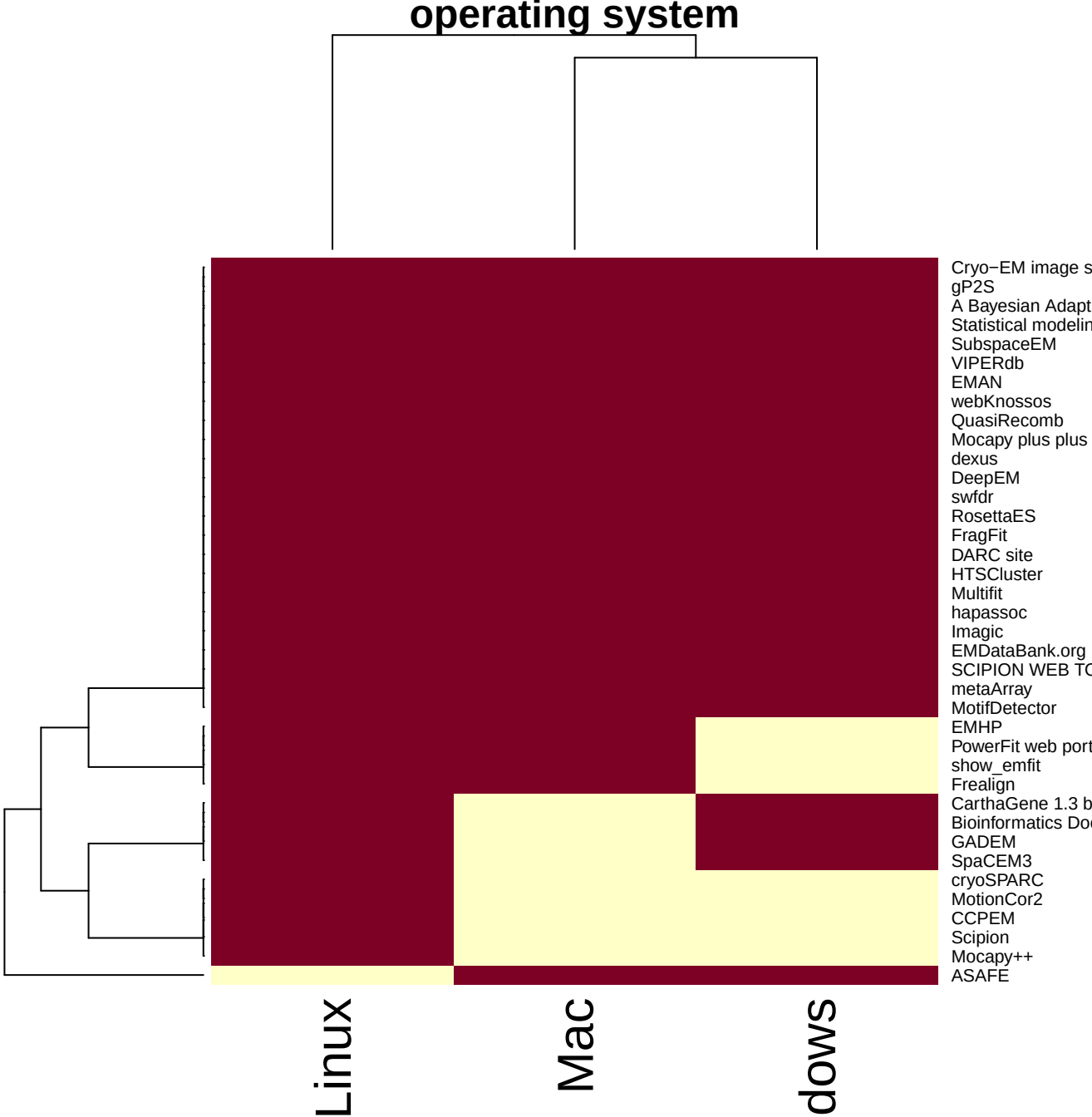
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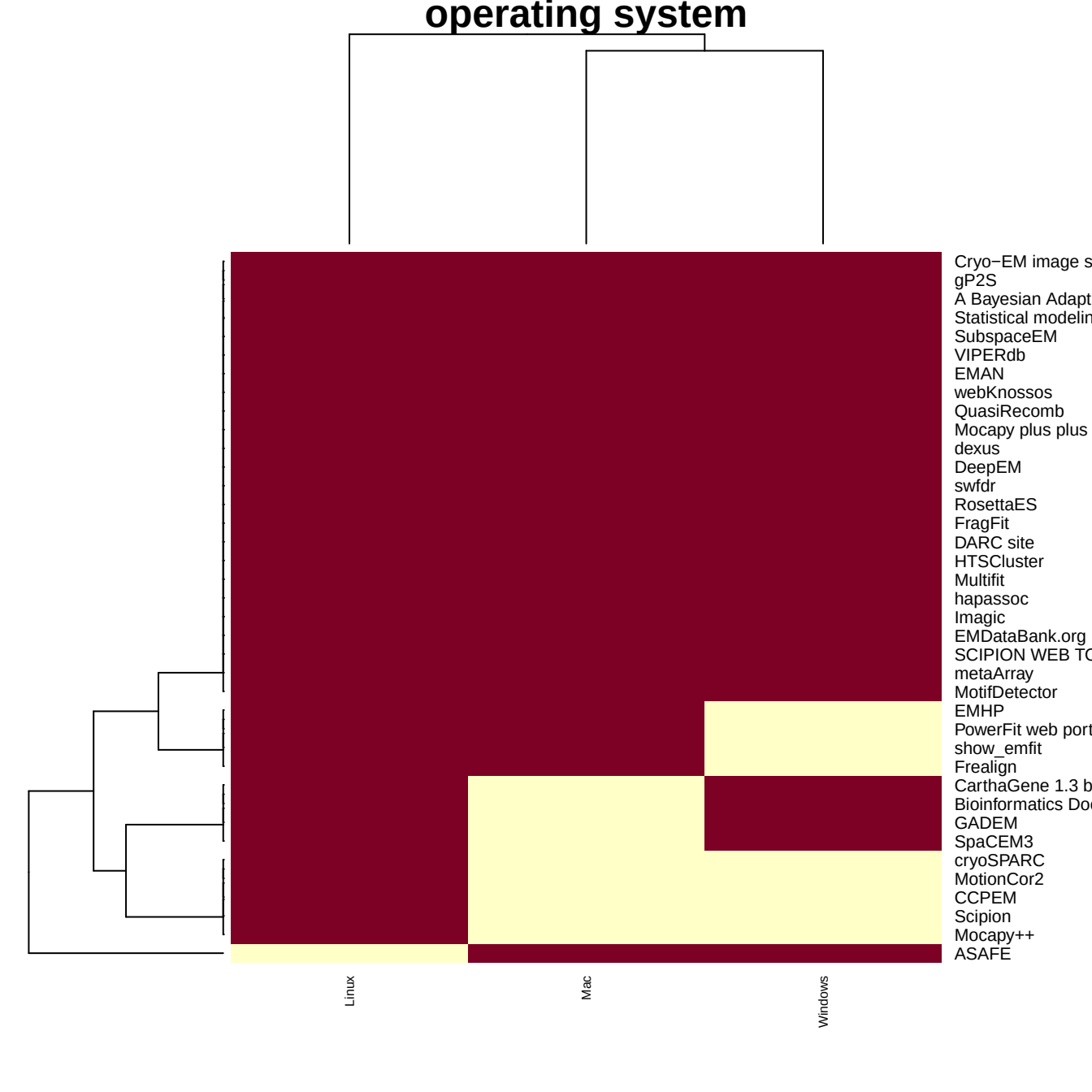
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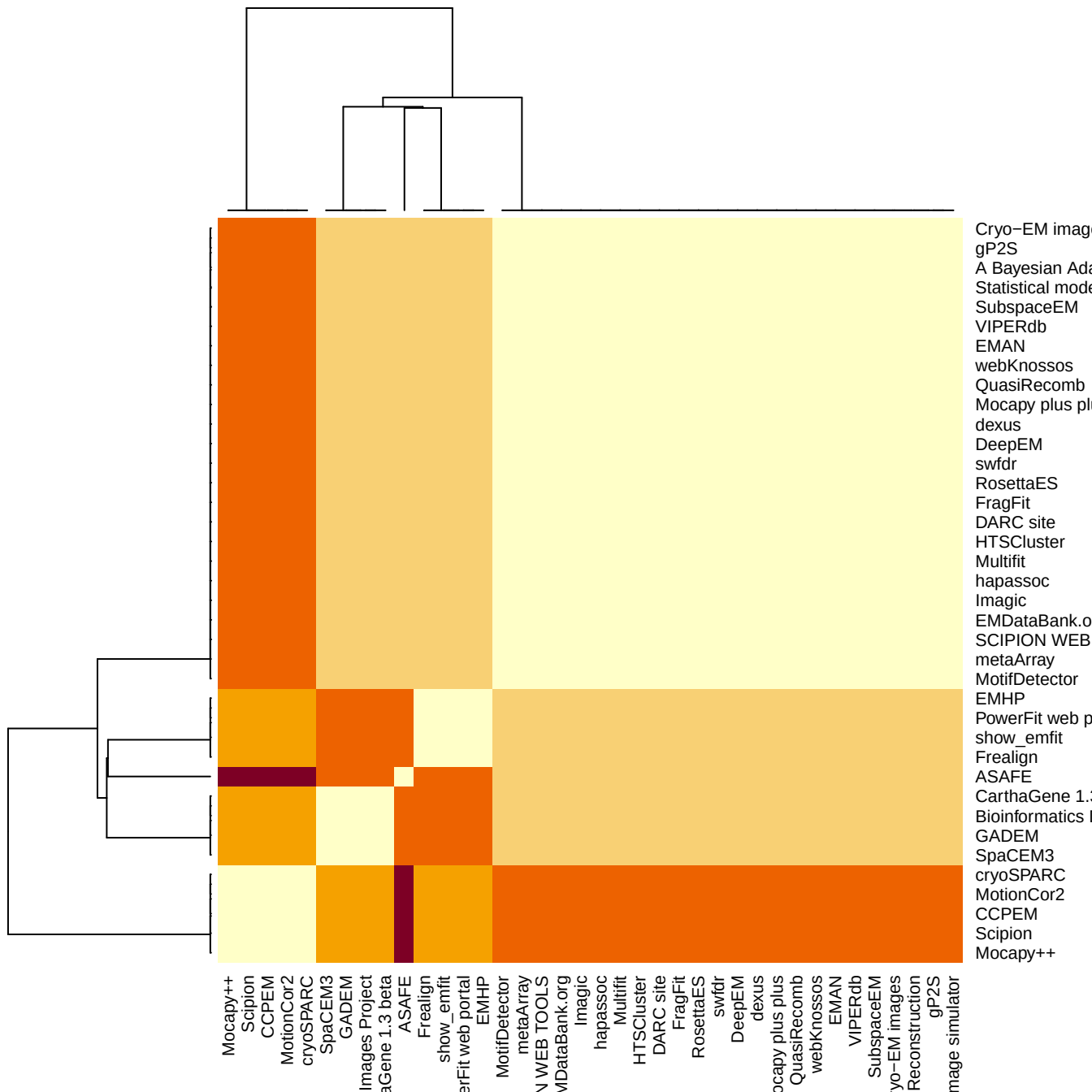
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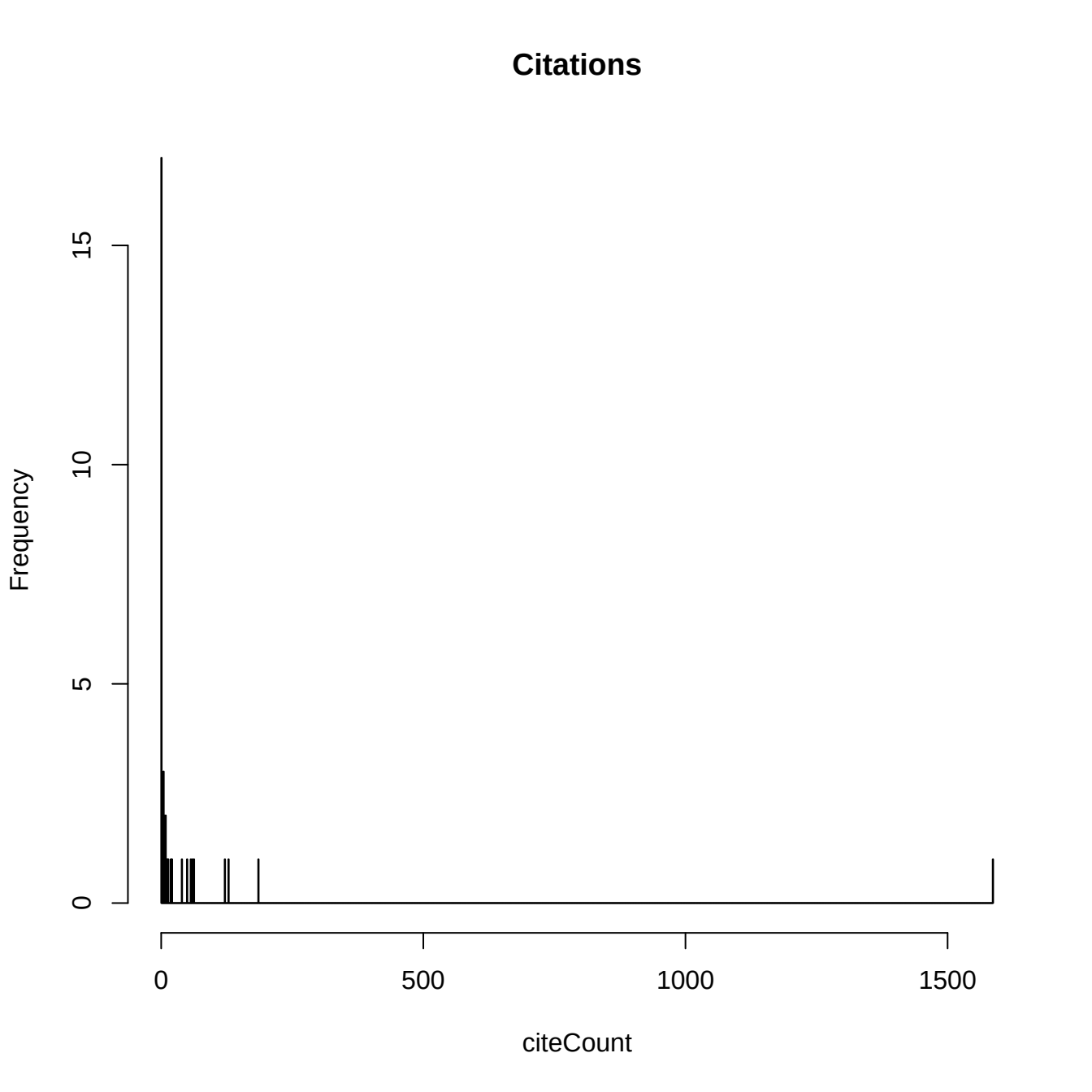
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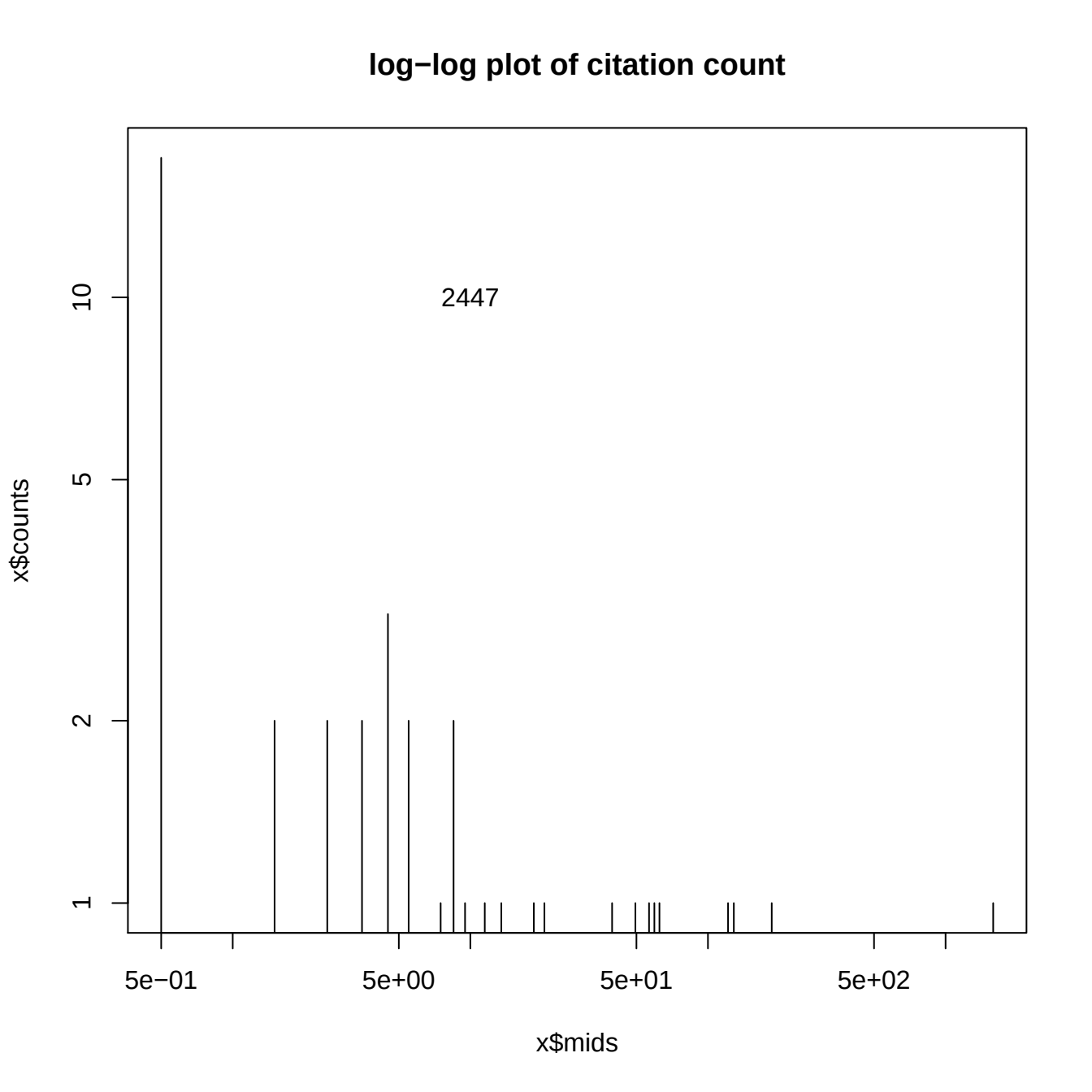
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