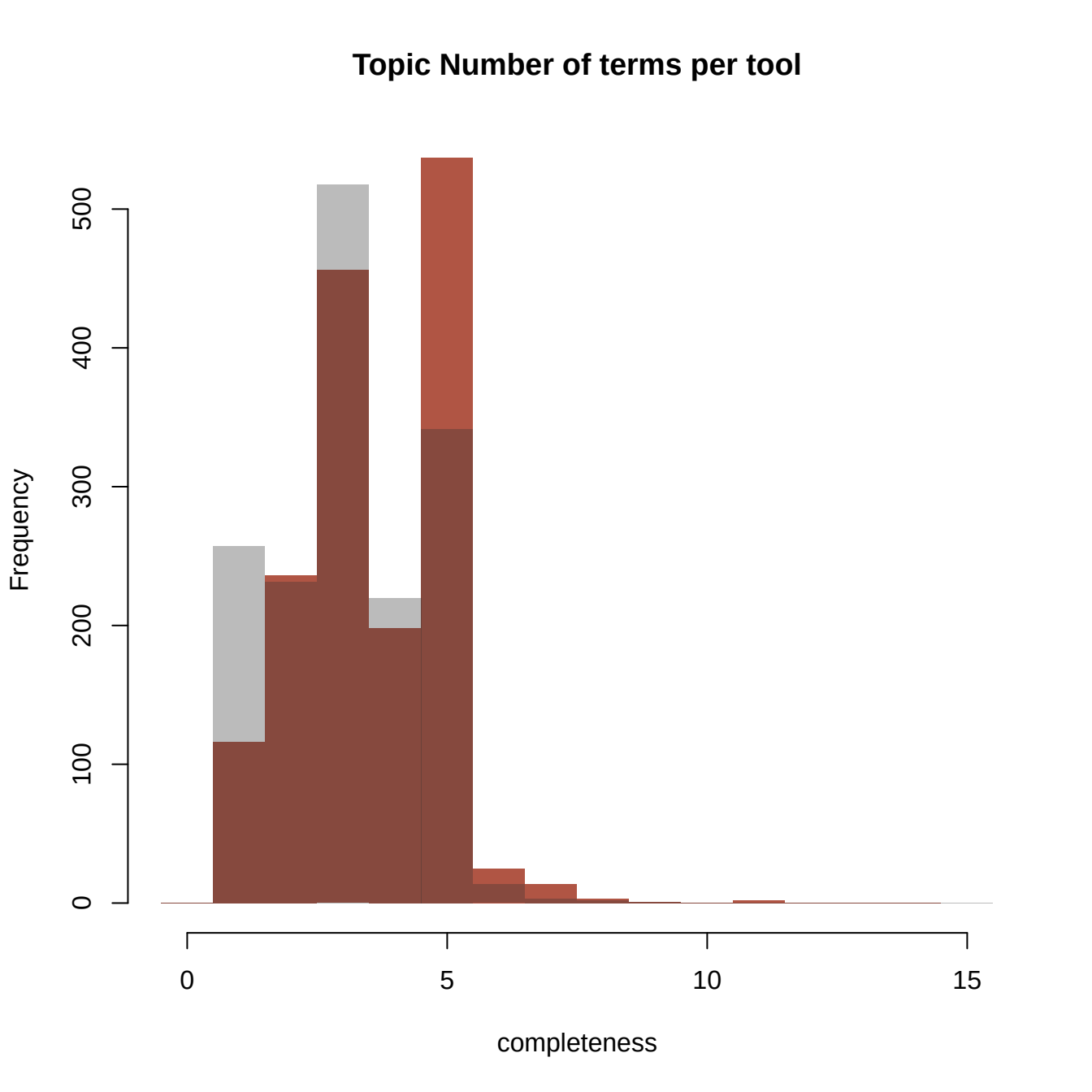
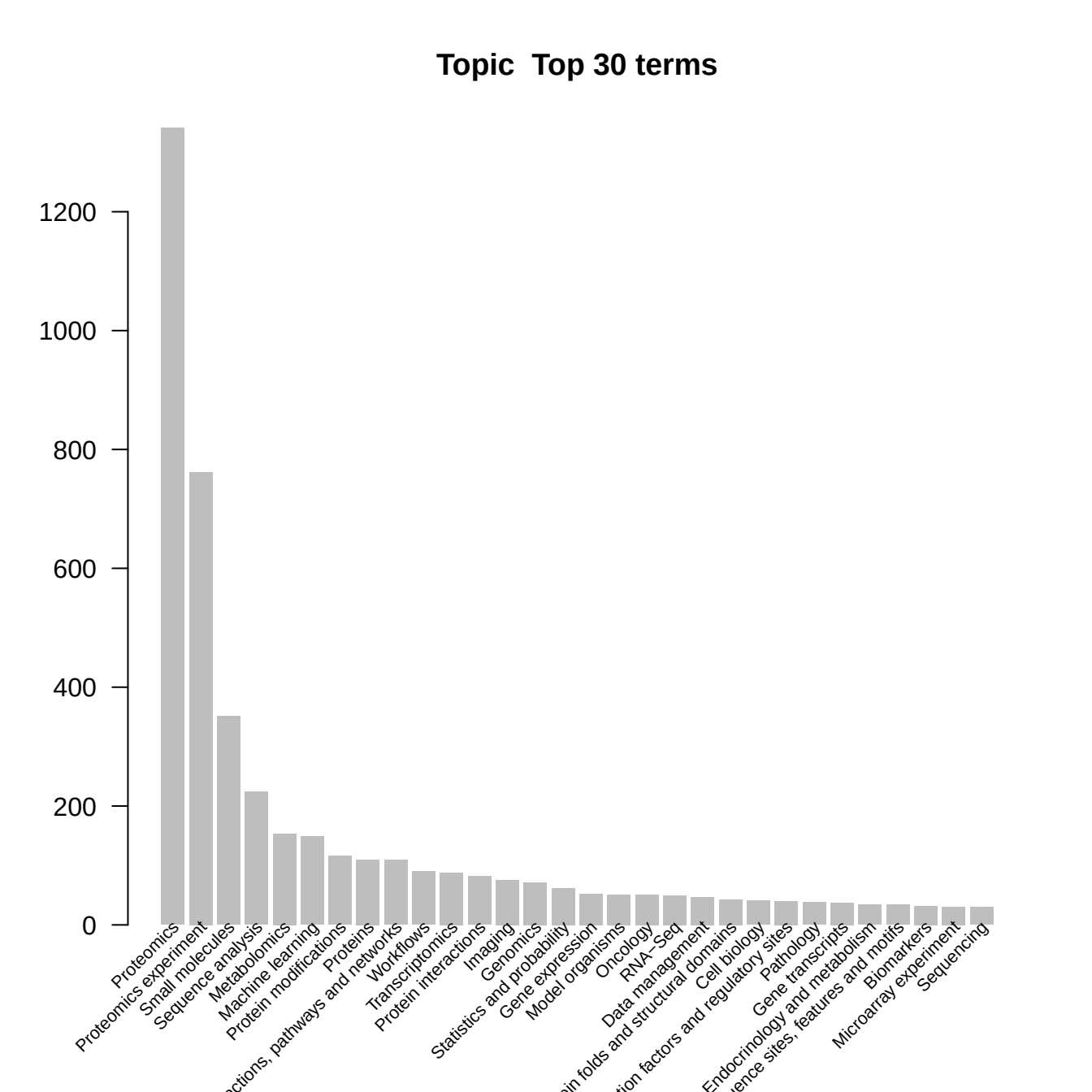
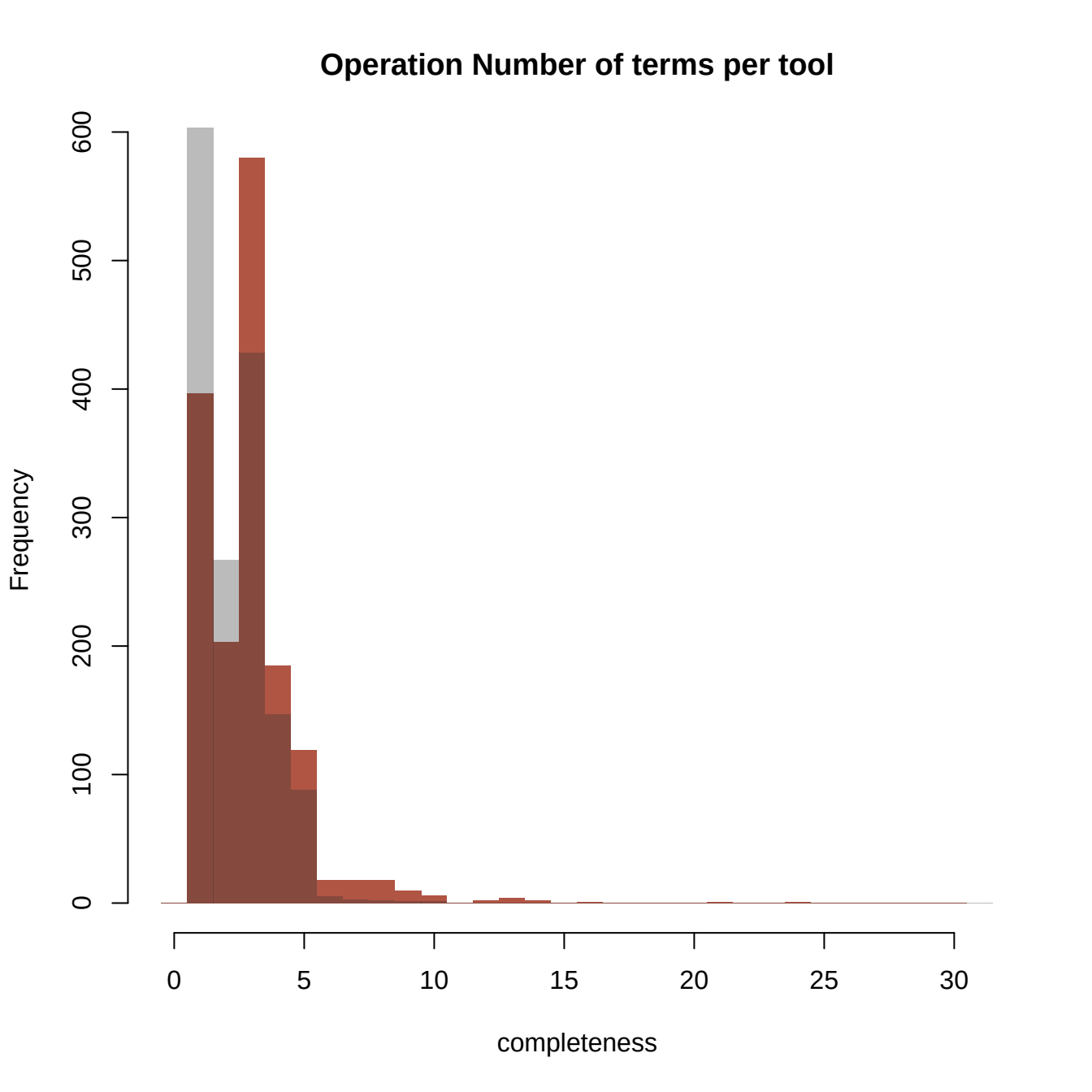

Topic Number of terms per tool
Frequency
0
100
200
300
400
500
0
5
10
15
completeness


Topic Top 30 terms
1200
1000
800
600
400
200
0
Proteomics
Proteomics experiment
Small molecules
Sequence analysis
Metabolomics
Machine learning
Protein modifications
Proteins
Pathways and networks
Workflows
Transcriptomics
Protein interactions
Imaging
Genomics
Statistics and probability
Gene expression
Model organisms
Oncology
RNA−Seq
Data management
Cell biology
Pathology
Gene transcripts
Endocrinology and metabolism
Microarray experiment
Biomarkers
Sequencing


Operation Number of terms per tool
Frequency
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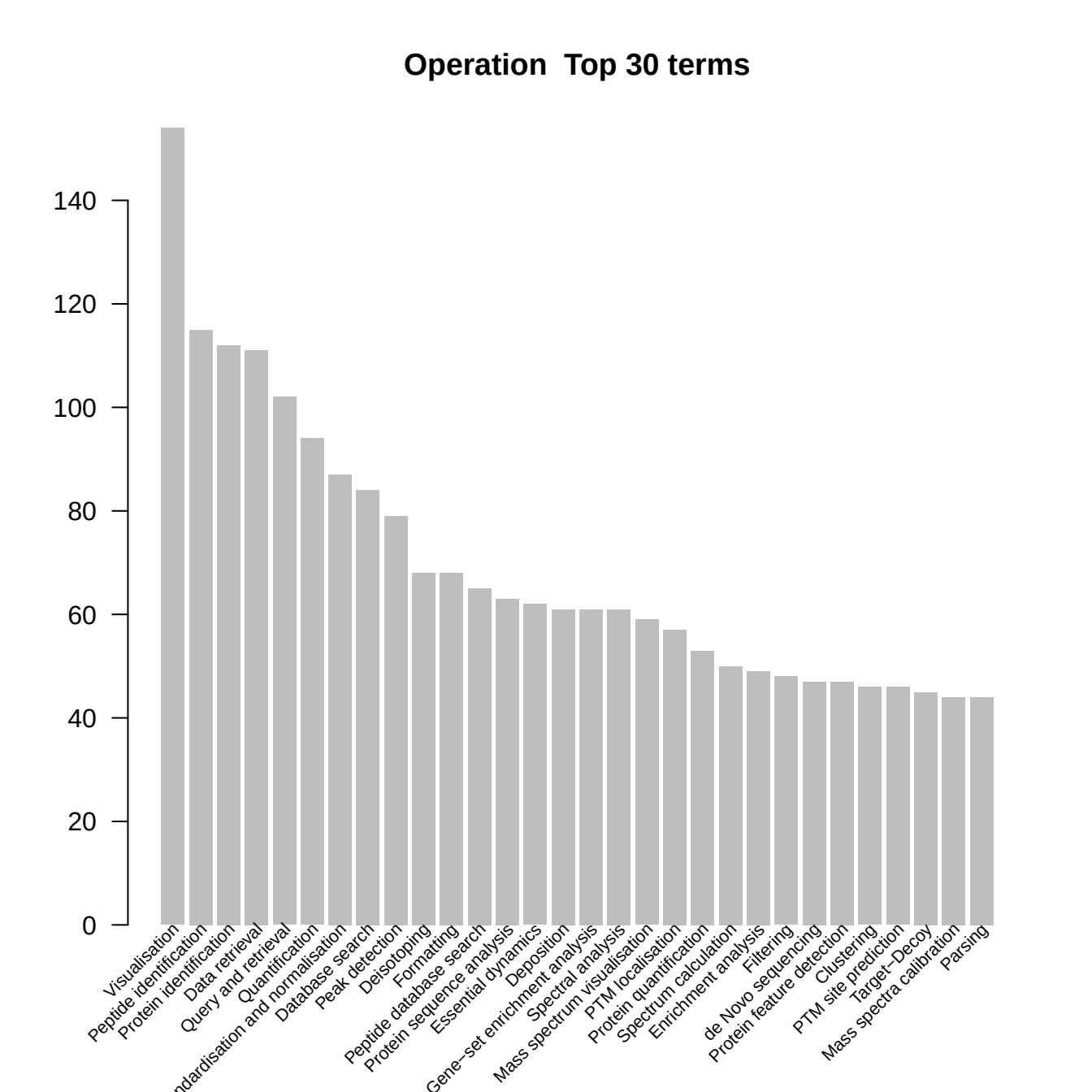
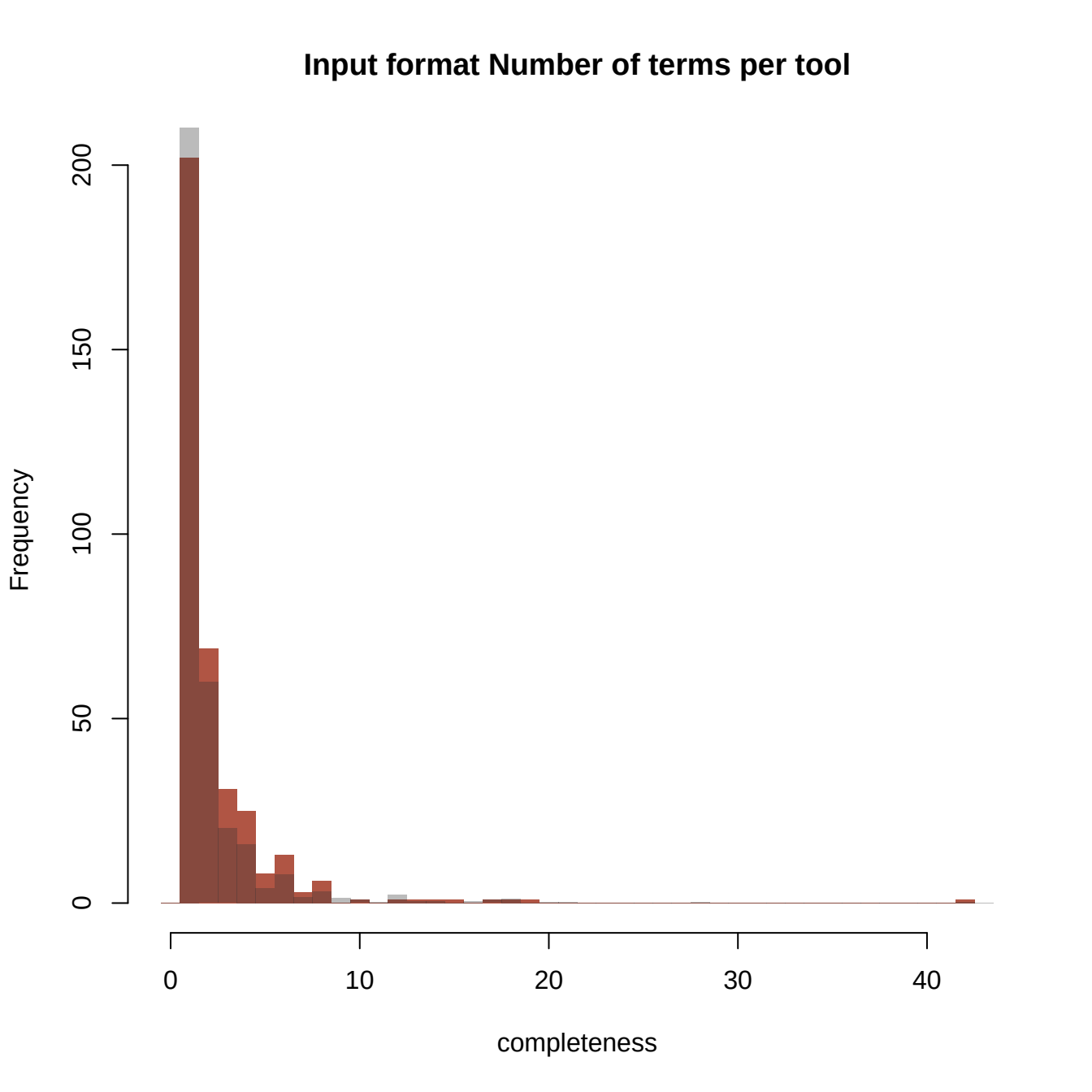
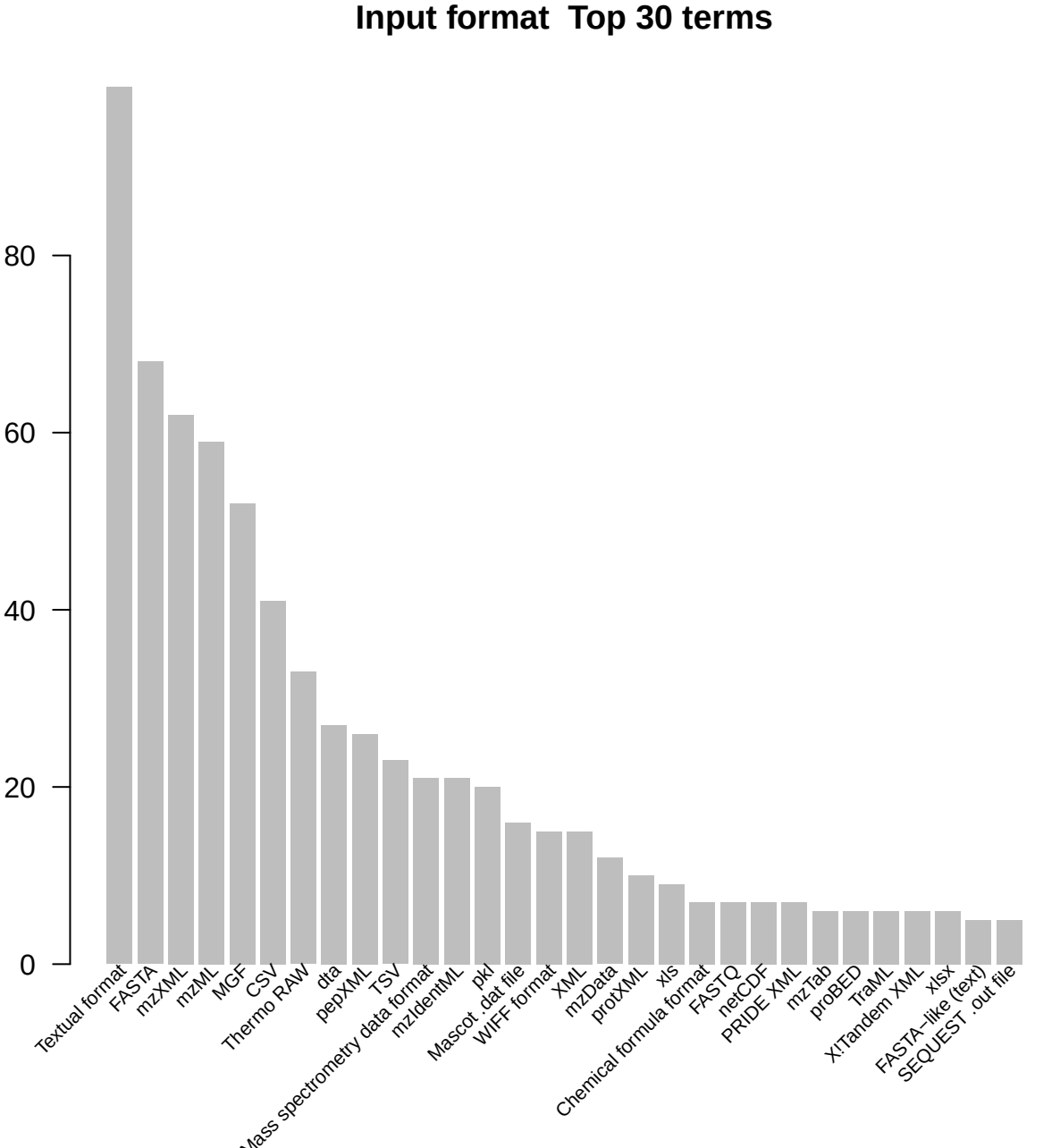
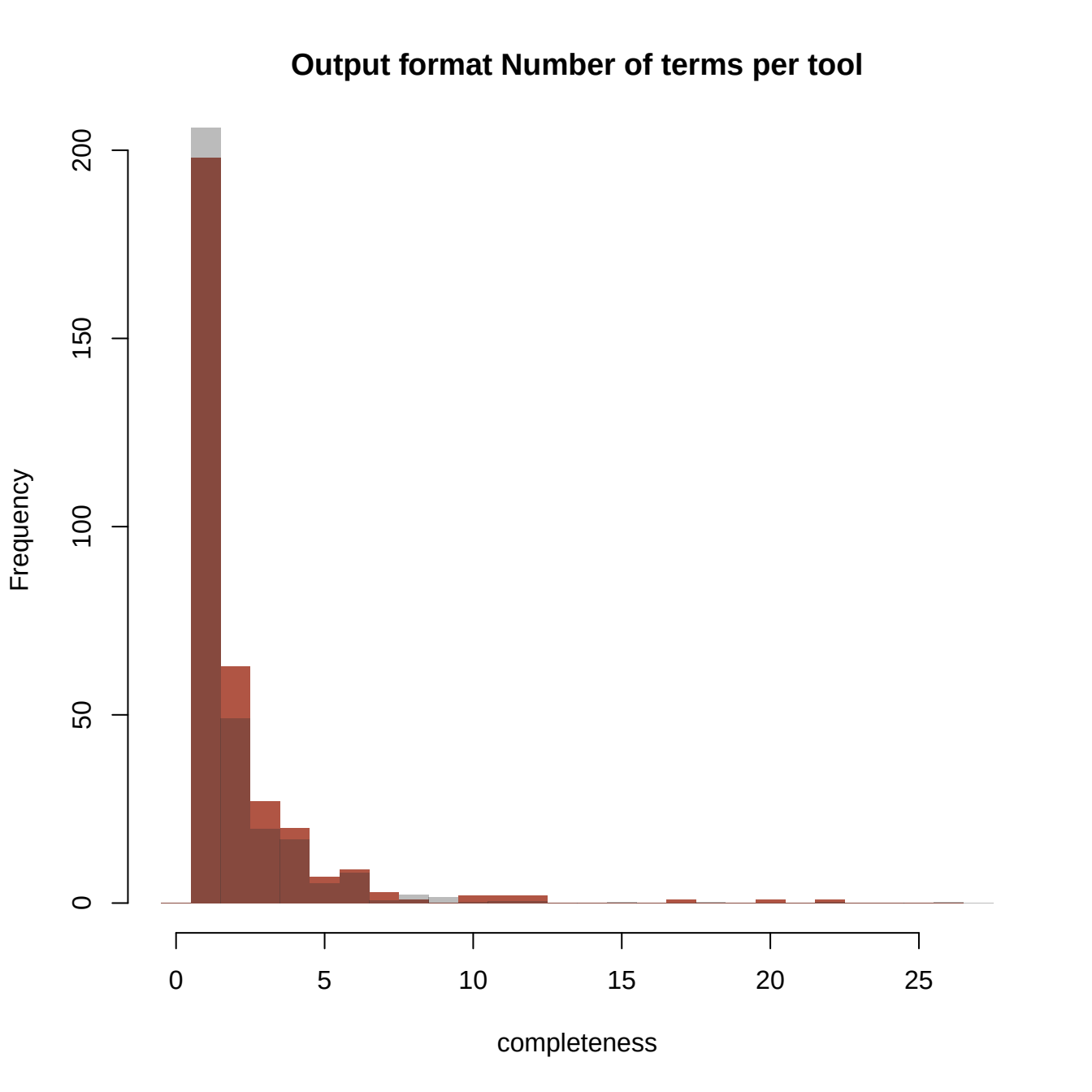
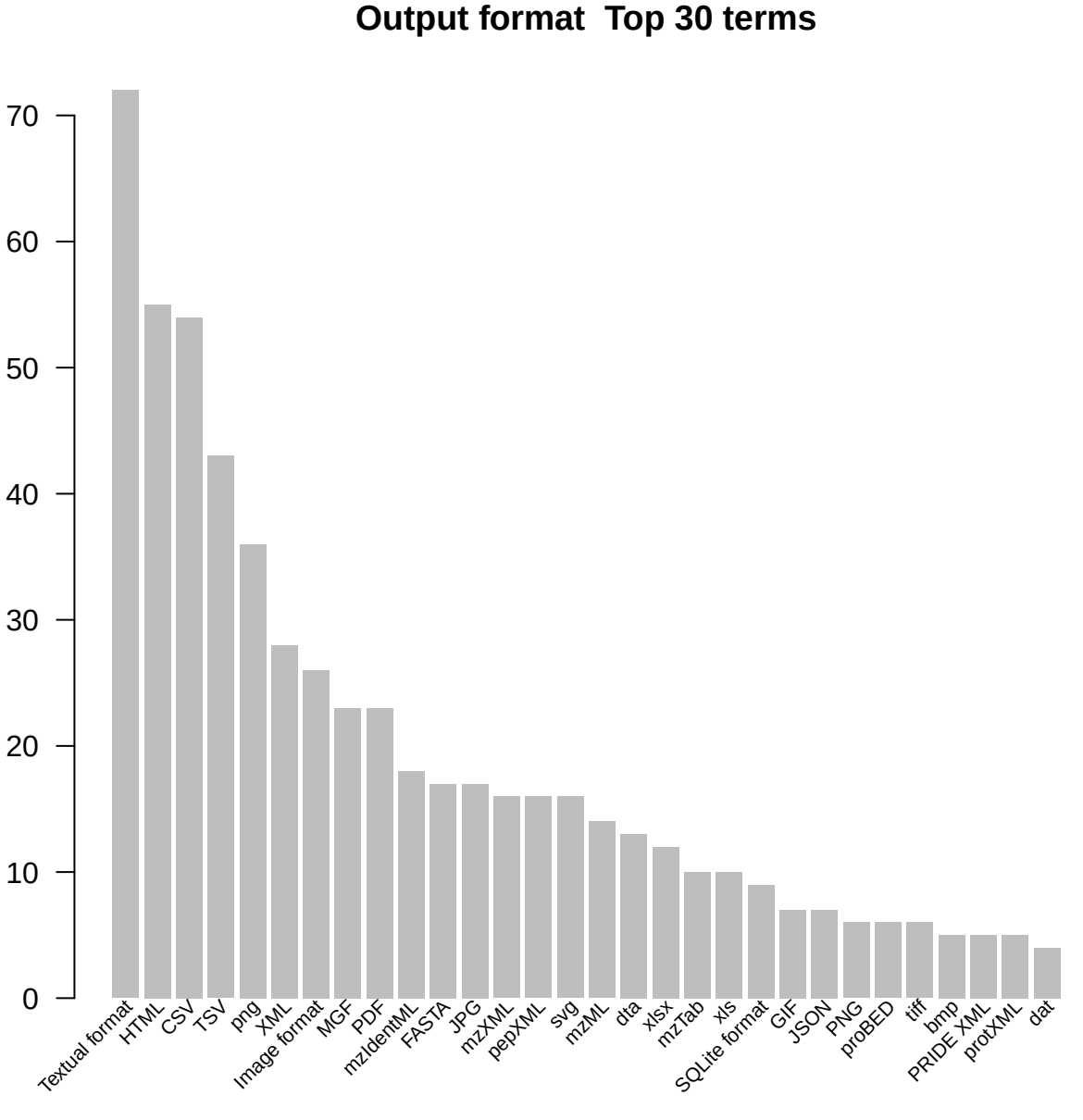
400
500
600
0
5
10
15
20
25
30
completeness

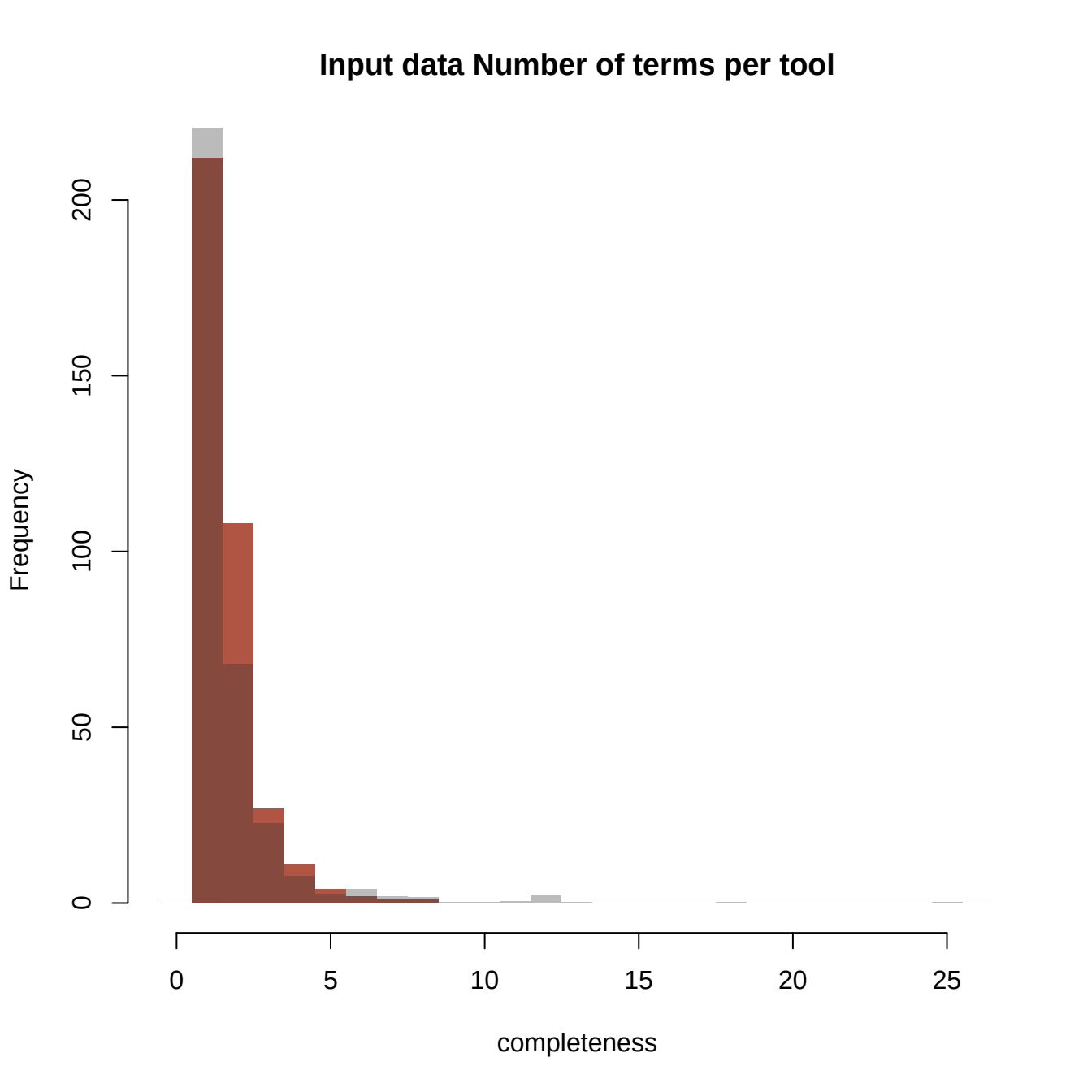

Operation Top 30 terms
140
120
100
80
60
40
20
0
Visualisation
Peptide identification
Protein identification
Data retrieval
Query and retrieval
Quantification
ndardisation and normalisation
Database search
Peak detection
Deisotoping
Formatting
Peptide database search
Protein sequence analysis
Essential dynamics
Deposition
Gene−set enrichment analysis
Spectral analysis
Mass spectrum visualisation
PTM localisation
Protein quantification
Spectrum calculation
Enrichment analysis
Filtering
de Novo sequencing
Protein feature detection
Clustering
PTM site prediction
Target−Decoy
Mass spectra calibration
Parsing

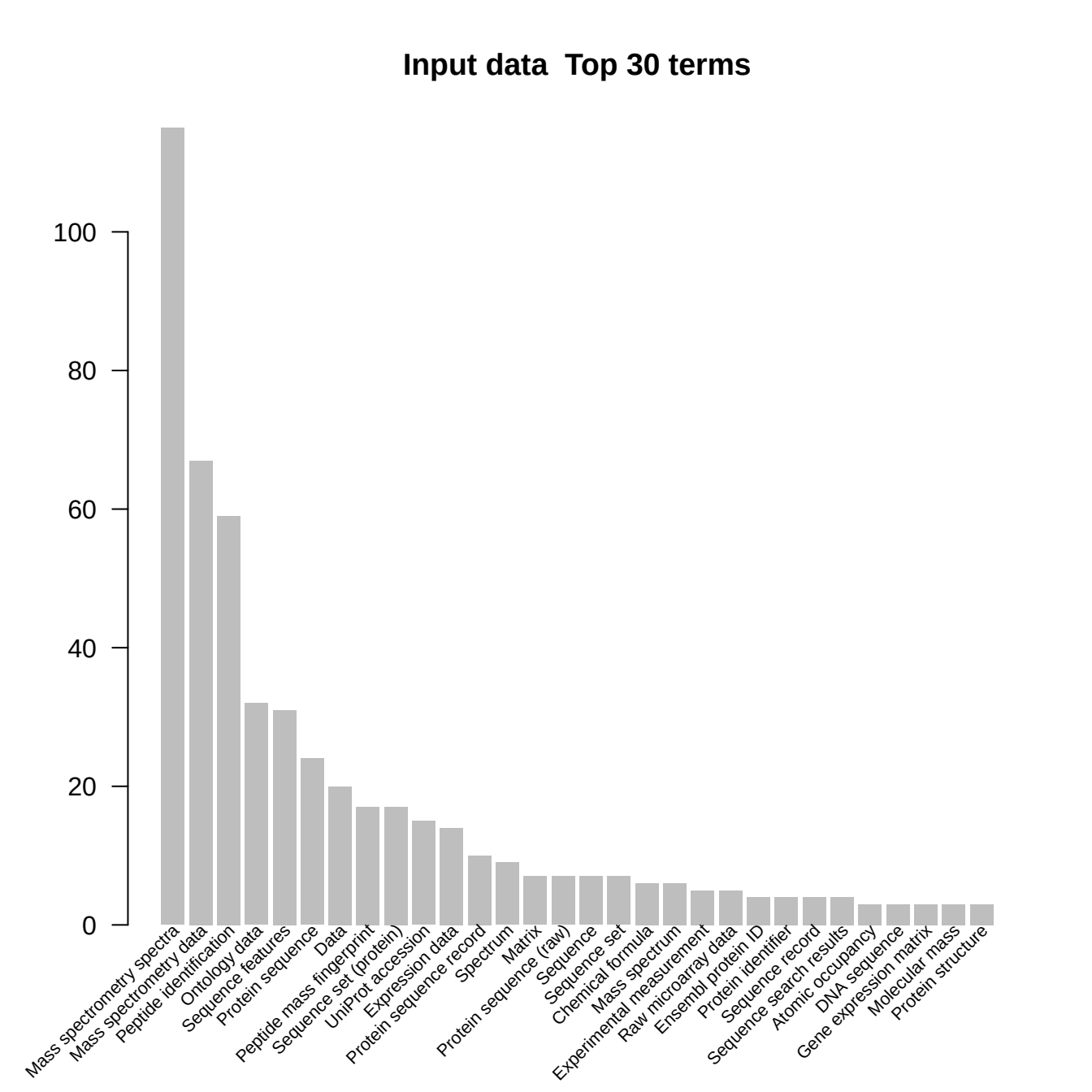

Input format Number of terms per tool
Frequency
0
50
100
150
200
0
10
20
30
40
completeness

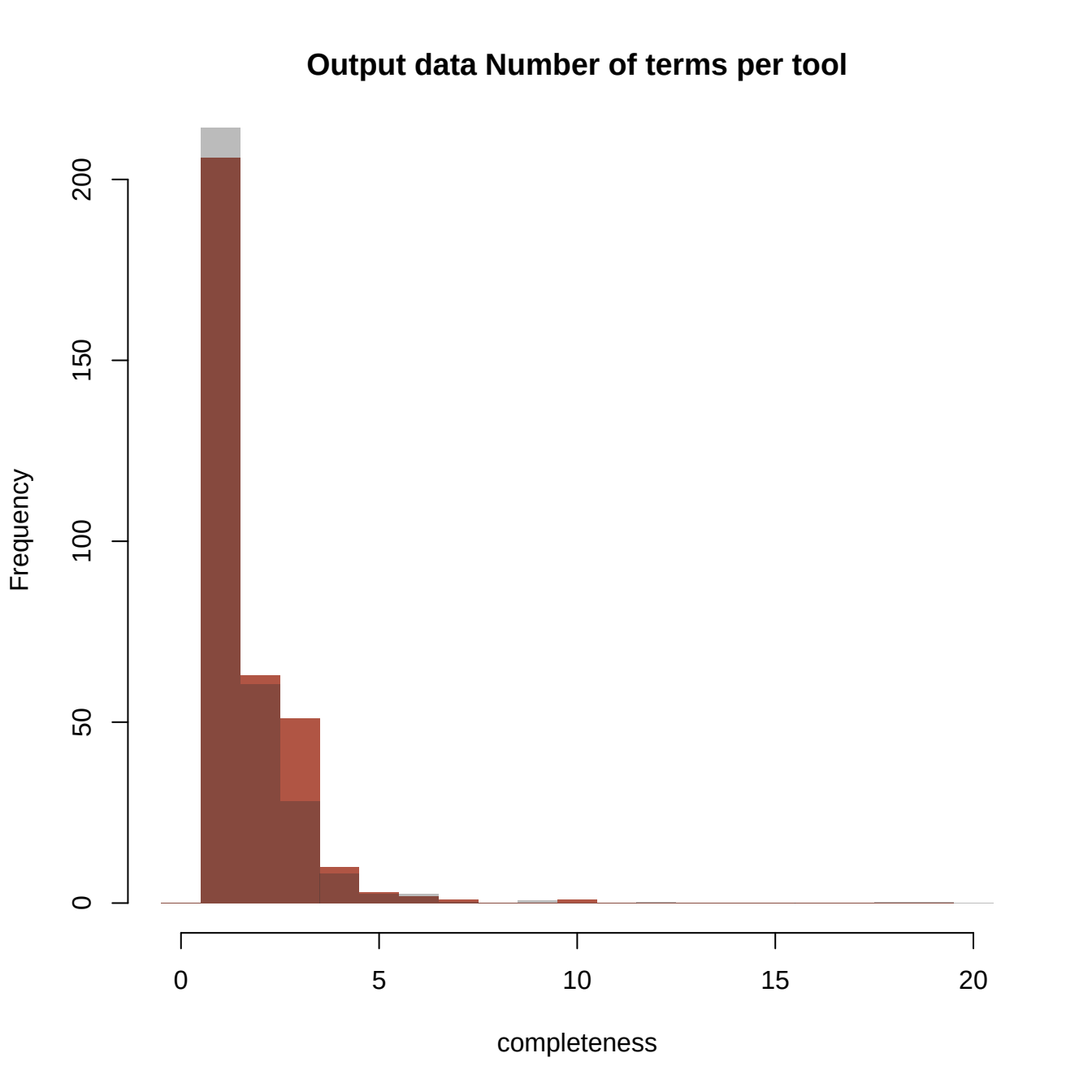

Input format Top 30 terms
80
60
40
20
0
Textual format
FASTA
mzXML
mzML
MGF
CSV
Thermo RAW
dta
pepXML
TSV
Mass spectrometry data format
mzIdentML
pkl
Mascot .dat file
WIFF format
XML
mzData
protXML
xls
Chemical formula format
FASTQ
netCDF
PRIDE XML
mzTab
proBED
TraML
X!Tandem XML
xlsx
FASTA-like (text)
SEQUEST .out file

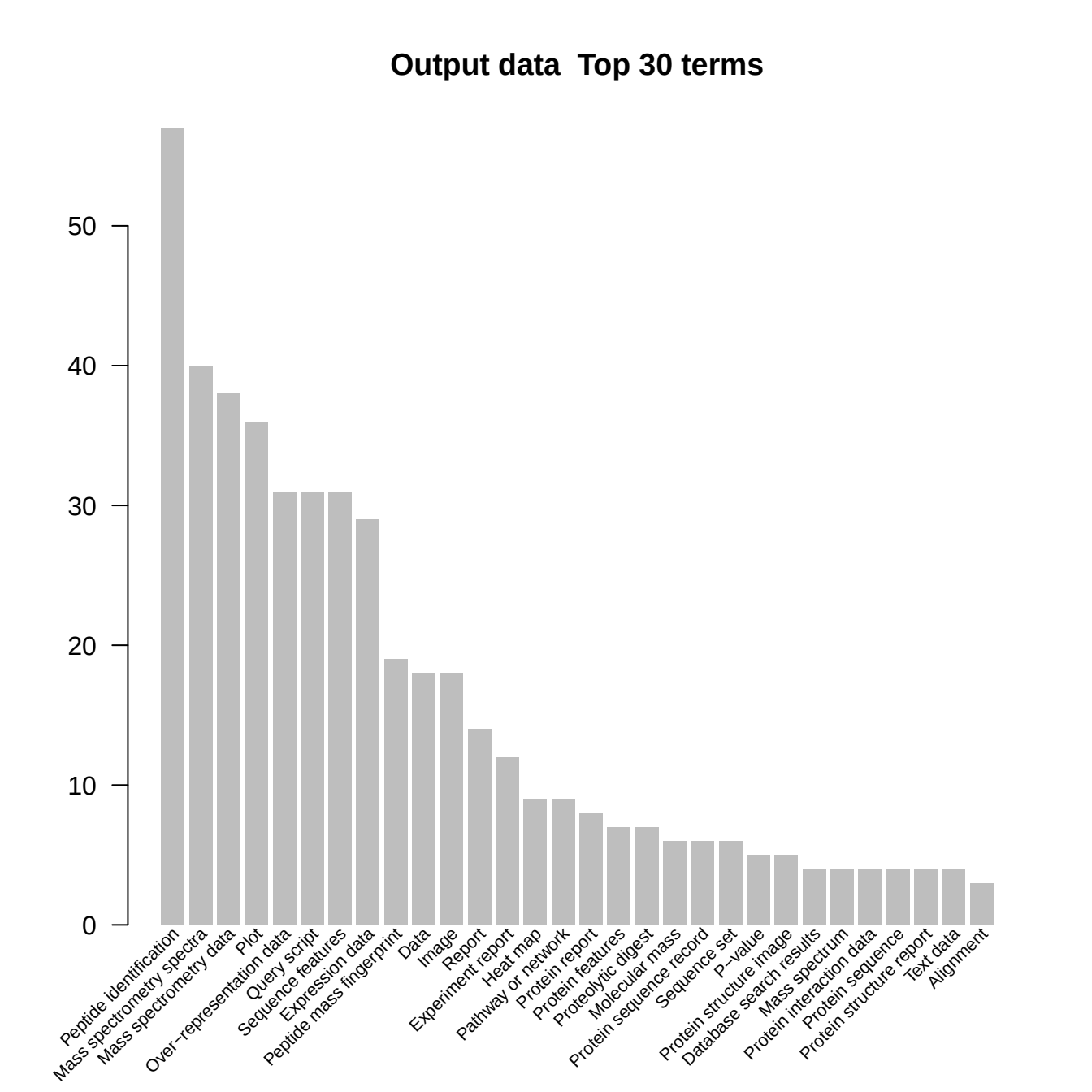

Output format Number of terms per tool
Frequency
0
50
100
150
200
0
5
10
15
20
25
completeness

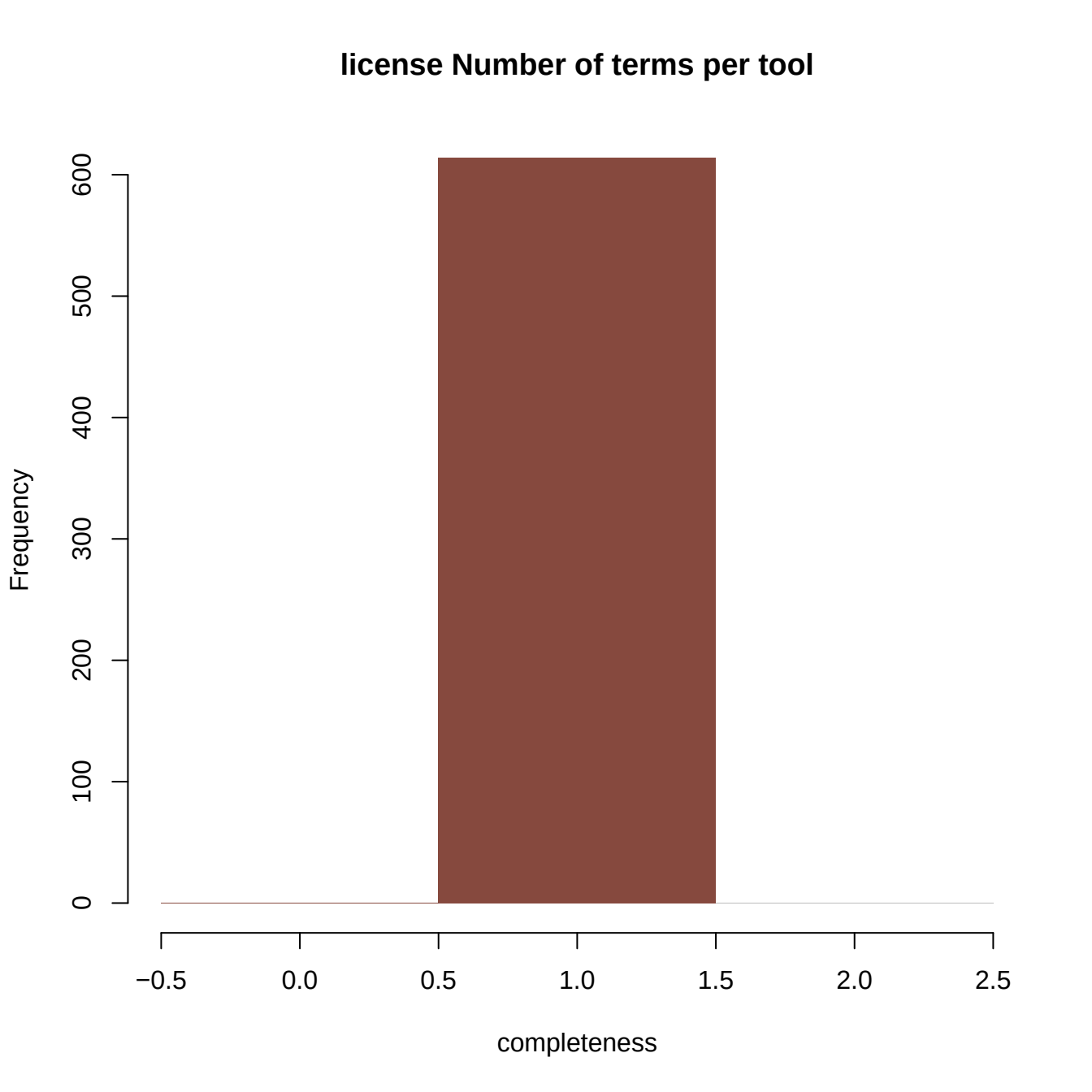

Output format Top 30 terms
70
60
50
40
30
20
10
0
Textual format
HTML
CSV
TSV
png
XML
Image format
MGF
PDF
mzIdentML
FASTA
JPG
mzXML
pepXML
svg
mzML
dta
xlsx
mzTab
xls
SQLite format
GIF
JSON
PNG
proBED
tiff
bmp
PRIDE XML
protXML
dat

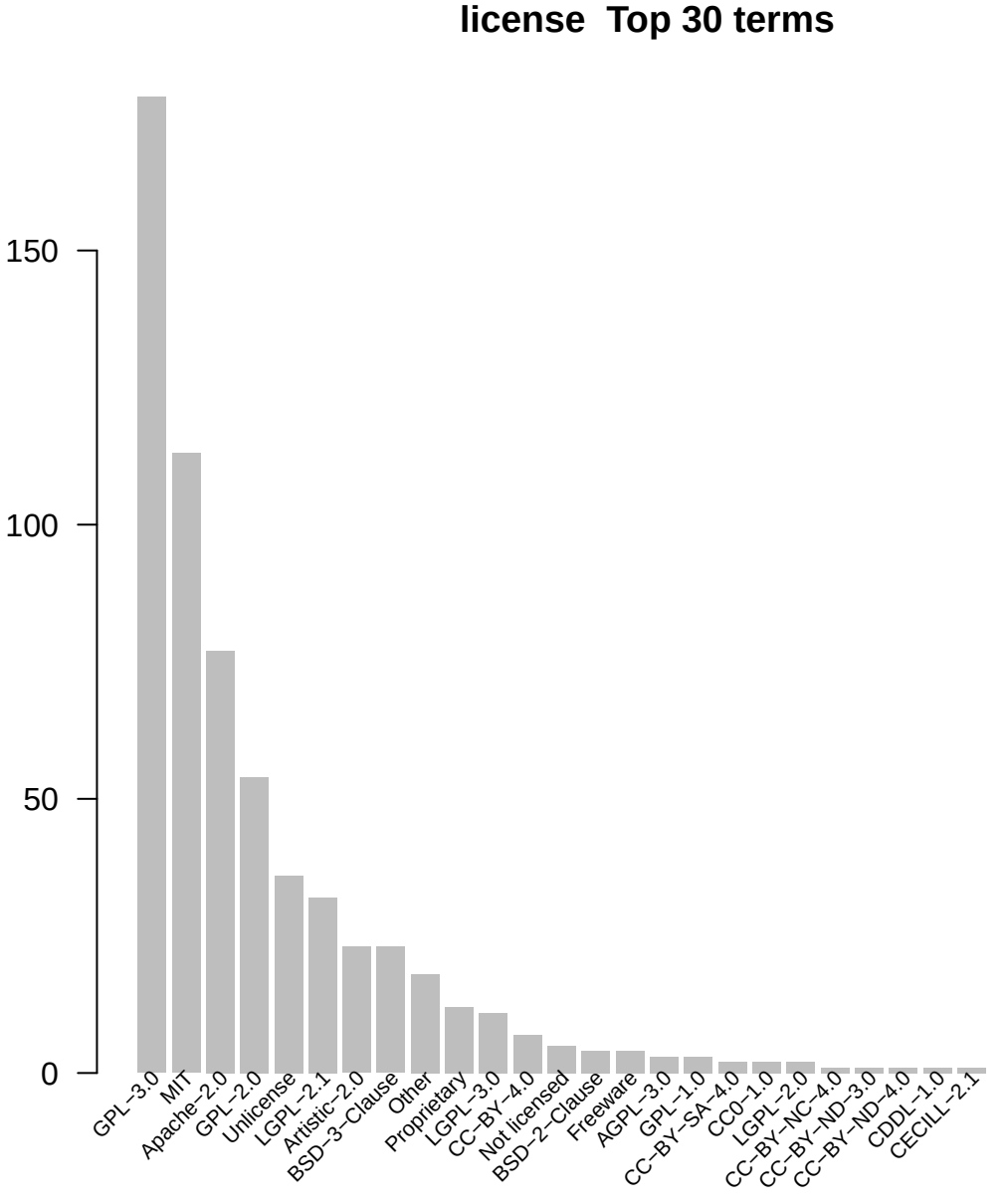

Input data Number of terms per tool
Frequency
0
50
100
150
200
0
5
10
15
20
25
completeness

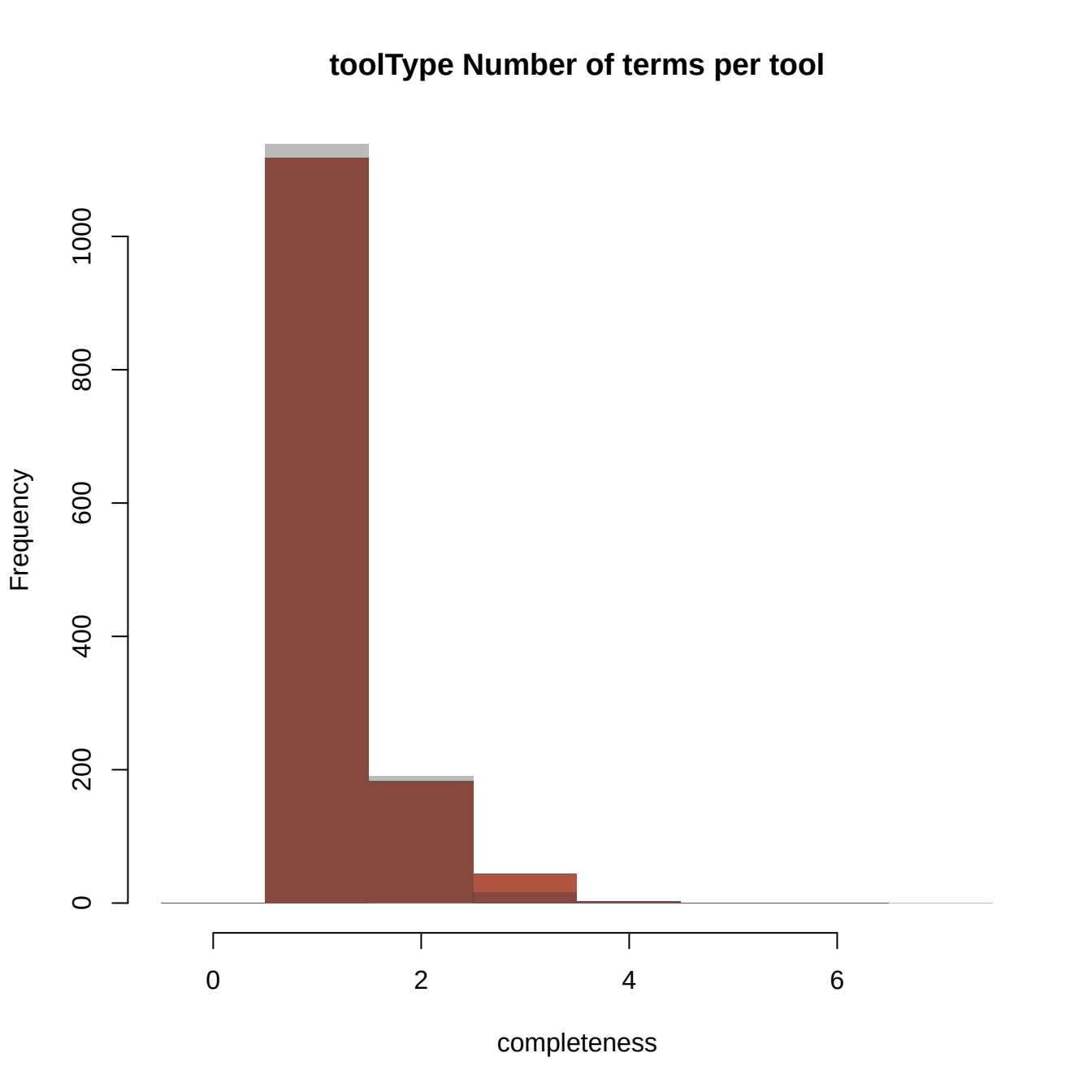

Input data Top 30 terms
100
80
60
40
20
0
Mass spectrometry spectra
Mass spectrometry data
Peptide identification
Ontology data
Sequence features
Protein sequence
Data
Peptide mass fingerprint
Sequence set (protein)
UniProt accession
Expression data
Protein sequence record
Spectrum
Matrix
Protein sequence (raw)
Sequence
Sequence set
Chemical formula
Mass spectrum
Experimental measurement
Raw microarray data
Ensembl protein ID
Protein identifier
Sequence record
Sequence search results
Atomic occupancy
DNA sequence
Gene expression matrix
Molecular mass
Protein structure

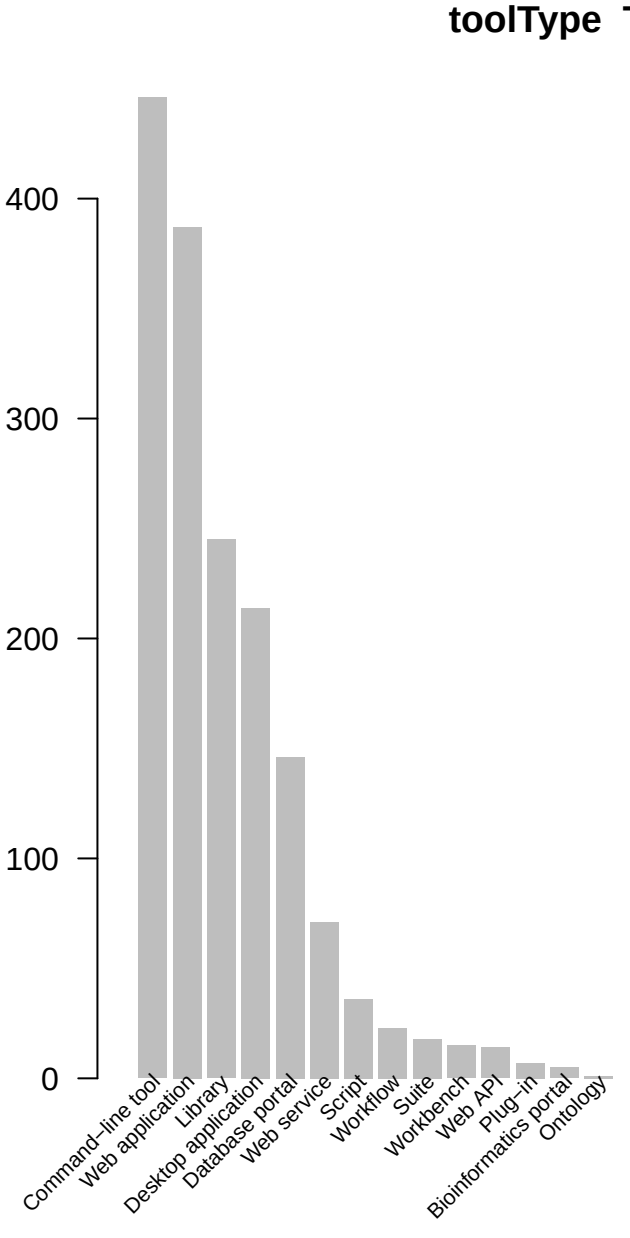

Output data Number of terms per tool
Frequency
0
50
100
150
200
0
5
10
15
20
completeness

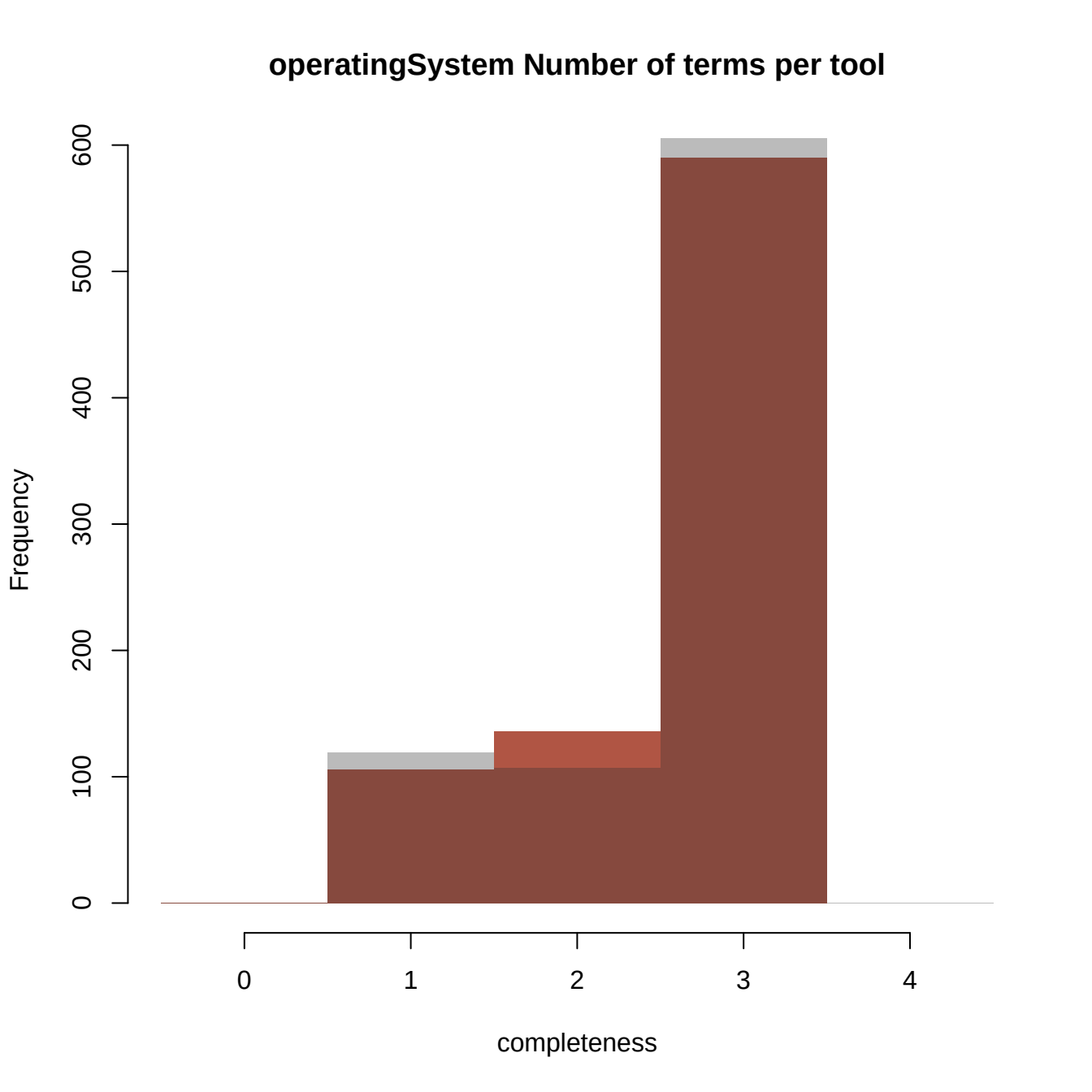

Output data Top 30 terms
0
10
20
30
40
50
Peptide identification
Mass spectrometry spectra
Mass spectrometry data
Plot
Over−representation data
Query script
Sequence features
Expression data
Peptide mass fingerprint
Data
Image
Report
Experiment report
Heat map
Pathway or network
Protein report
Protein features
Proteolytic digest
Molecular mass
Protein sequence record
Sequence set
P−value
Protein structure image
Database search results
Mass spectrum
Protein interaction data
Protein sequence
Protein structure report
Text data
Alignment

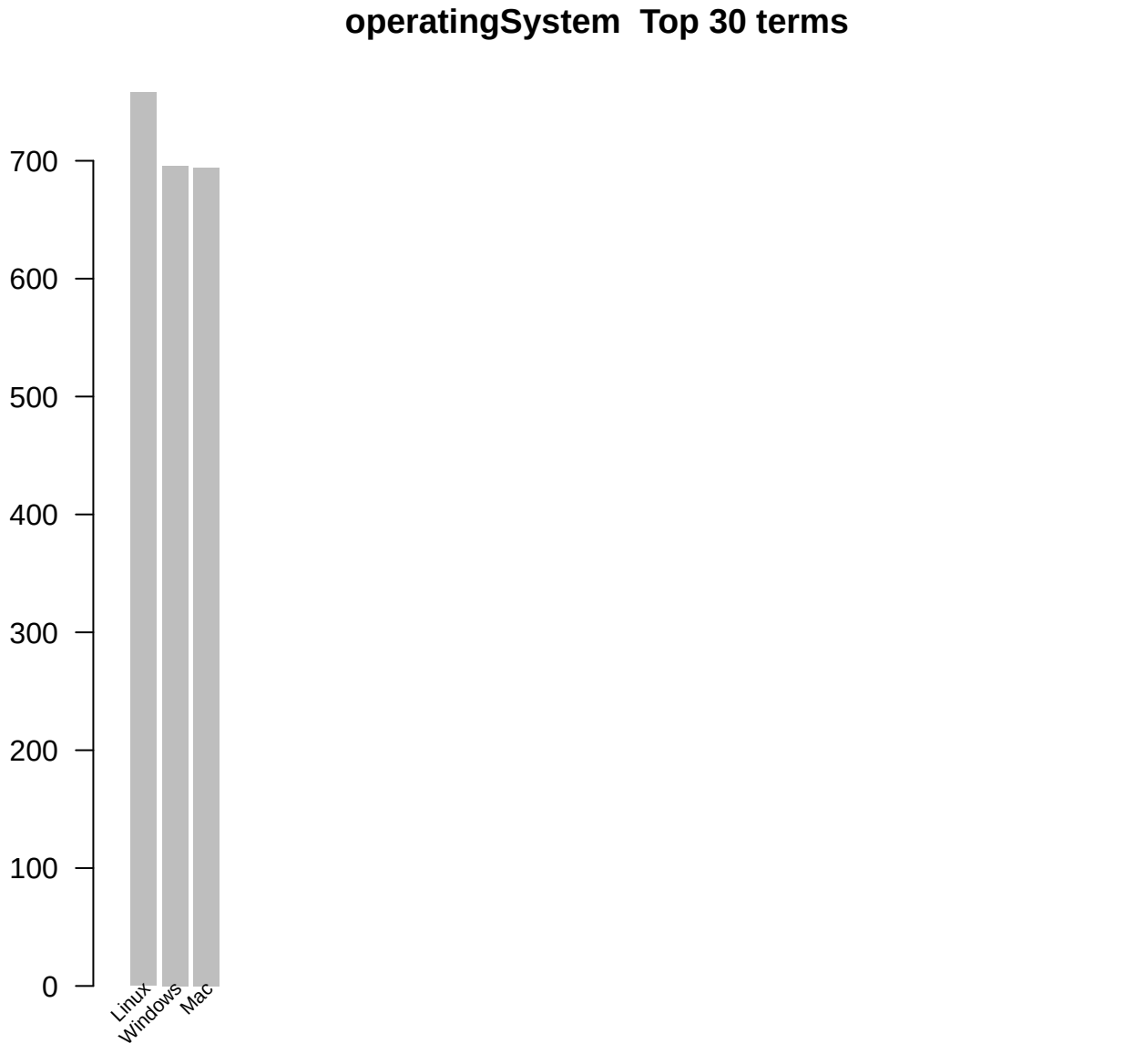

license Number of terms per tool
Frequency
0
100
200
300
400
500
600
−0.5
0.0
0.5
1.0
1.5
2.0
2.5
completeness

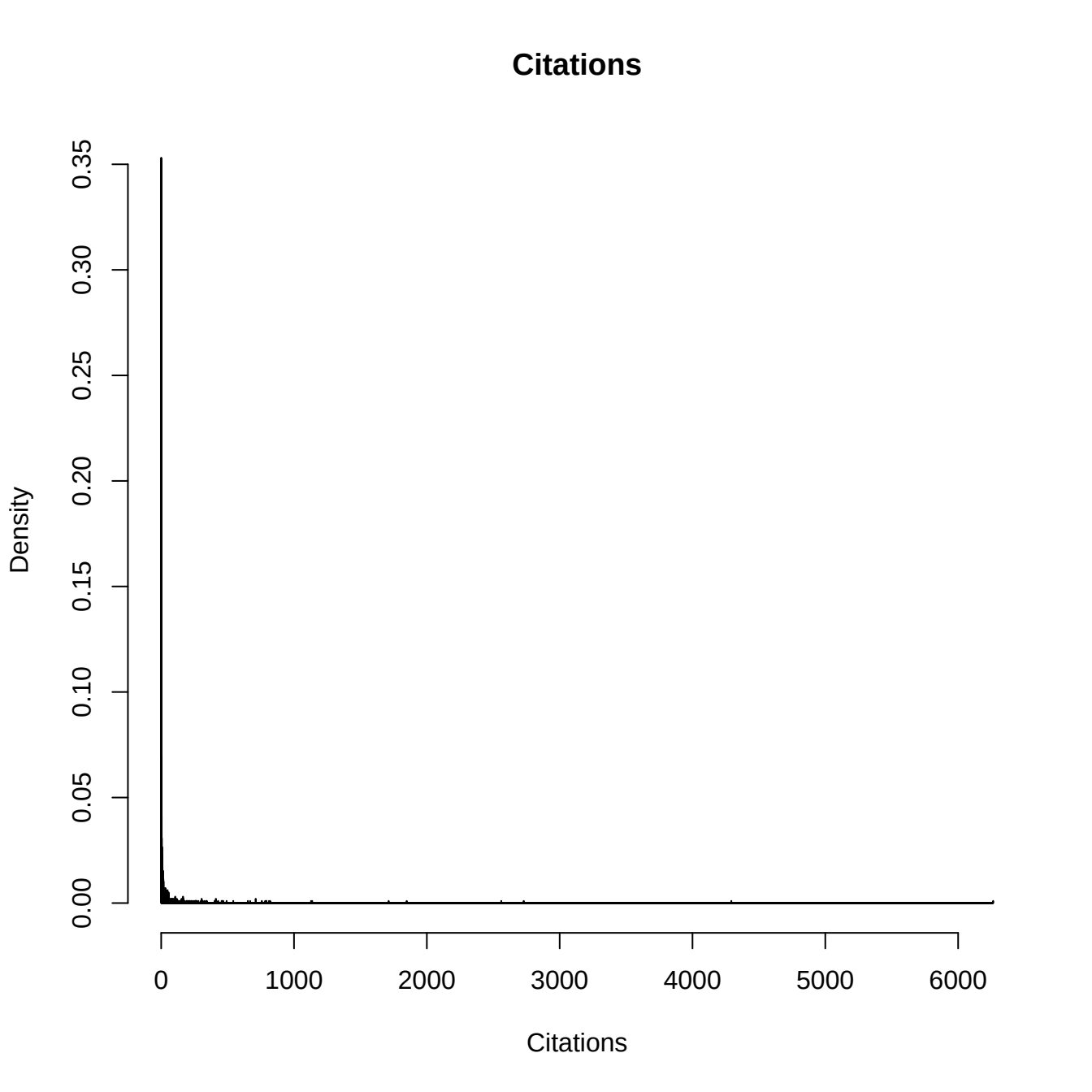

license Top 30 terms
150
100
50
0
GPL−3.0
MIT
Apache−2.0
GPL−2.0
Unlicense
LGPL−2.1
Artistic−2.0
BSD−3−Clause
Other
Proprietary
LGPL−3.0
CC−BY−4.0
Not licensed
BSD−2−Clause
Freeware
AGPL−3.0
GPL−1.0
CC−BY−SA−4.0
CC0−1.0
LGPL−2.0
CC−BY−NC−4.0
CC−BY−ND−3.0
CC−BY−ND−4.0
CDDL−1.0
CECILL−2.1


toolType Number of terms per tool
Frequency
0
200
400
600
800
1000
0
2
4
6
completeness


toolType Top 30 terms
400
300
200
100
0
Command−line tool
Web application
Library
Desktop application
Database portal
Web service
Script
Workflow
Suite
Workbench
Web API
Plug−in
Bioinformatics portal
Ontology


operatingSystem Number of terms per tool
Frequency
0
100
200
300
400
500
600
0
1
2
3
4
completeness


operatingSystem Top 30 terms
700
600
500
400
300
200
100
0
Linux
Windows
Mac


Citations
Density
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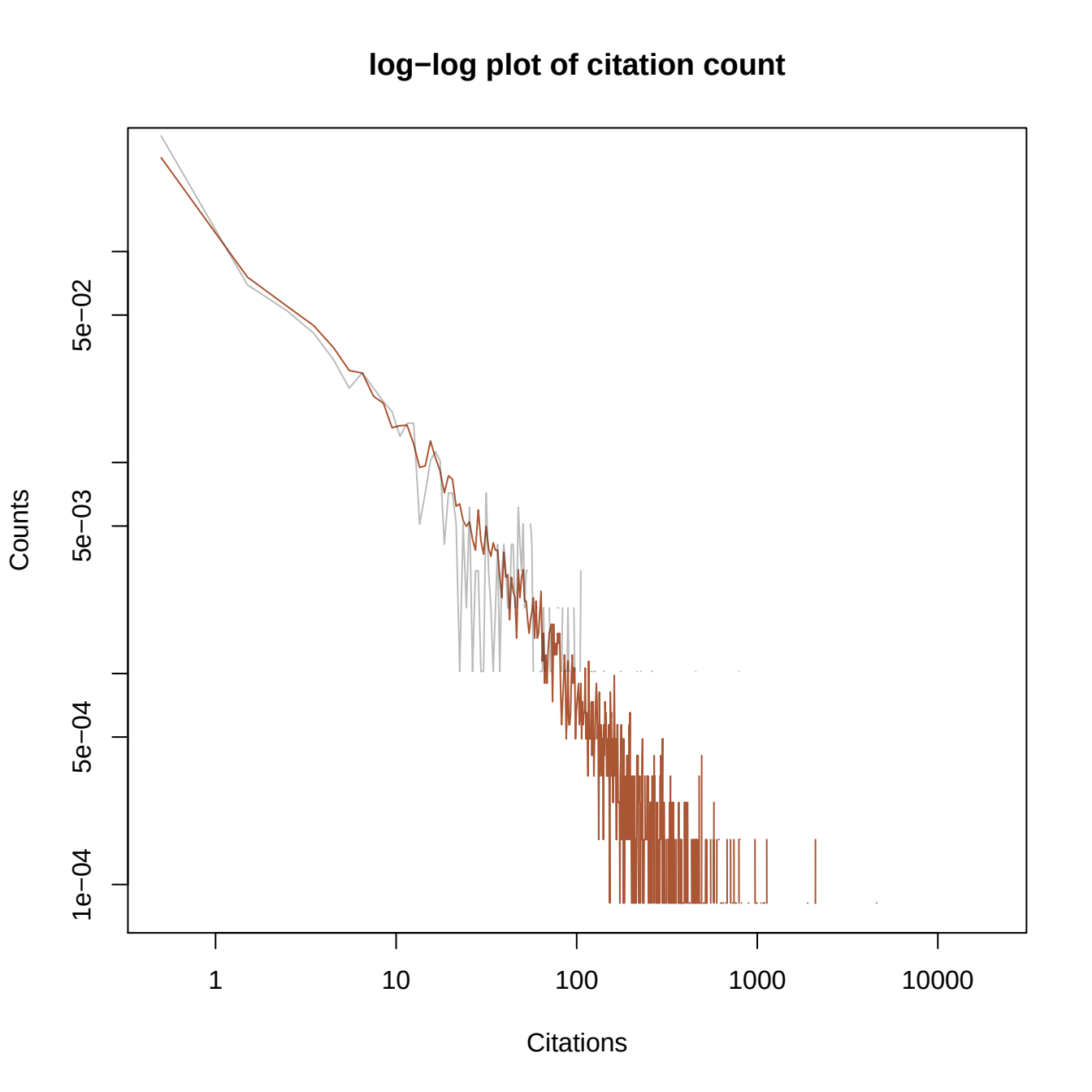
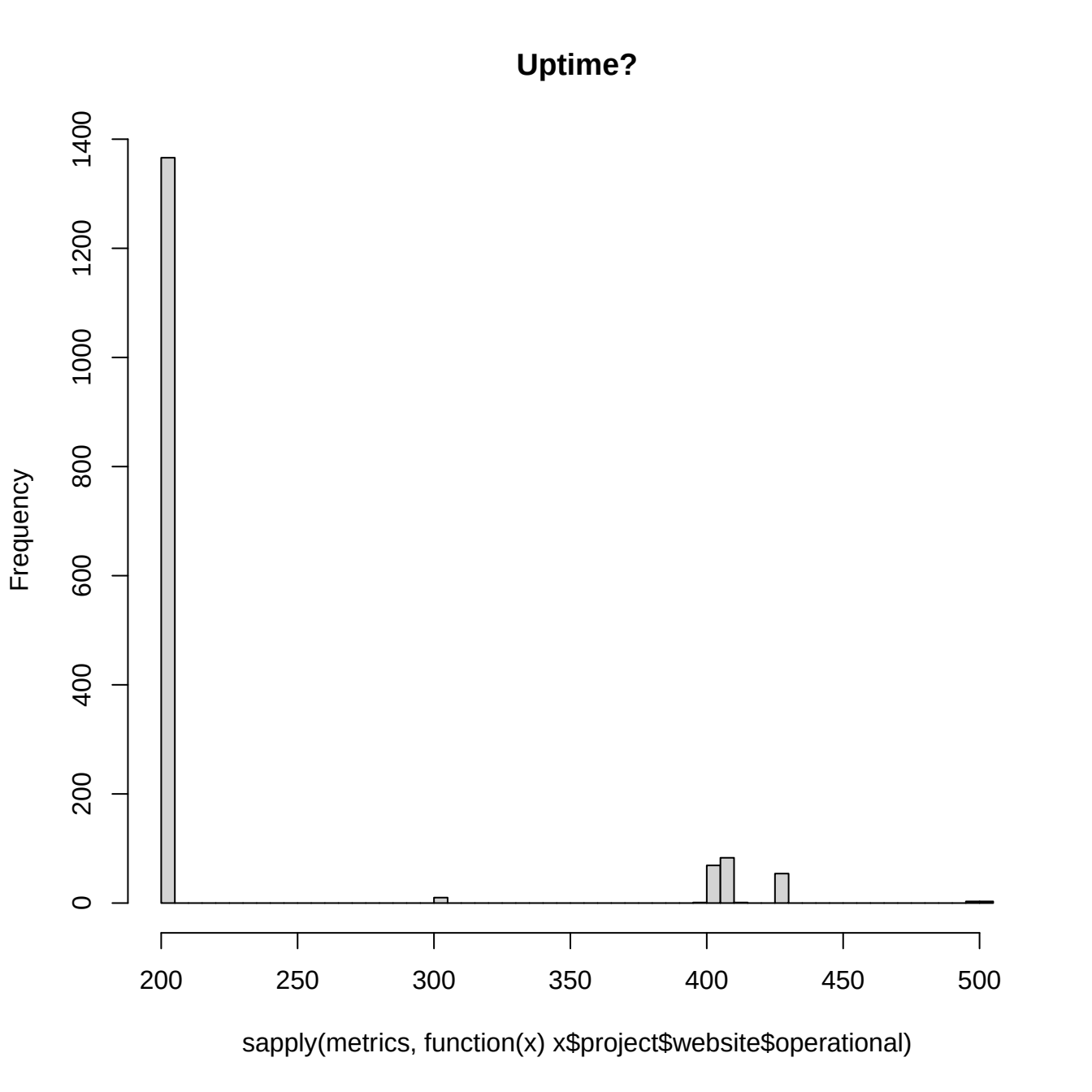
0
1000
2000
3000
4000
5000
6000
Citations


log−log plot of citation count
Counts
5e−02
5e−03
5e−04
1e−04
1
10
100
1000
10000
Citations


Uptime?
Frequency
0
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600
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1400
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250
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350
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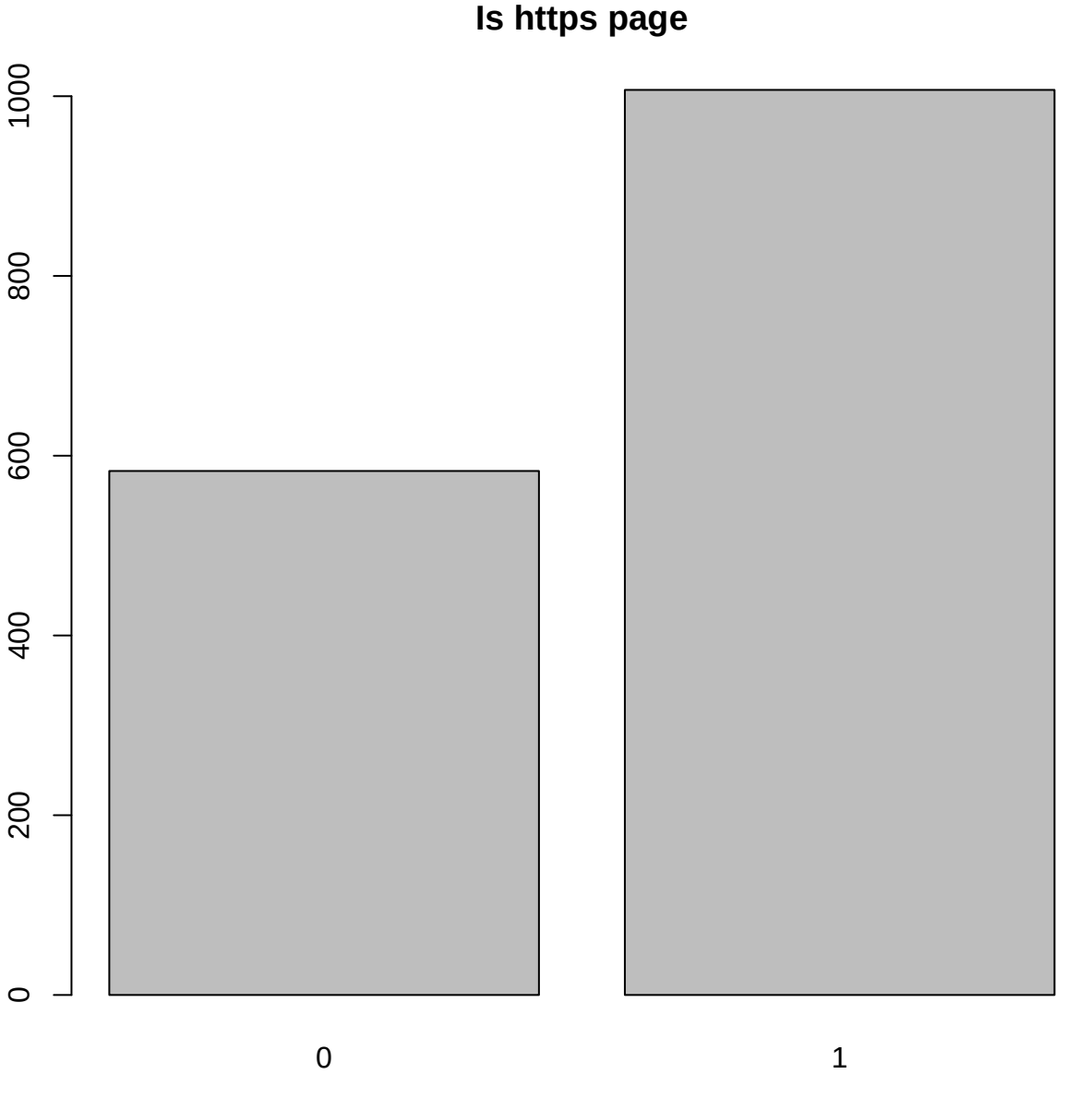
450
500
sapply(metrics, function(x) x$project$website$operational)


Is https page
0
200
400
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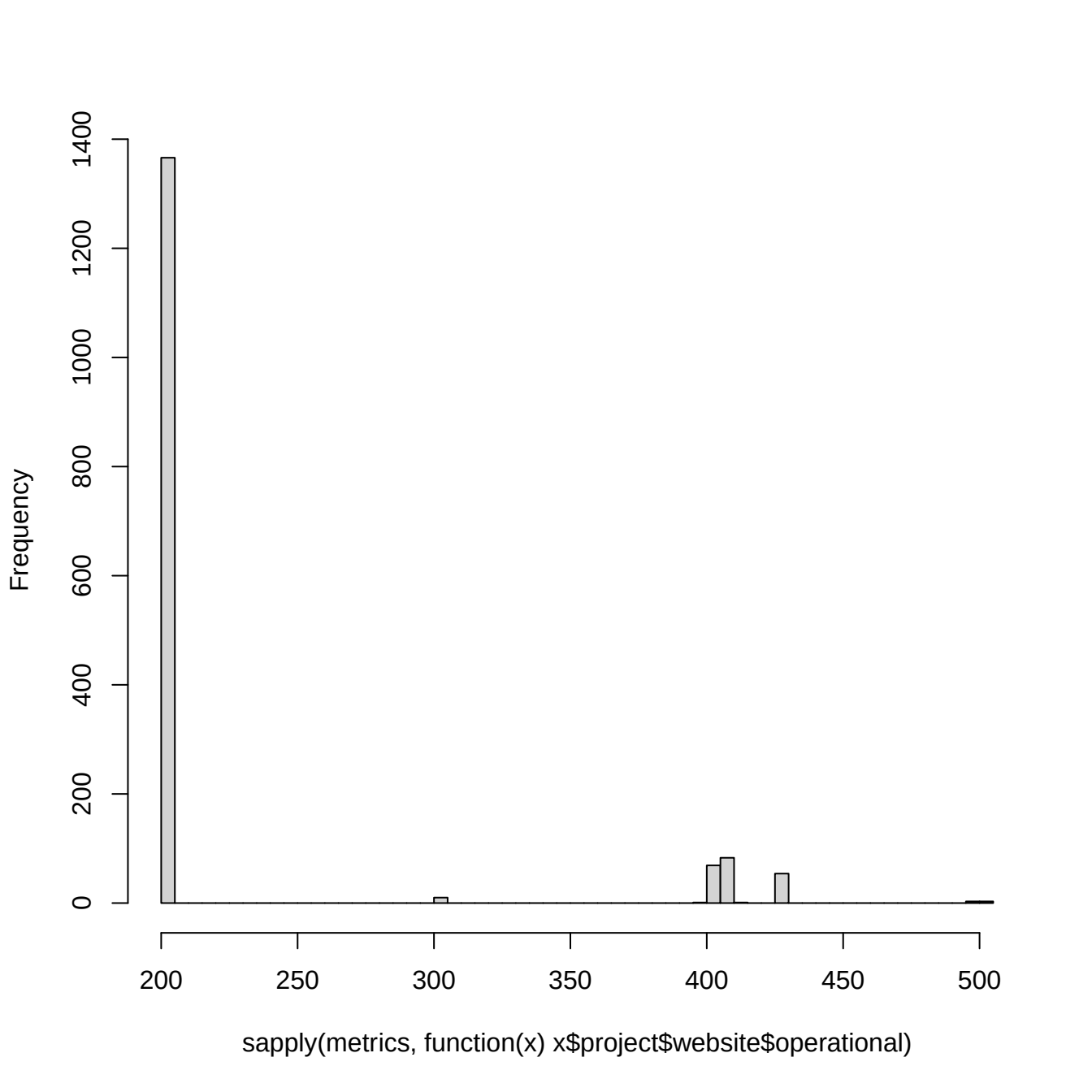
800
1000
0
1


Frequency
0
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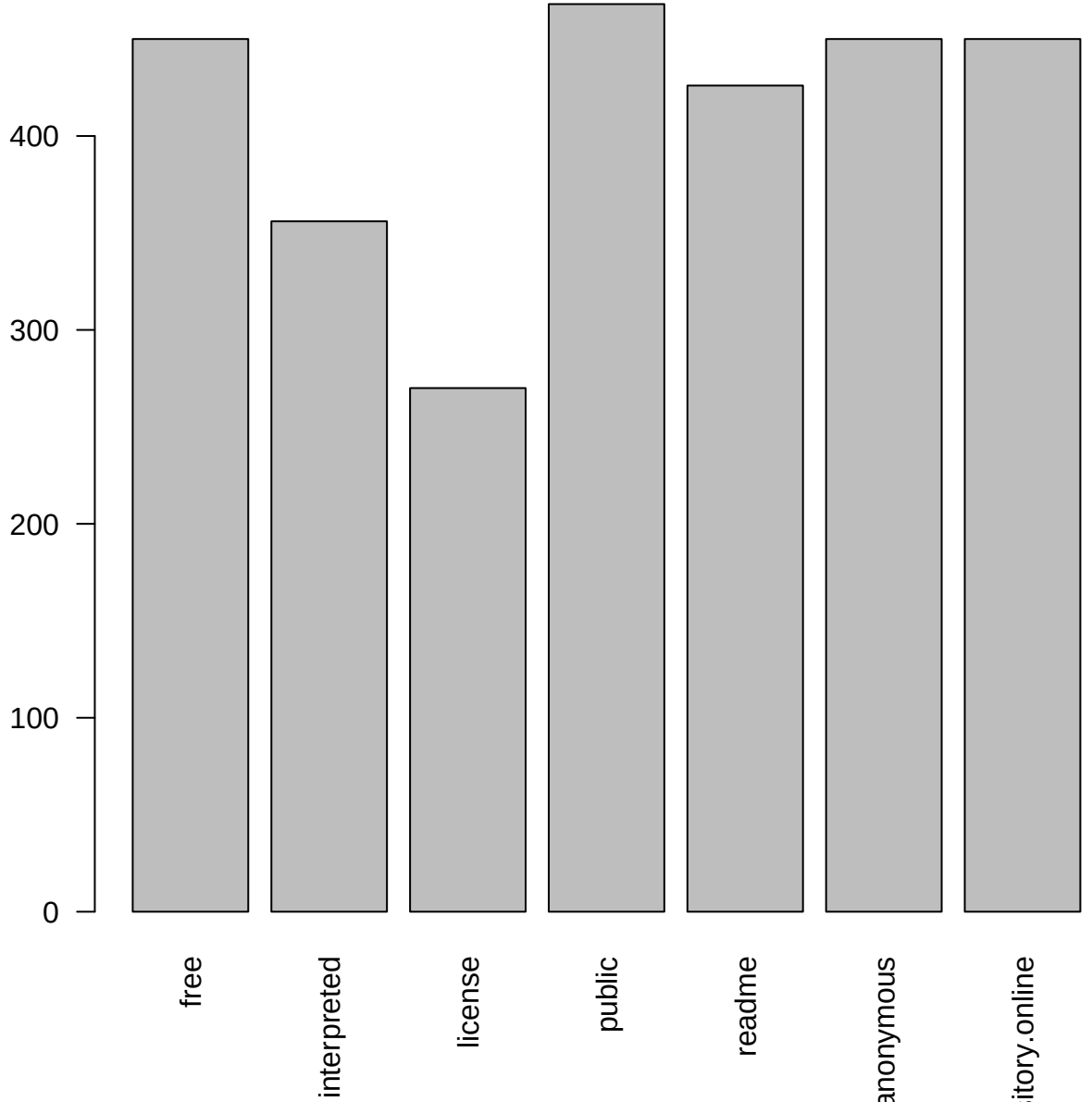
1200
1400
200
250
300
350
400
450
500
sapply(metrics, function(x) x$project$website$operational)


400
300
200
100
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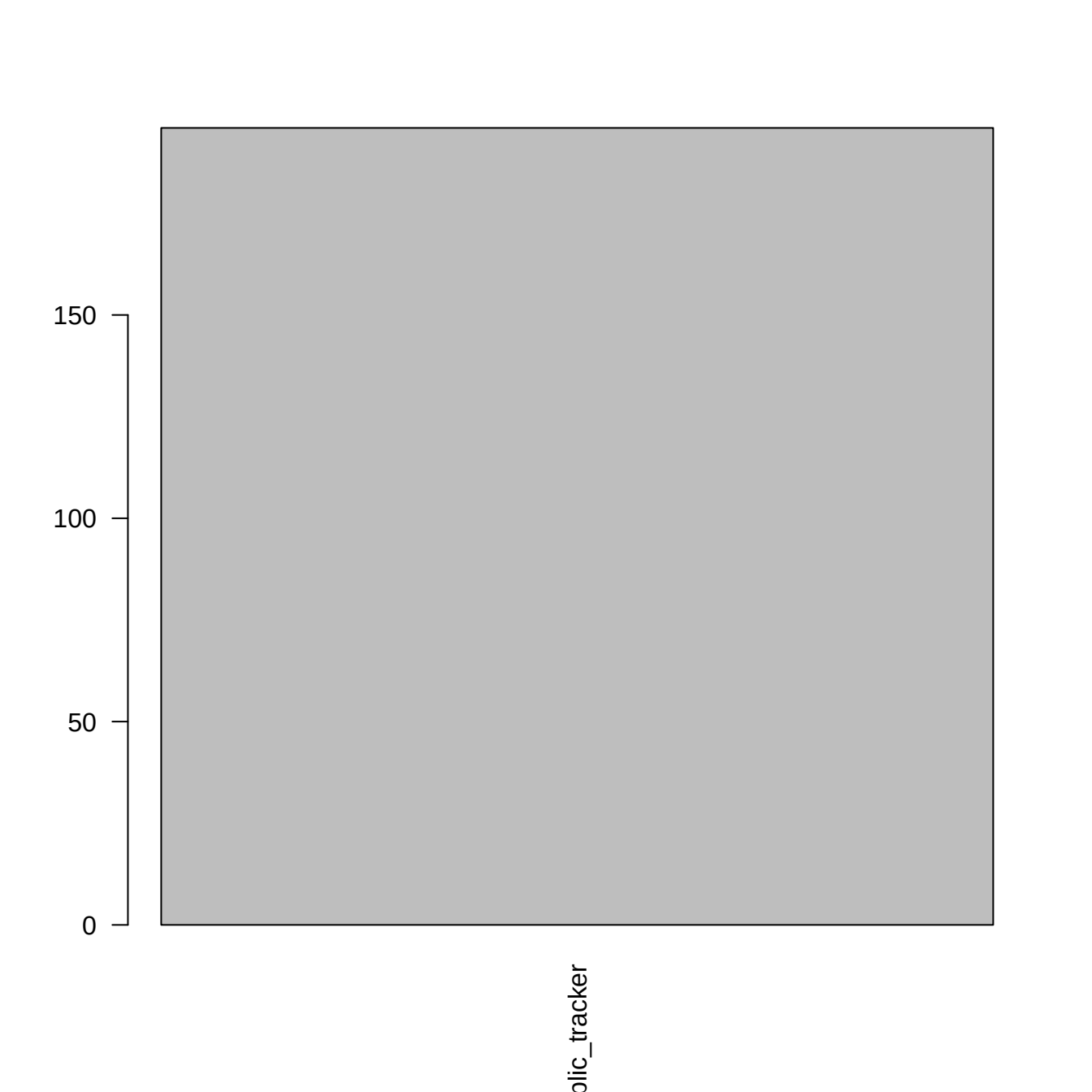
free
interpreted
license
public
readme
anonymous
itory.online


150
100
50
0
olic_tracker