Electron microscopy volume map

Raw image

Sequence

Protein sequence

Image

3D EM Mask

EM Micrograph

Hidden Markov model

Gene identifier

Structure image

Protein structure

Image format

FASTA

PDB

Freeware

other

Apache-2.0

GPL-2.0

LGPL-3.0

AGPL-3.0

Artistic-2.0

BSD-2-Clause

MIT

BSD-3-Clause

GPL-3.0

Mac
Linux
Windows

Sequence motif discovery

Regression analysis

Statistical inference

Simulation analysis

Principal component visualisation

Sequence annotation

Rigid body refinement

Surface rendering

RNA-Seq quantification

Virtual screening

Scatter plot plotting

Protein interaction analysis

Reverse complement

Image analysis

Molecular model refinement

Genetic variation analysis

Molecular dynamics

Mapping

Peak detection

Local alignment

Deposition

Clustering

Loop modelling

Heat map generation

Enrichment analysis

Essential dynamics

Comparison

Base-calling

Phasing

Data handling

Genotyping

Neurite measurement

Read binning

Coding region prediction

Analysis

Database search

Formatting

3D profile generation

Pathway analysis

Backbone modelling

Fold recognition

Classification

Chimera detection

Parsing

Editing

Collapsing methods

Scaffolding

de Novo sequencing

Sequence analysis

Copy number estimation

Query and retrieval

Differential gene expression analysis

Image annotation

Data retrieval

Imputation

Phylogenetic tree analysis

Expression analysis

Prediction and recognition

Haplotype mapping

Molecular docking

Modelling and simulation

Optimisation and refinement

Nucleic acid curvature calculation

Principal component analysis

Protein geometry calculation

Protein model validation

Protein geometry validation

Protein modelling (mutation)

Protein signal peptide detection

Protein structure analysis

Sequence alignment

Protein threading

Visualisation

Structure analysis

Protein secondary structure prediction

Protein secondary structure prediction (helices)
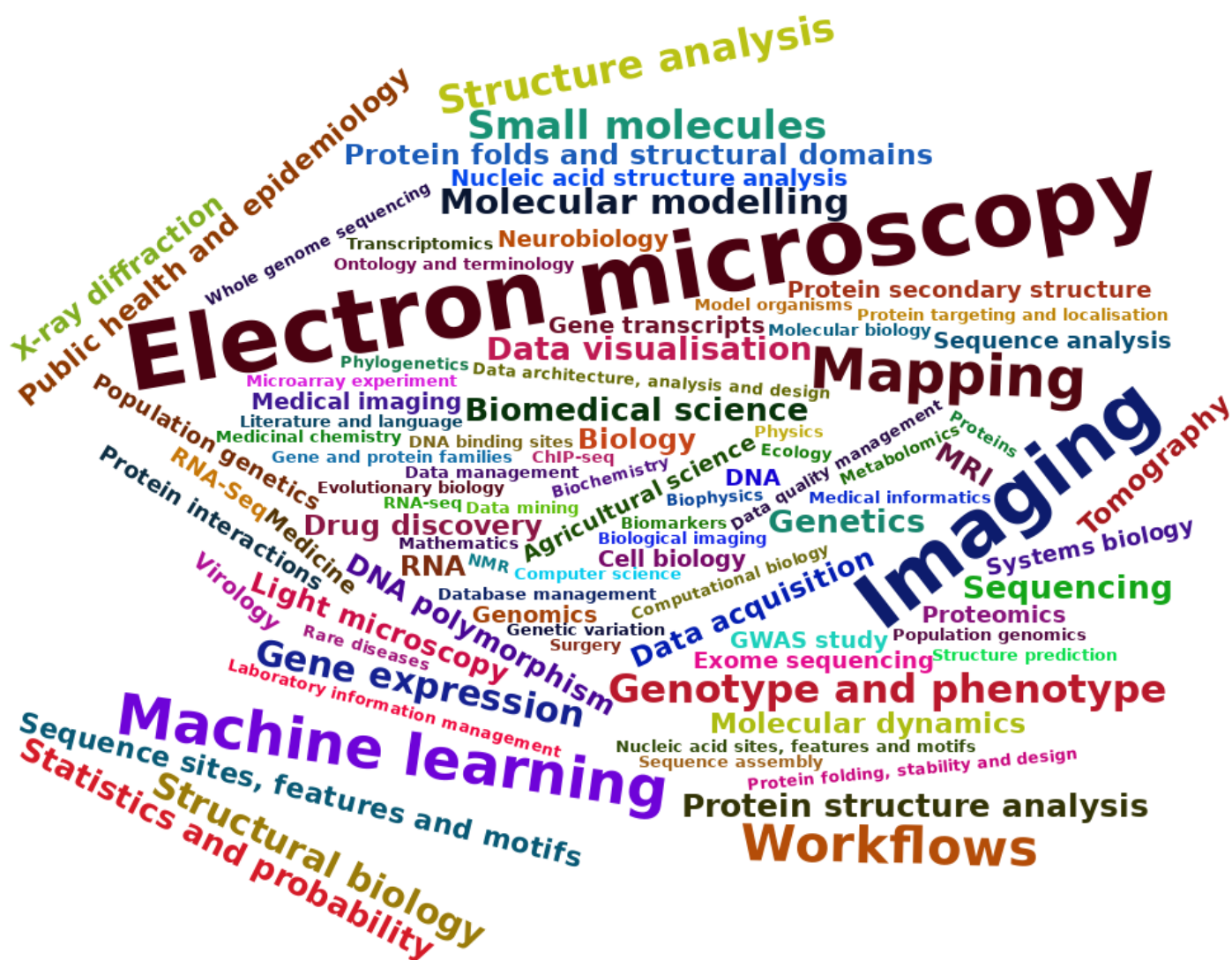
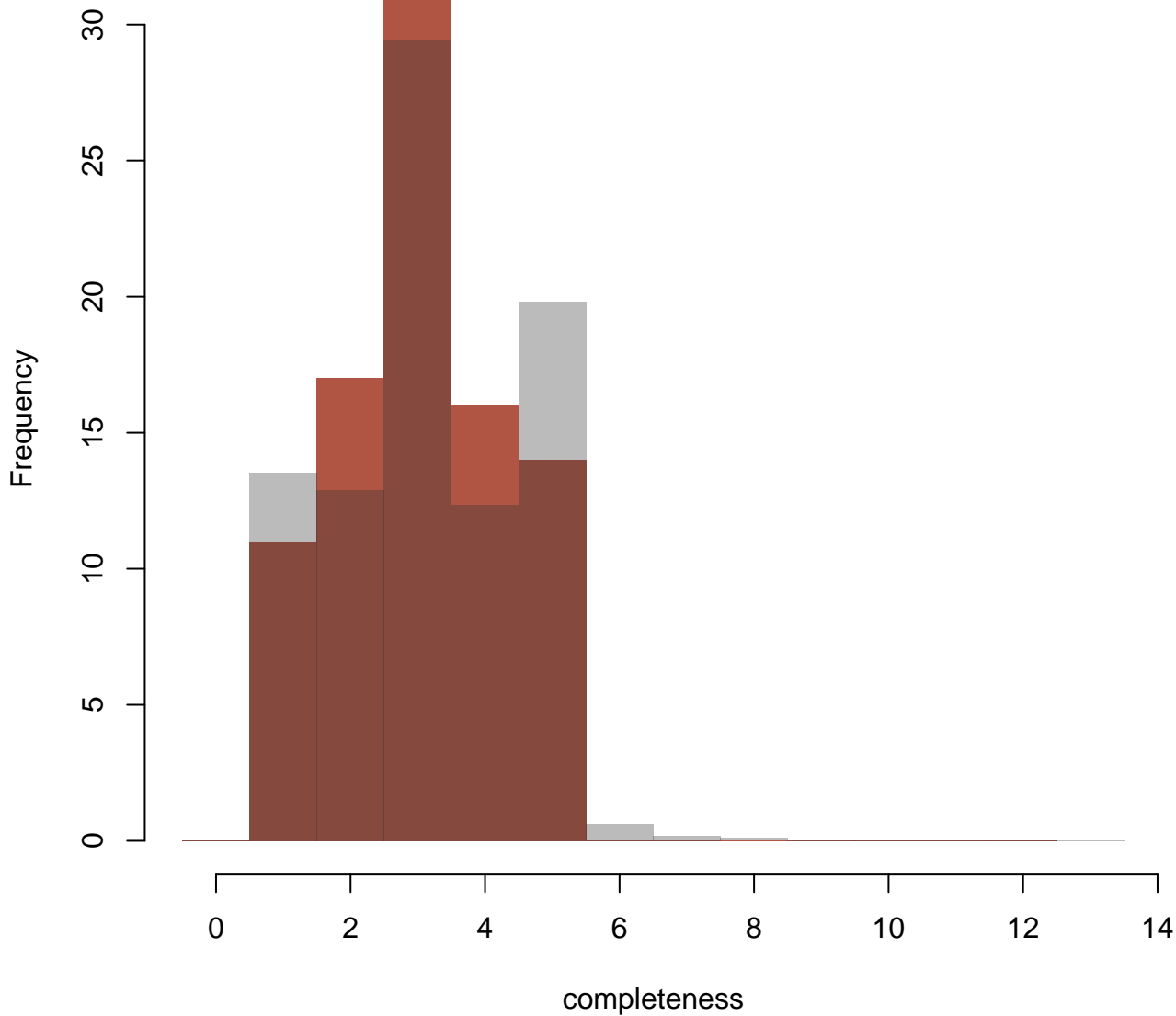# Structural profile

Statistical estimate score

Protein structure

Hidden Markov model

Pathway or network

Structure

Nucleic acid features

Structure image
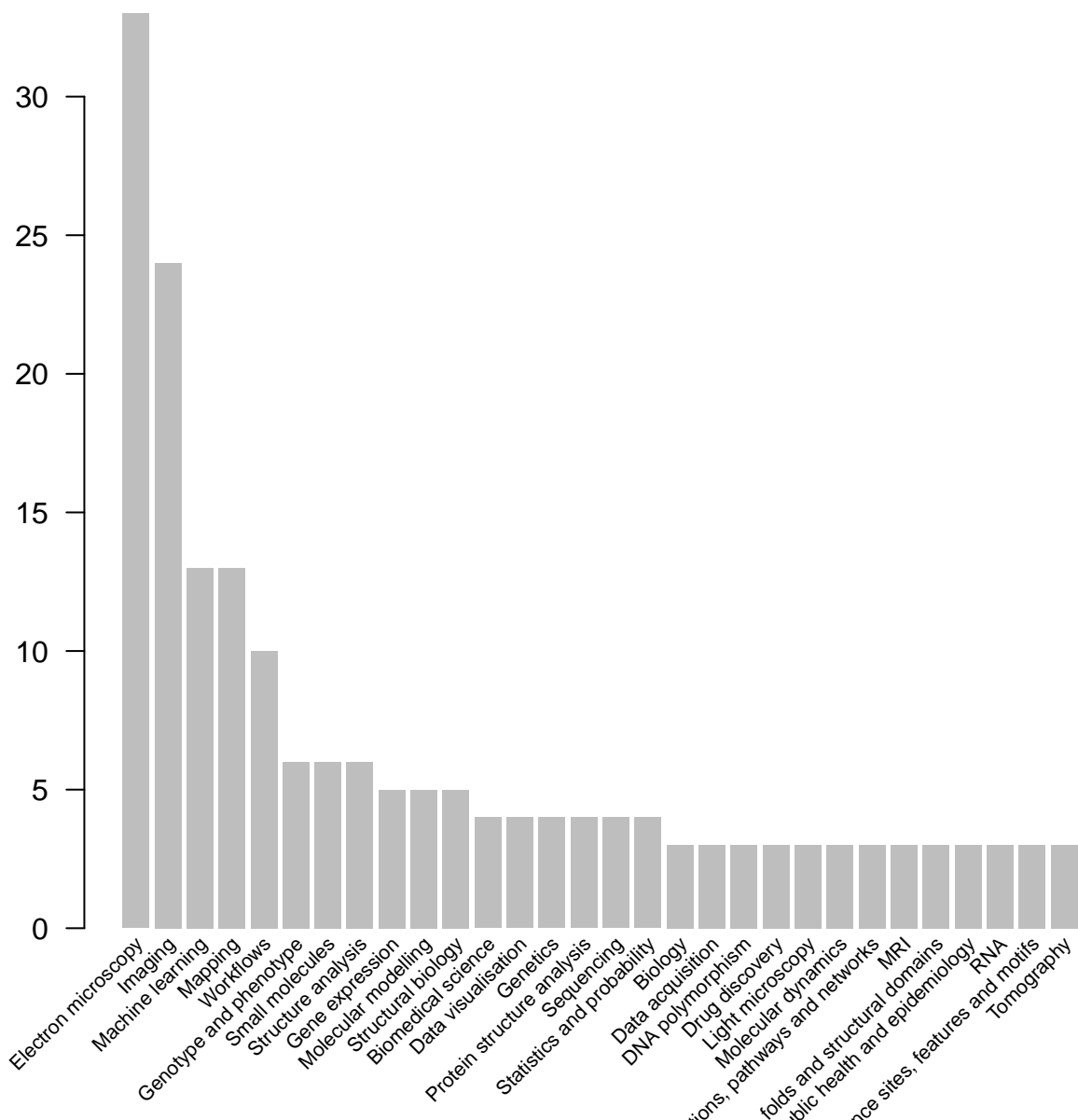
Image format

Workflow format

Web application

Workbench

Database portal

Workflow Suite

Command-line tool

Ontology

Plug-in Script

Library

Desktop application

Structure analysis

Small molecules

X-ray diffraction

Protein folds and structural domains

Nucleic acid structure analysis

Public health and epidemiology

Whole genome sequencing

Molecular modelling

Transcriptomics Neurobiology

Ontology and terminology

Electron microscopy

Protein secondary structure

Model organisms Protein targeting and localisation

Gene transcripts Molecular biology Sequence analysis

Data visualisation Mapping

Phylogenetics Data architecture, analysis and design

Microarray experiment

Population genetics

Medical imaging Biomedical science

Literature and language Physics

Medicinal chemistry DNA binding sites Biology Ecology Metabolomics Proteins

Gene and protein families ChIP-seq Biochemistry DNA MRI

Data management Agricultural science

Protein interactions

Evolutionary biology RNA-seq Data mining Biophysics Data quality management Medical informatics Tomography

RNA-Seq Medicine Drug discovery Biomarkers Genetics

Mathematics NMR Biological imaging Systems biology

RNA Computer science Computational biology Sequencing

Virology Database management Data acquisition Proteomics

Genomics Genetic variation GWAS study Population genomics

Light microscopy Rare diseases Surgery Exome sequencing Structure prediction

DNA polymorphism

Gene expression Genotype and phenotype

Laboratory information management Molecular dynamics

Machine learning Nucleic acid sites, features and motifs

Sequence assembly

Sequence sites, features and motifs Protein folding, stability and design

Structural biology Protein structure analysis

Statistics and probability Workflows

Topic Number of terms per tool

Topic Top 30 terms

Operation Number of terms per tool

Frequency

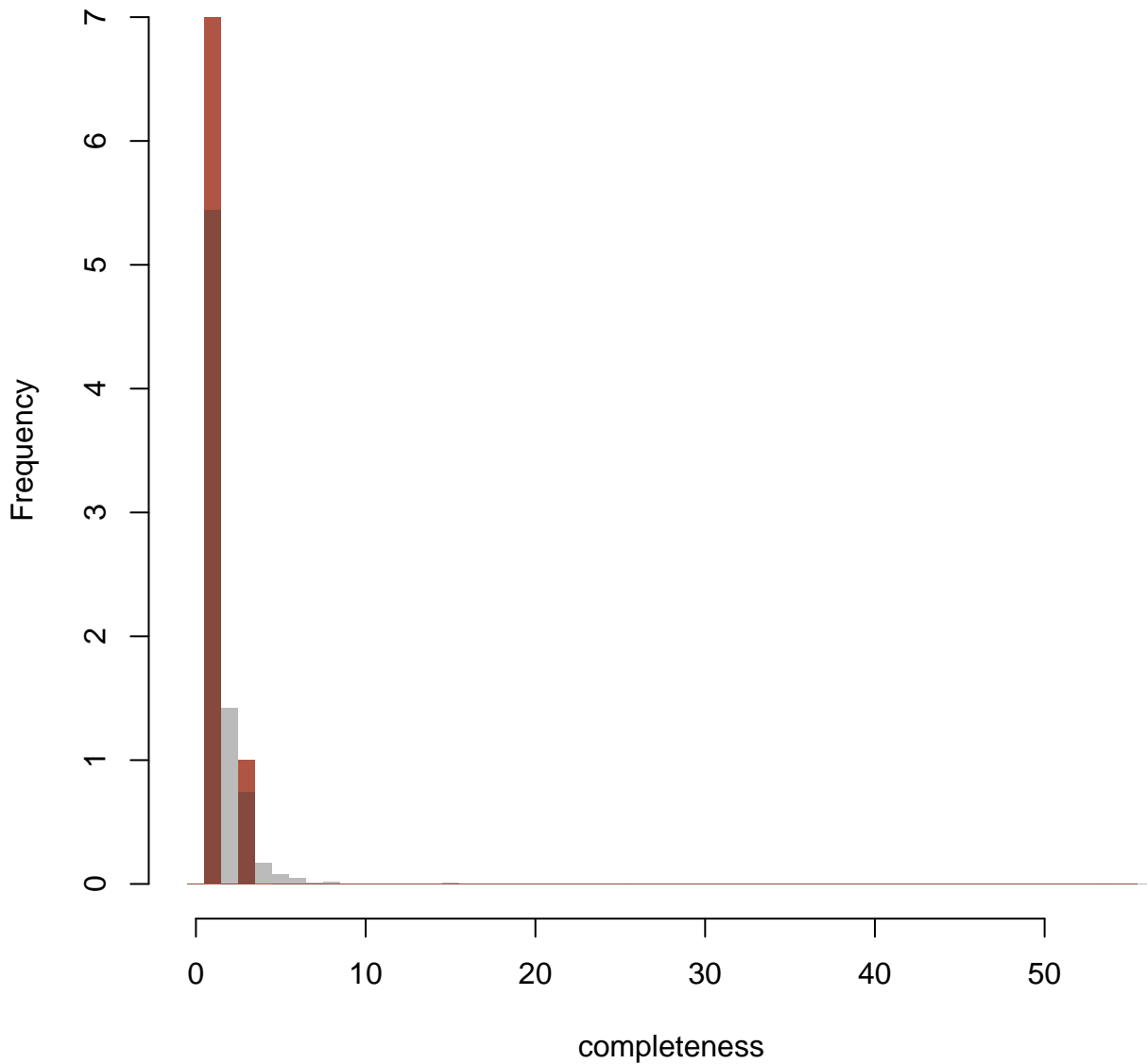completeness
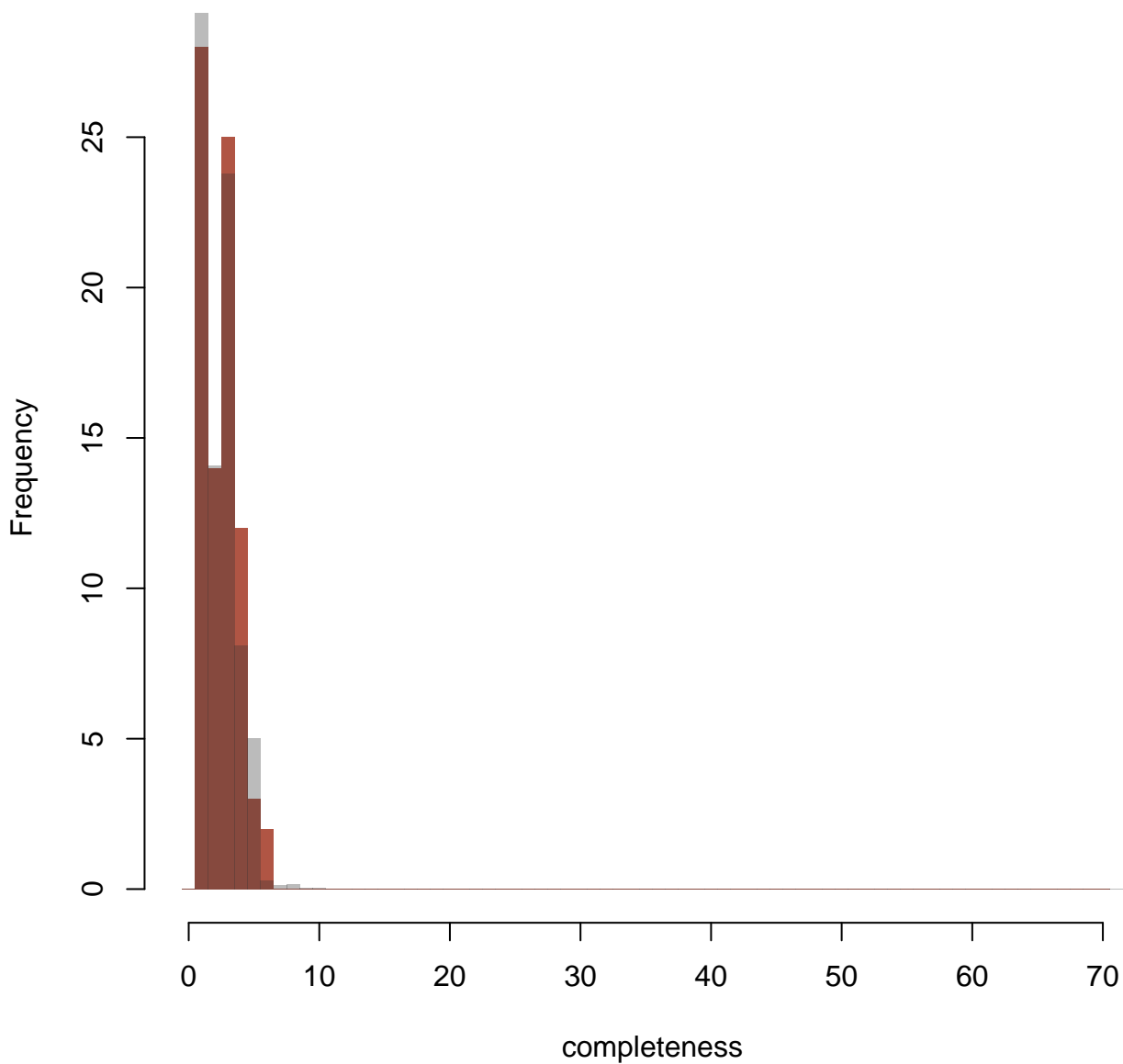
Operation Top 30 terms
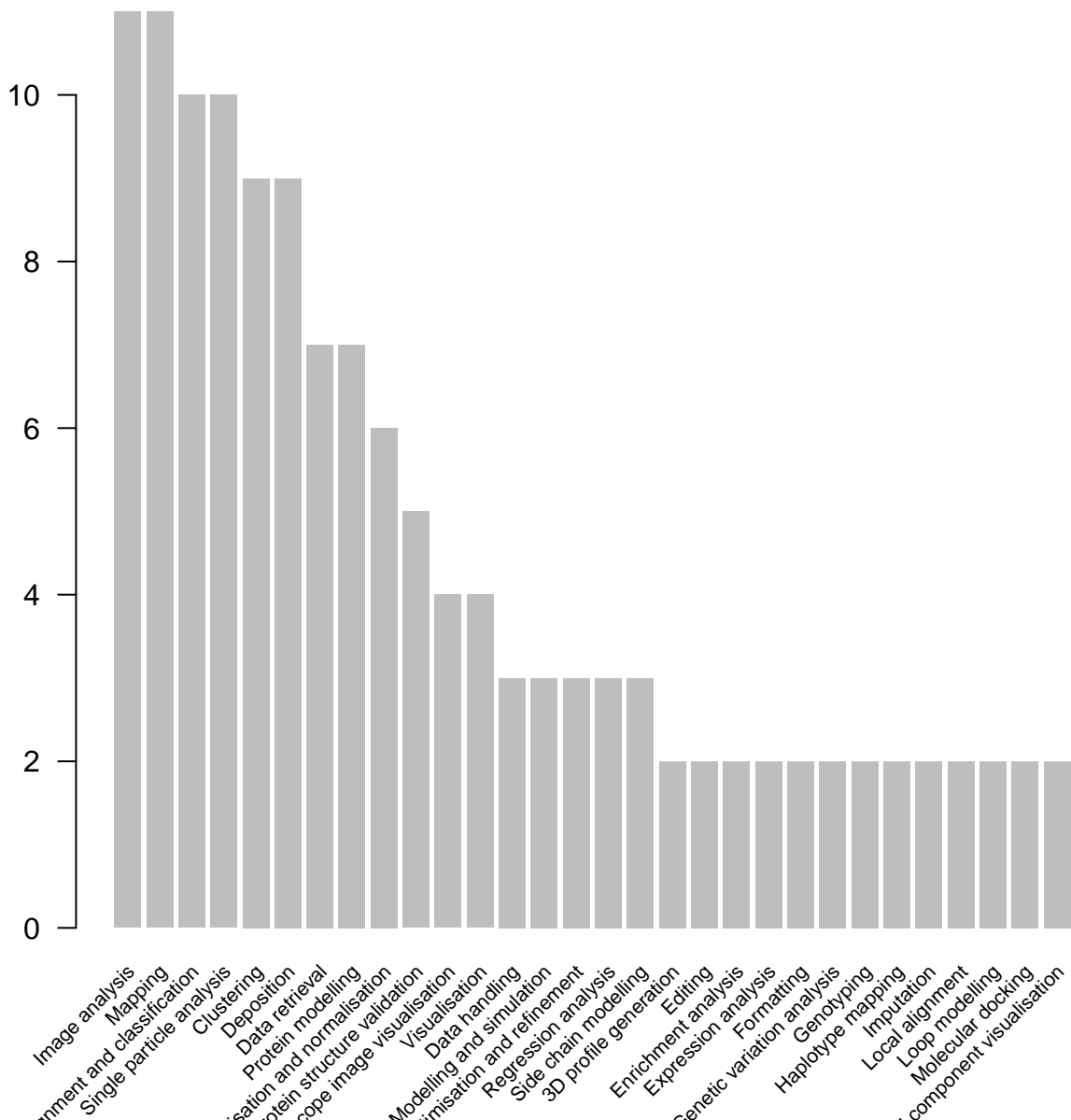
Input format Number of terms per tool
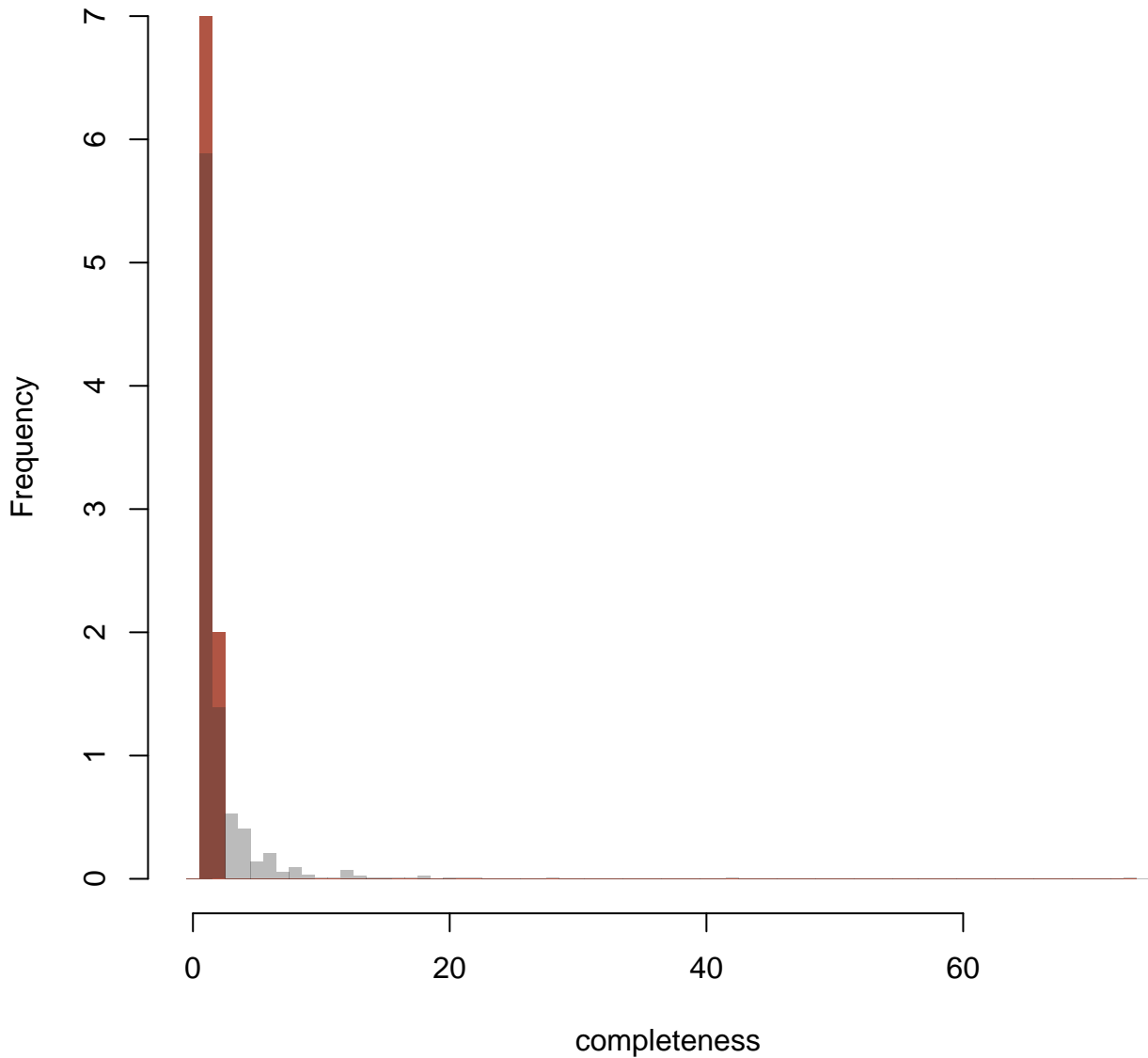
Input format Top 30 terms

Output format Number of terms per tool

Frequency

completeness
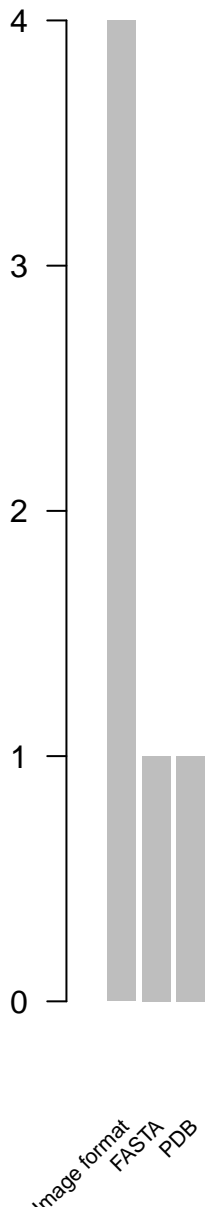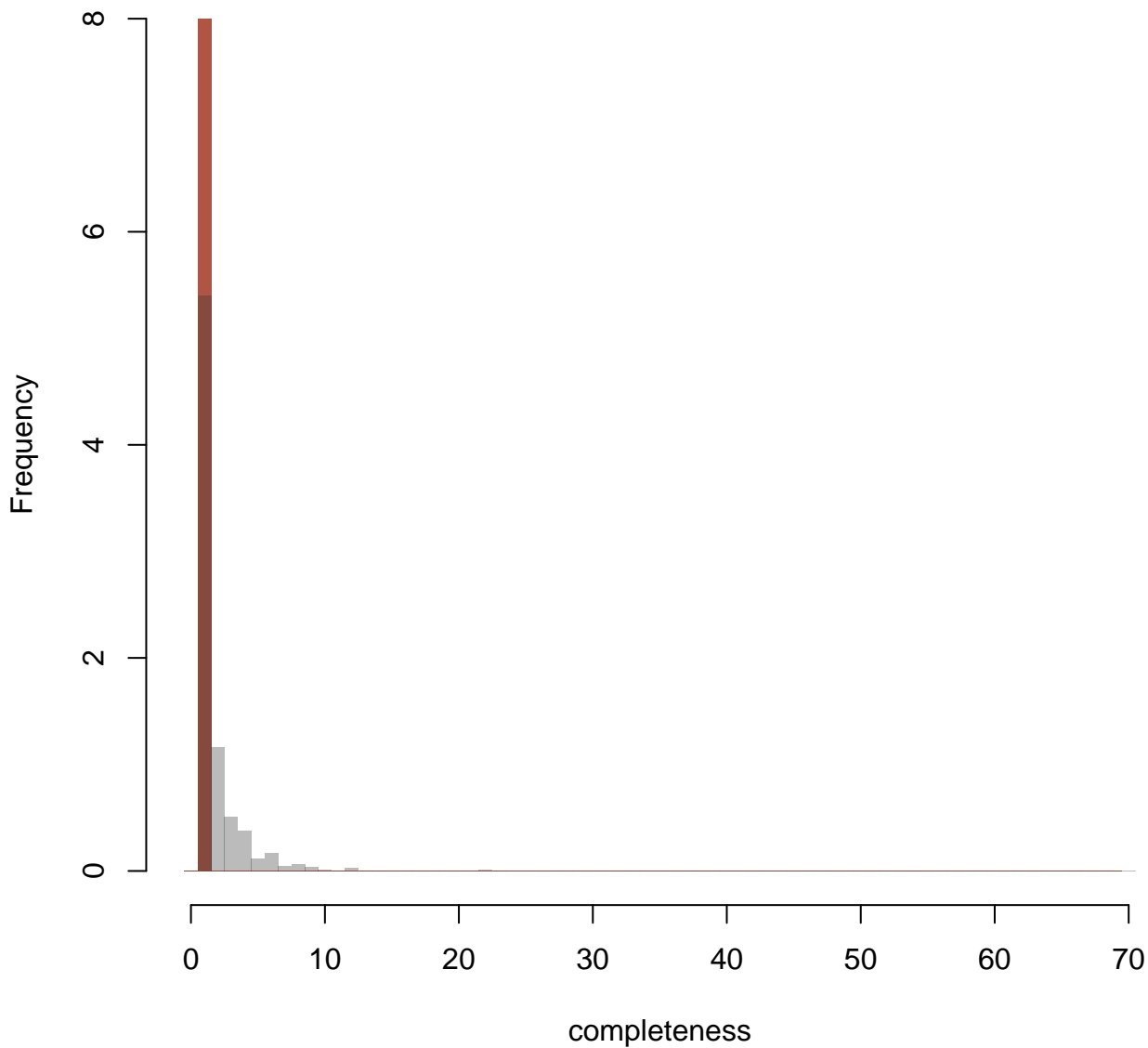
Output format Top 30 terms

Input data Number of terms per tool

Frequency (y-axis)

completeness (x-axis)
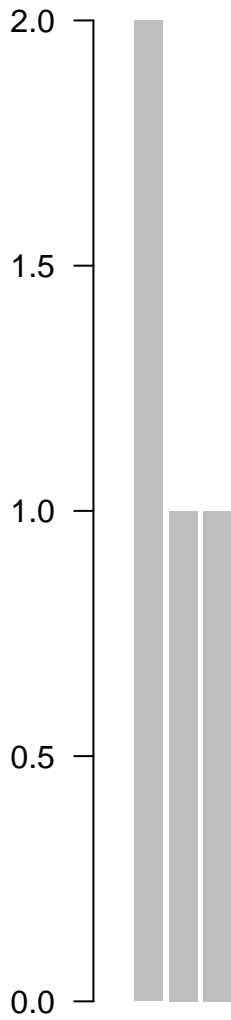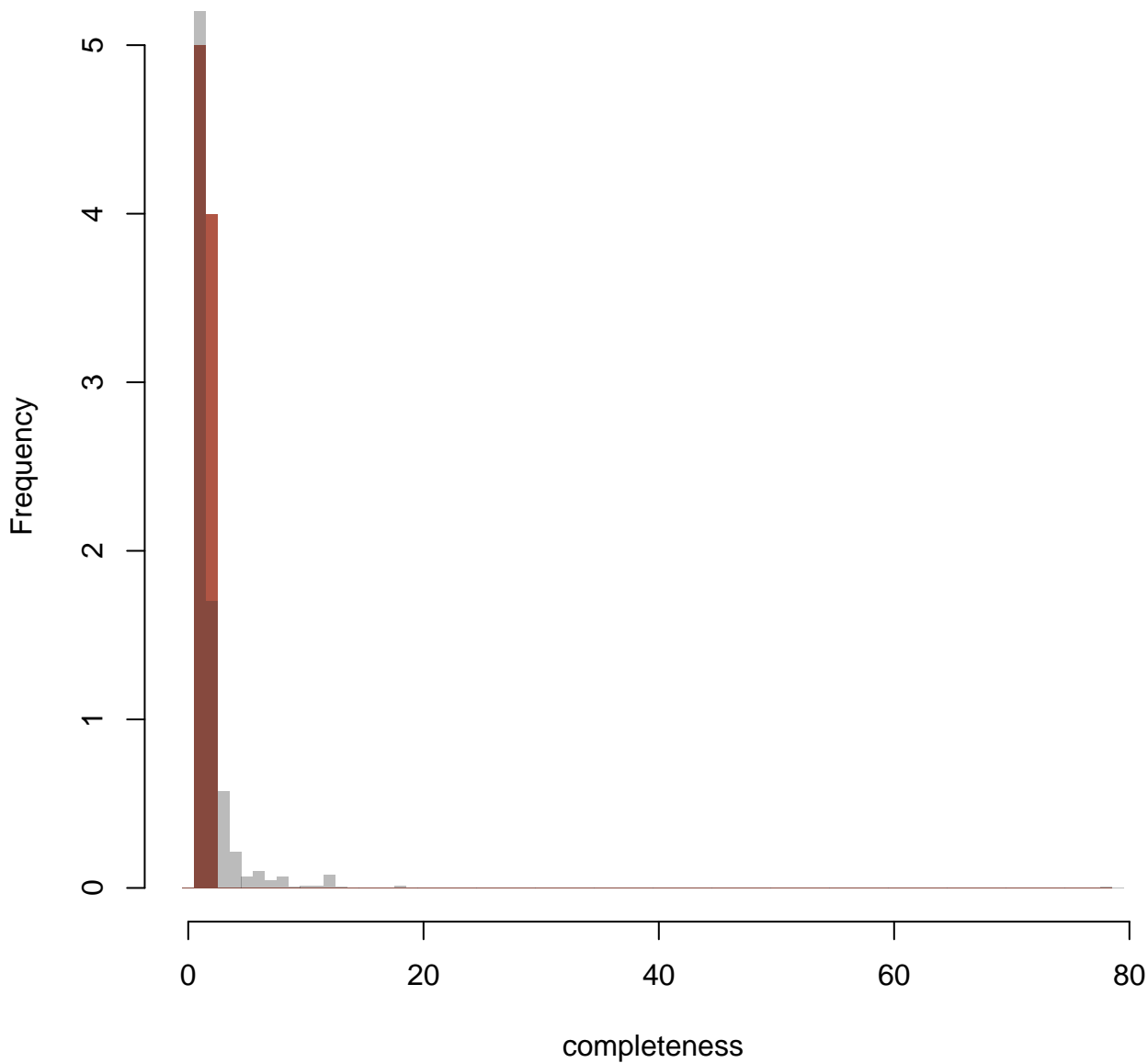
Input data Top 30 terms

Output data Number of terms per tool

Frequency

completeness
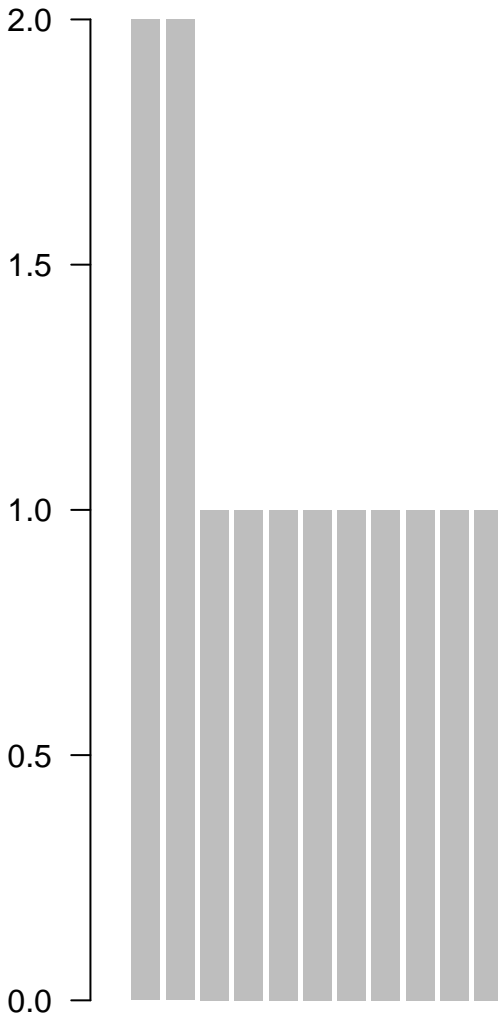
Output data Top 30 terms
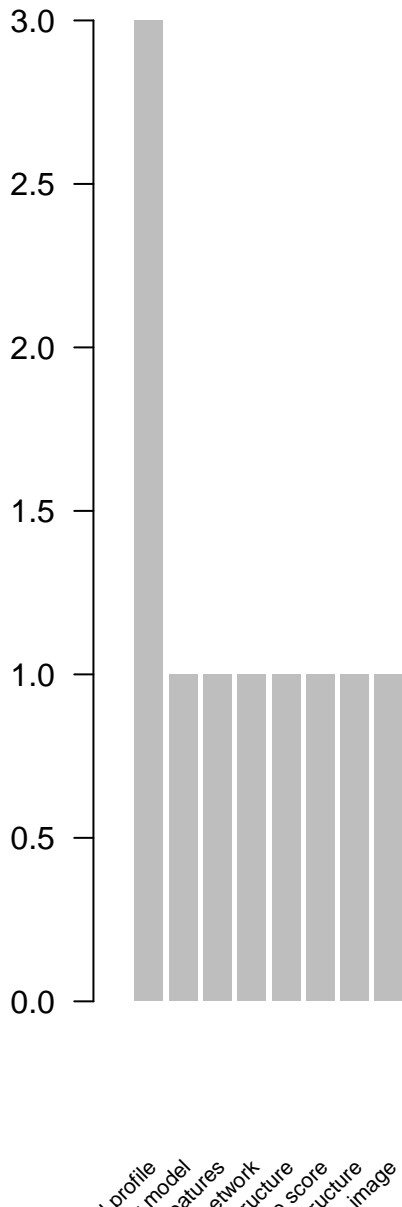
license Number of terms per tool

Frequency

completeness
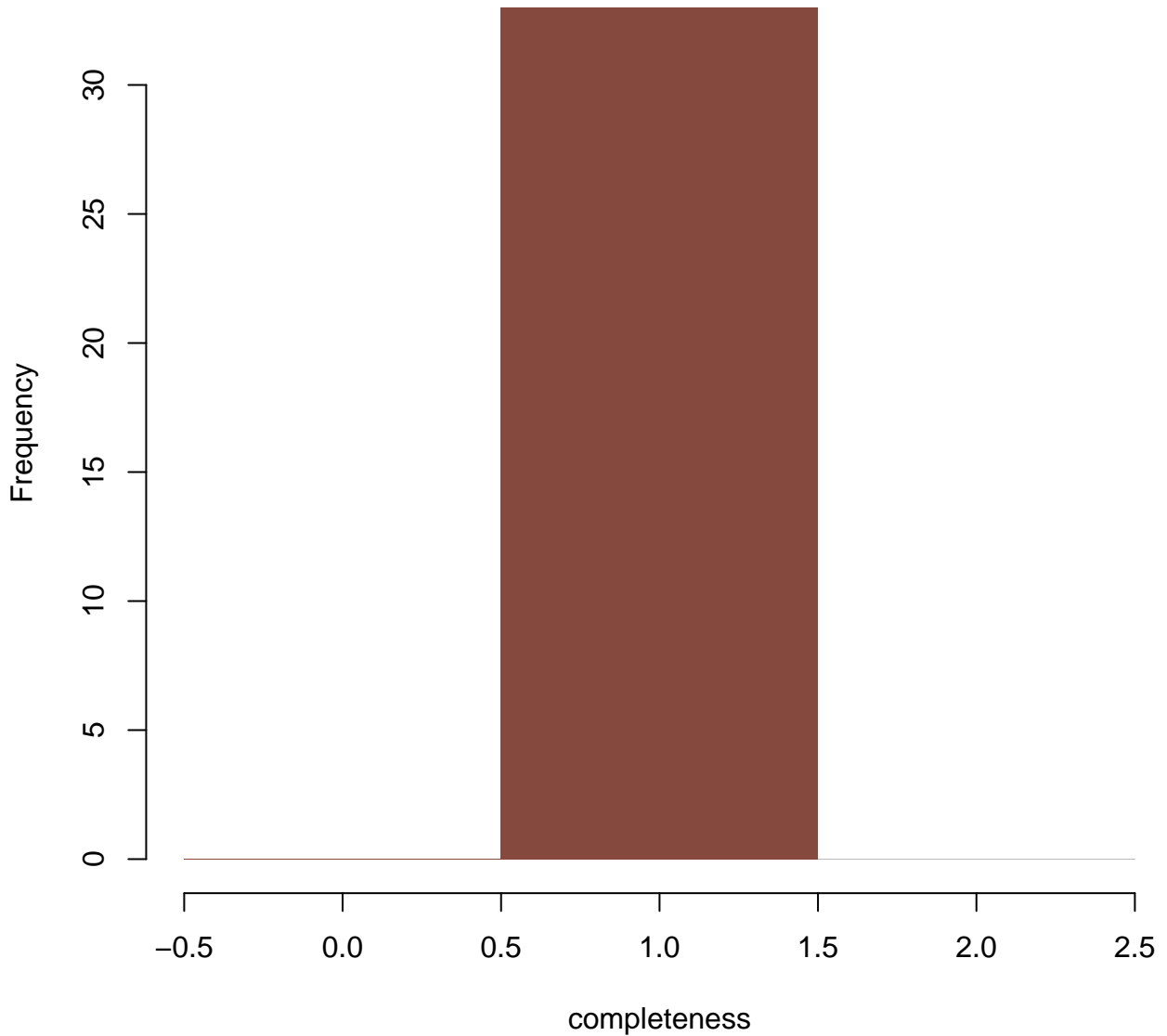
license Top 30 terms
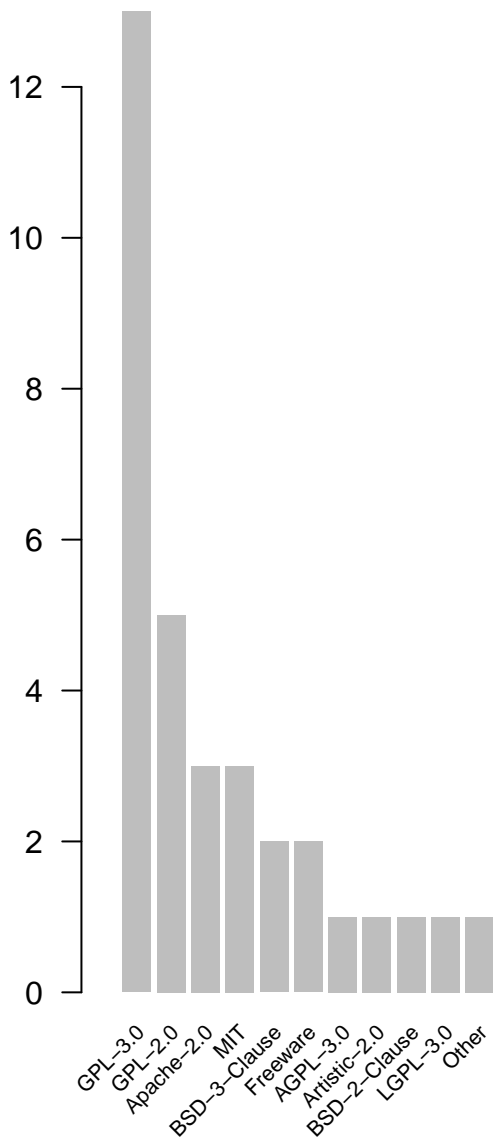
toolType Number of terms per tool
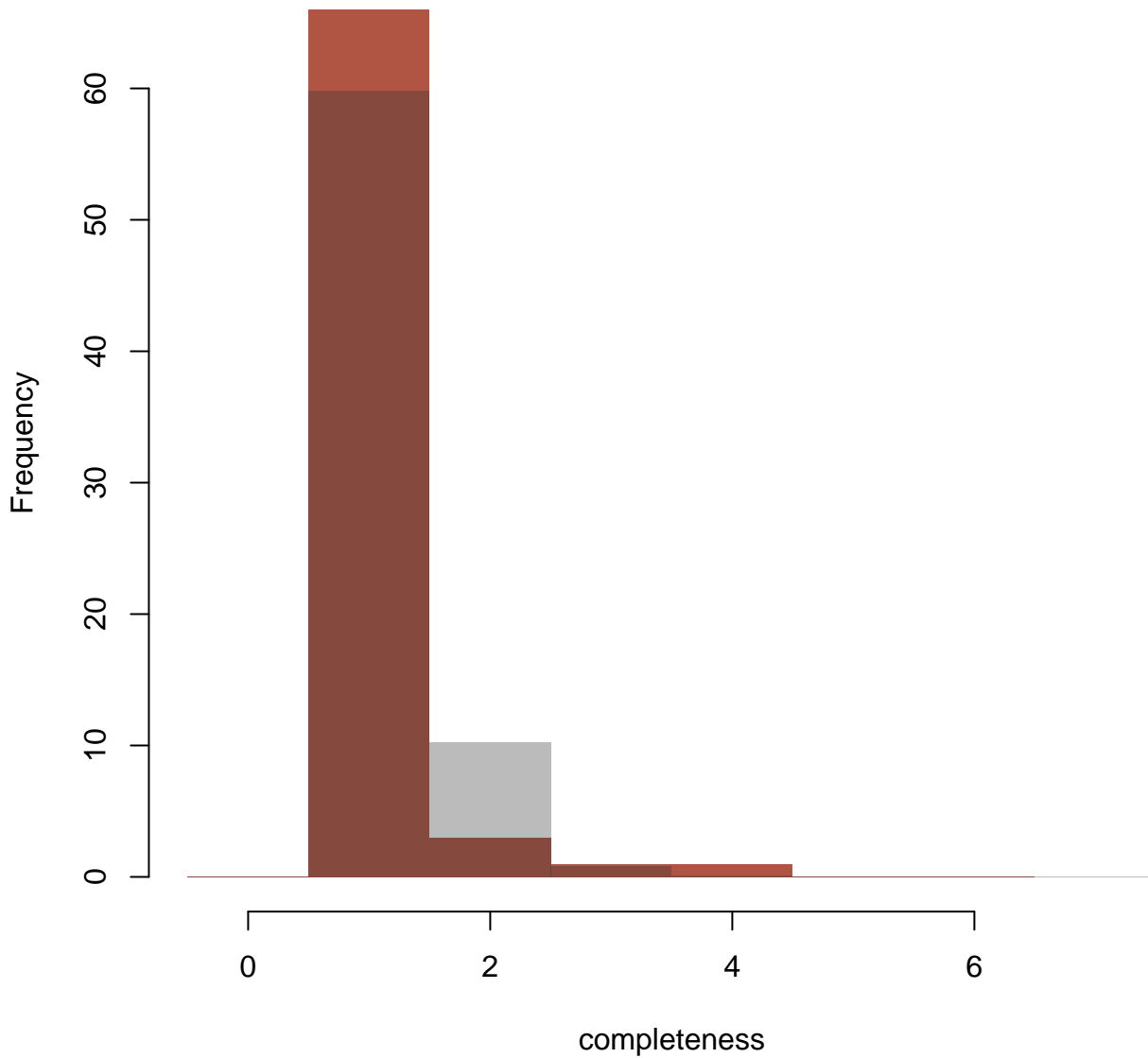
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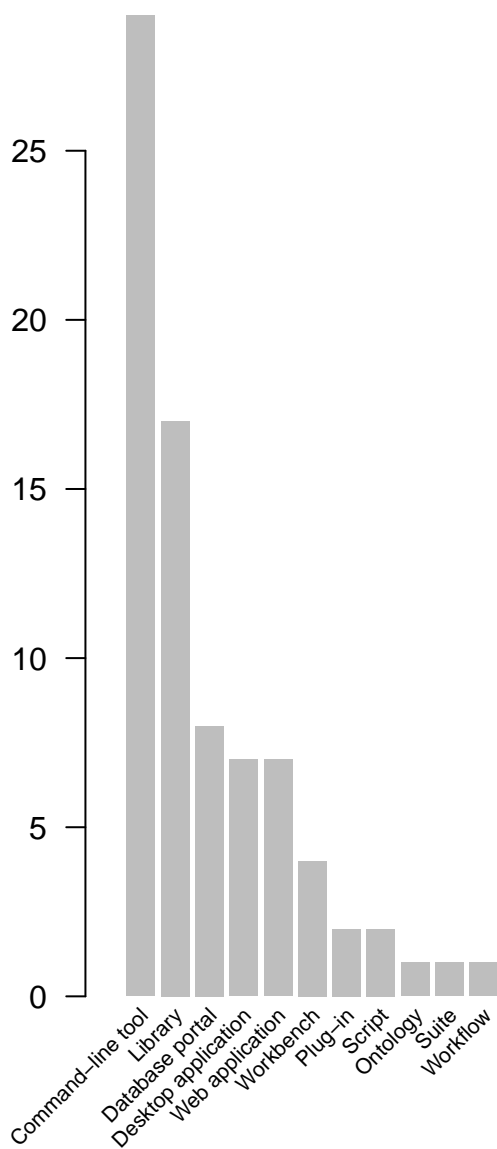
operatingSystem Number of terms per tool
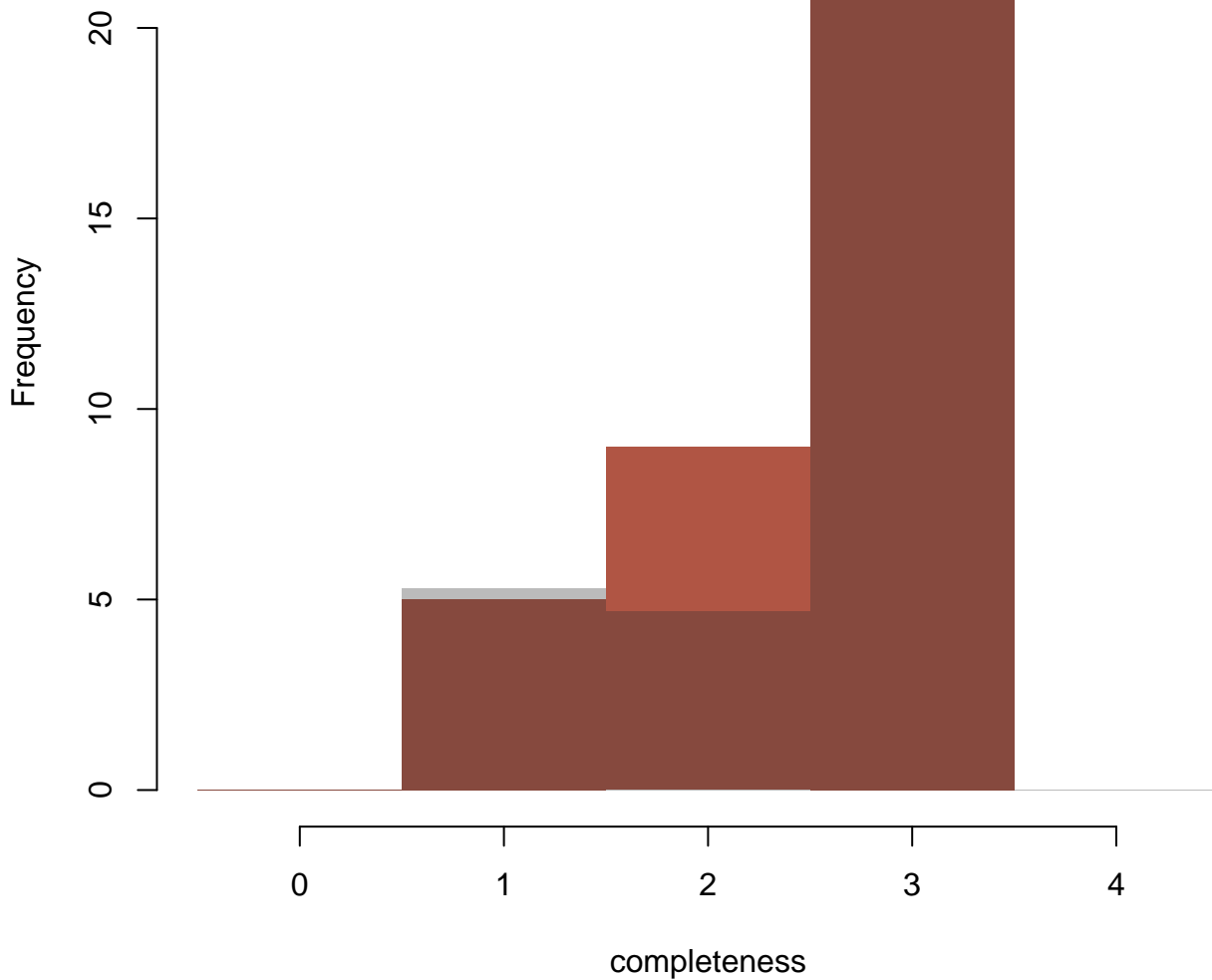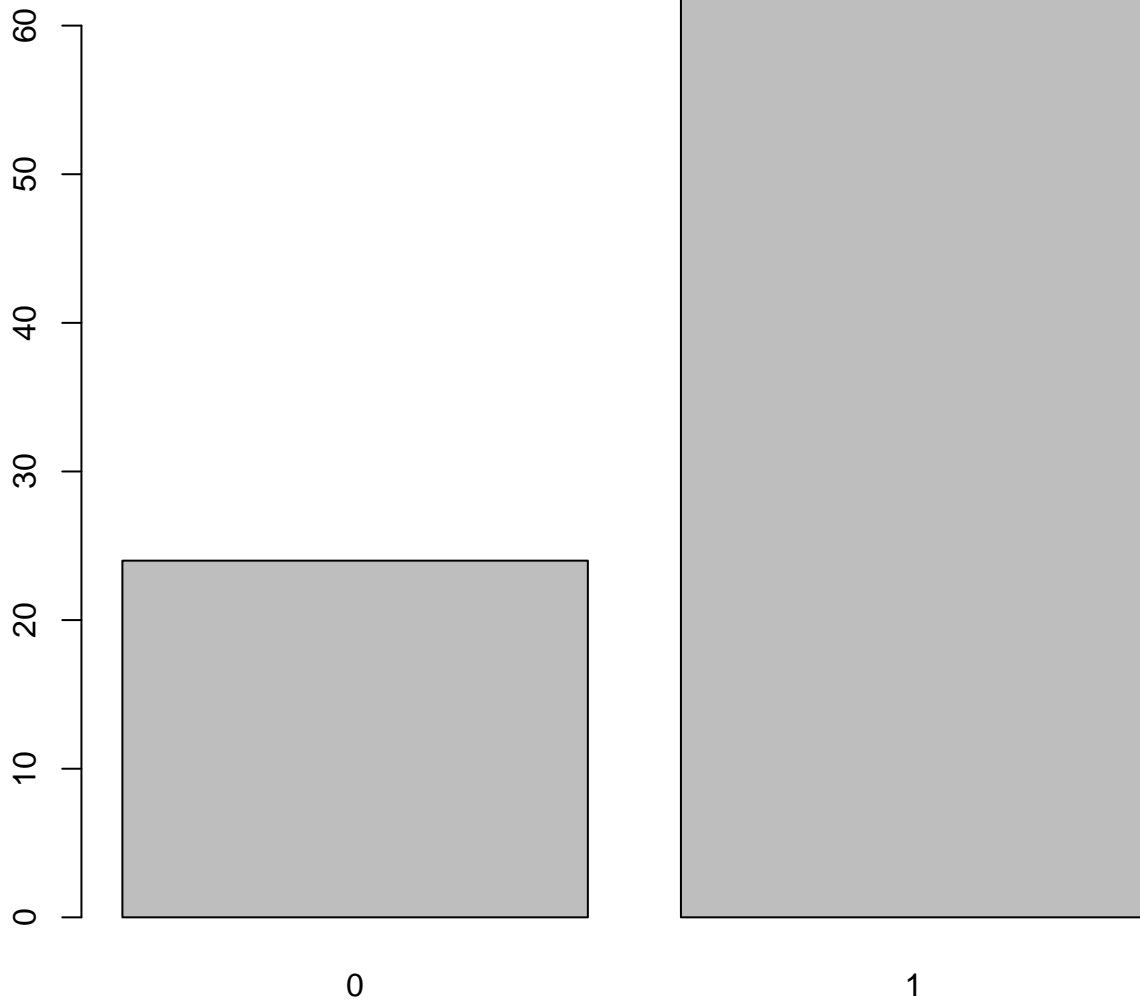
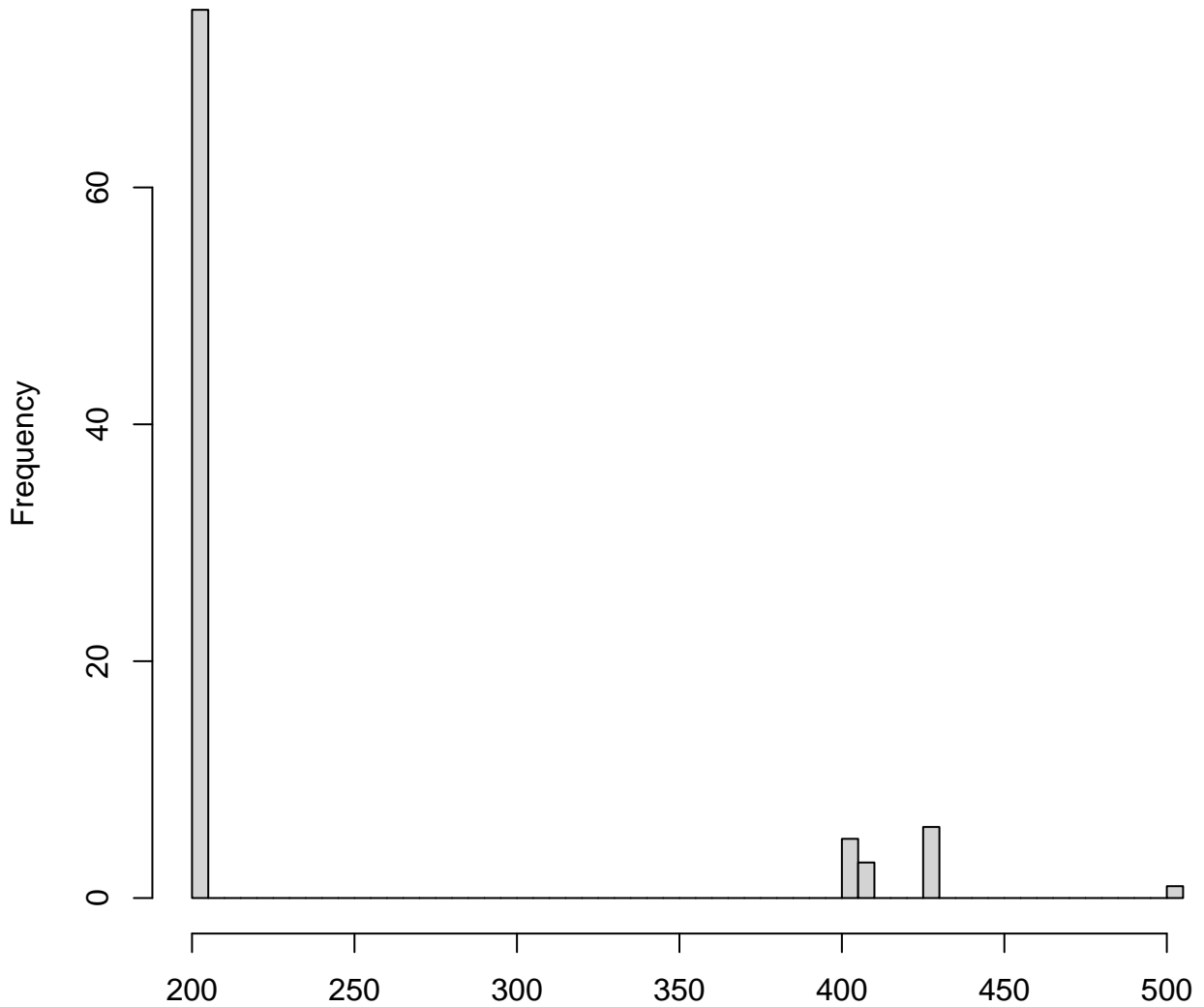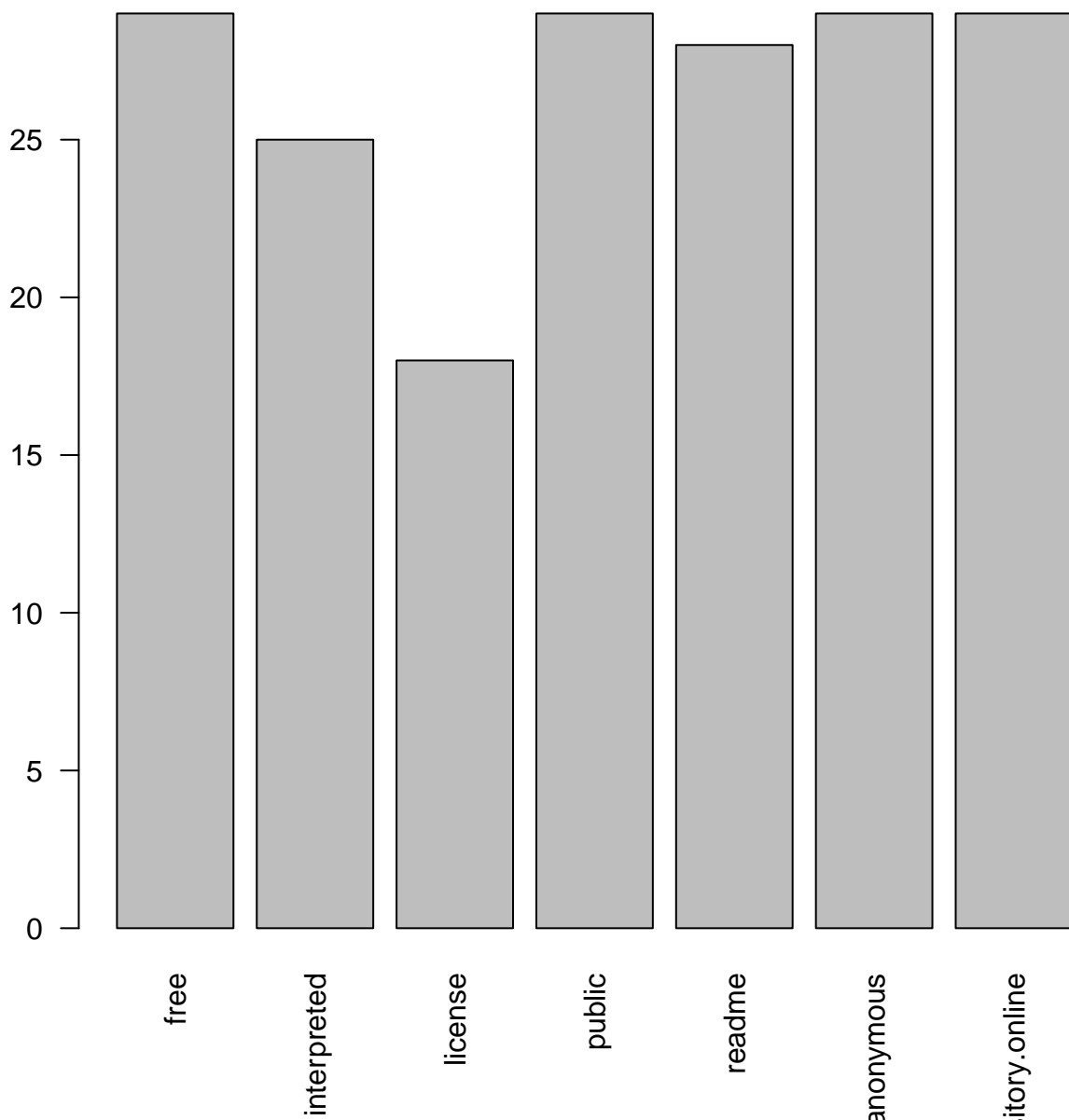# operatingSystem Top 30 terms
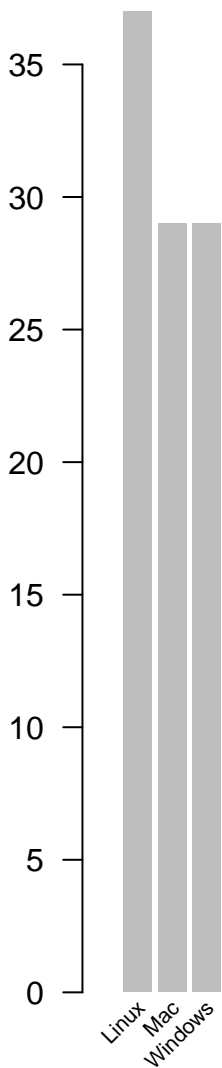
Citations
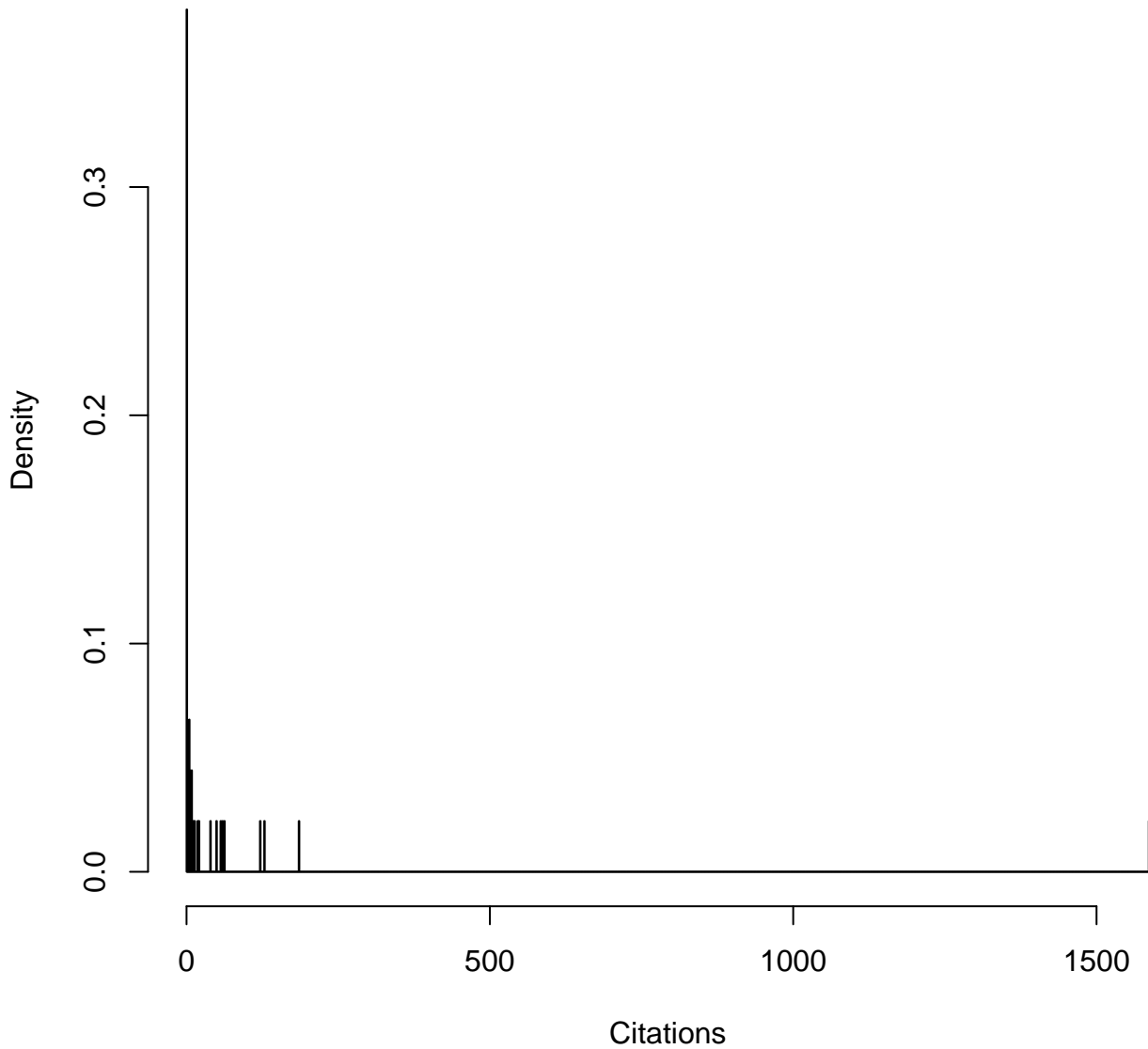
log−log plot of citation count

Uptime?

Frequency

sapply(metrics, function(x) x$project$website$operational)
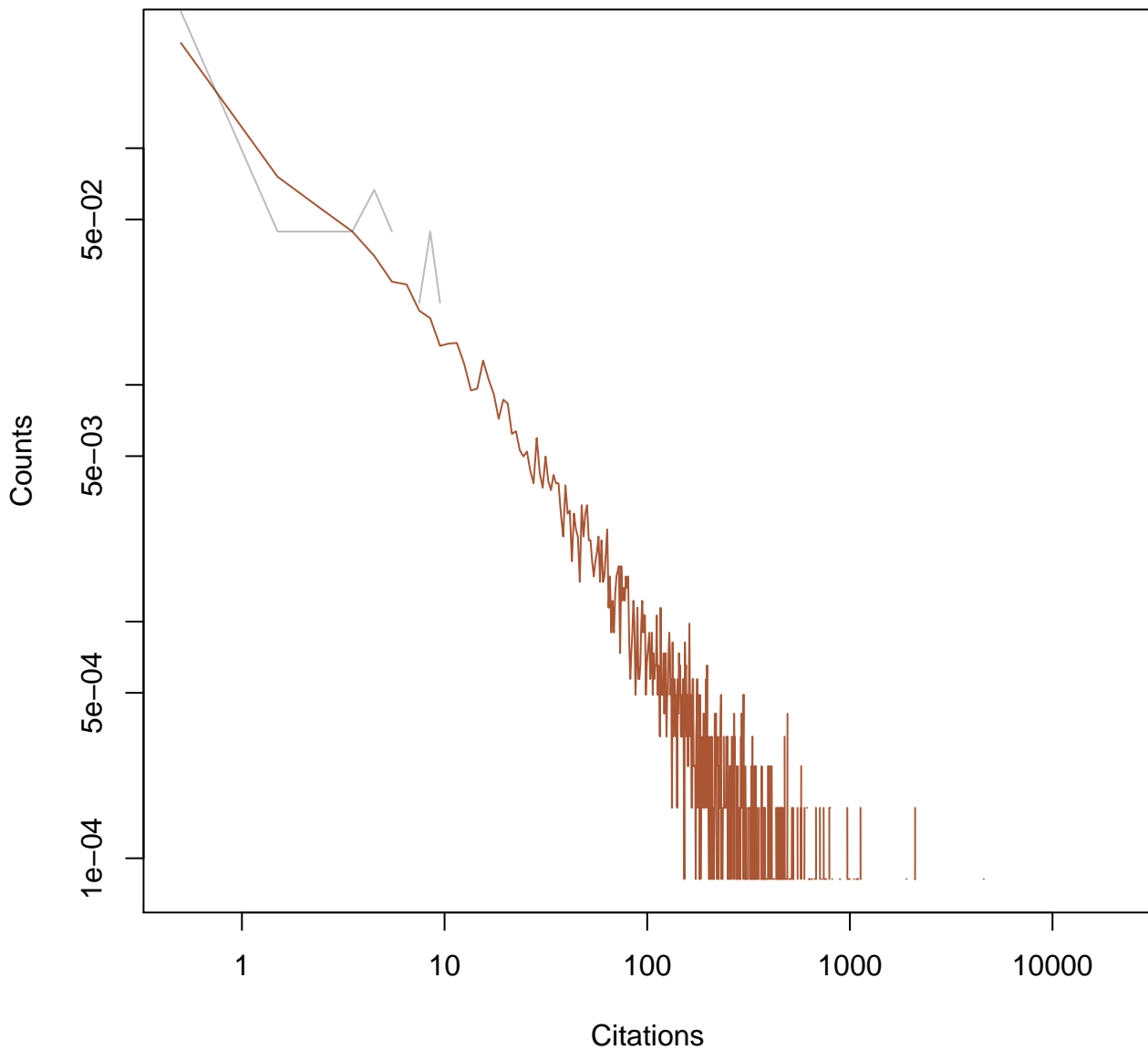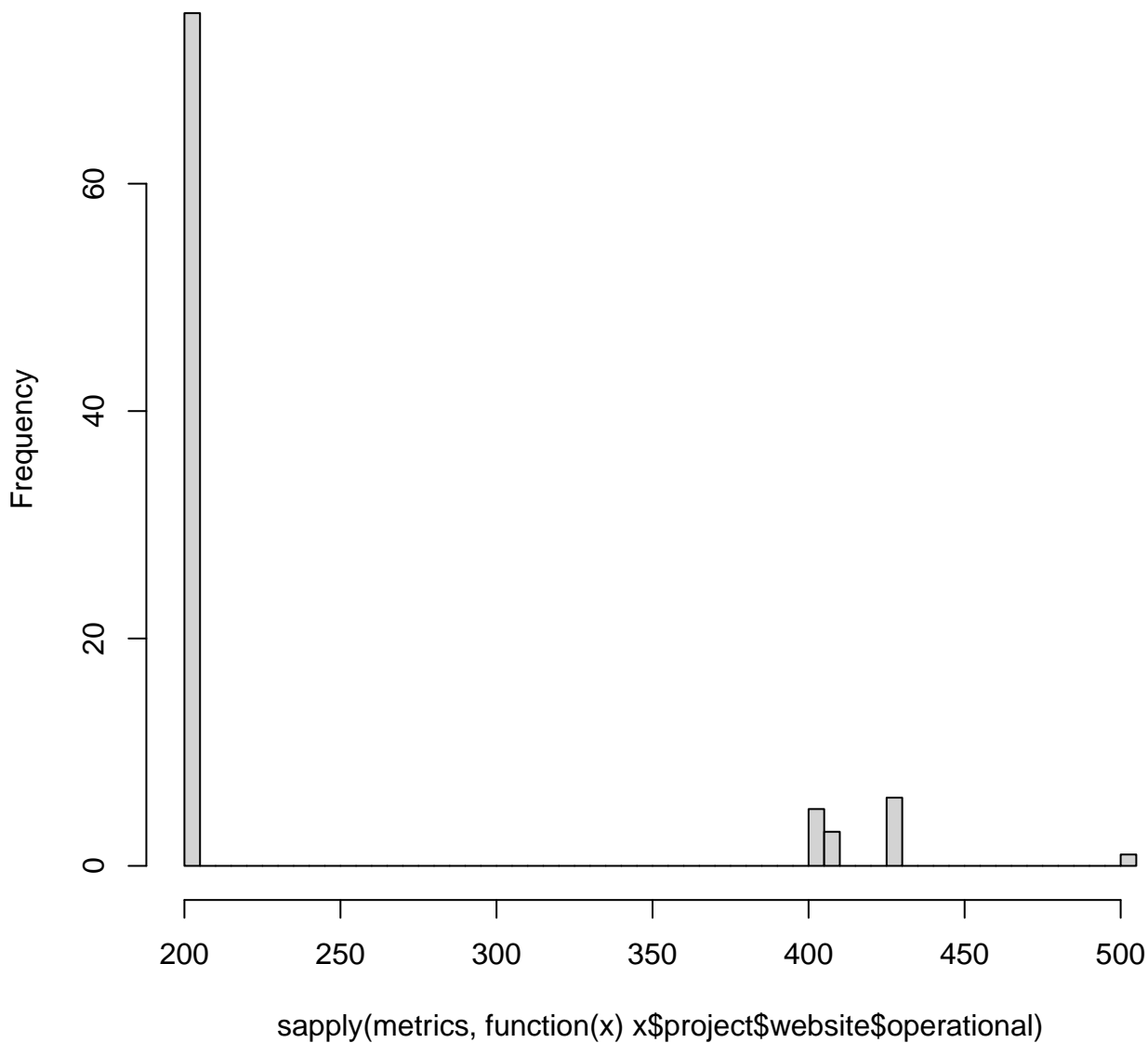
Is https page

Operational web page

Source code

Issue tracker