#### Molecule

Molecule()

Molecule (Molecule mol)

Molecule (Molecule mol, List<Bool> atoms,

List<Bool> bonds, Bool adjustHydrogens)

Int numAtoms()

Iter<Atom> atoms()

Atom atom(Int index)

Atom addAtom()

Void removeAtom(Atom atom)

Int numBonds()

Iter<Bond> bonds()

Bond bond(Int index)

Bond bond(Atom source, Atom target)

Bond addBond()

Void removeBond(Bond bond)

Void clear()

### **Bond**

Int index()

Atom source()

Atom target()

Atom other(Atom atom)

Int order()

Bool isAromatic()

Void setAromatic(Bool value)

Void setOrder(Int value)

# Ring

Int size()

List<Atom> atoms()

Atom atom(Int index)

Bool containsAtom(Atom atom)

List<Bond> bonds()

Bond bond(Int index)

Bool containsBond(Bond bond)

Bool isAromatic()

# Fingerprint [python]

Fingerprint(Int numWords)

String bin(Bool spaces = true)

String **hex**()

Void zero()

Int count()

Int count(Int begin, Int end)

Bool \_\_getitem\_\_(Int index)
Void \_\_setitem\_\_(Int index, Bool value)

Int numWords()

## **Atom**

Int index() Bool isOxygen()

Int degree() Bool isPhosphorus()

Iter<Bond> bonds() Bool isSulfur()

Iter<Atom> nbrs() Int heavyDegree() Bool isAromatic()

Int boSum() Int element() Int valence()

Int mass() Int connectivity()

Int hydrogens() Void **setAromatic**(Bool **value**) Int charge()

Void **setElement**(Int **value**) Bool isHydrogen() Void **setMass**(Int **value**)

Bool isCarbon() Void setHydrogens(Int value)

Bool isNitrogen() Void **setCharge**(Int **value**)

### **Element**

String element(Int element)

Int averageMass(Int element)

Bool addHydrogens(Int element)

Int valence(Int element, Int charge,

int degree)

# RingSet

RingSet(Molecule mol)

Int size()

List<Ring> rings()

Ring ring(Int index)

Bool isAtomInRing(Atom atom)

Bool isAtomInRingSize(Atom atom, Int size)

Int numRingNbrs(Atom atom)

Int numRings(Atom atom)

Bool isBondInRing(Bond bond)

Bool isBondInRingSize(Bond bond, Int size)

## DistanceMatrix

String \_\_str\_\_()

Int dim()

Int infinity()

Int operator()(Int i, Int j)

Int \_\_call\_\_(Int i, Int j)

#### **Error**

String what() [C++]

operator bool() [C++]

Bool \_\_nonzero\_\_() [python]

String \_\_str\_\_() [python]

## **Smiles**

Enum Flags: None, Mass, Charge, Hydrogens, Order, All

Smiles()

Bool **read**(String **smiles**, Molecule **mol**)

String write(Molecule mol, Flags flags = All)

String write(Molecule mol, List<Index> order, Flags flags = All)

String writeCanonical(Molecule mol)

Error error()

## **Smarts**

Smarts()

Mapping implementations: NoMapping.match, CountMapping.count,

SingleMapping.map, MappingList.maps

Error error()

Bool requiresCycles()

Bool **init**(String **smarts**)

Bool requiresExplicitHydrogens()

Bool findMapping(Molecule mol, RingSet rings, Mapping mapping, Bool uniqueComponents = false)

Bool findMapping(Molecule mol, Mapping mapping, Bool uniqueComponents = false)

Bool find(Molecule mol, RingSet rings, Bool uniqueComponents = false)

Bool find(Molecule mol, Bool uniqueComponents = false)

### **Smirks**

Smirks()

Void setFixMass(Bool value)

Void setFixHydrogens(Bool value)

Bool **init**(String **smirks**)

Bool init(String reactants, String products)

SmirksError error()

Bool requiresCycles()

Bool requiresExplicitHydrogens()

Bool apply(Molecule mol, RingSet rings)

Bool apply(Molecule mol)

List<Molecule **mol**, RingSet **rings**,

Int min = 1, Int max = 1)

List<Molecule> react(Molecule mol,

Int min = 1, Int max = 1)

# Memory Mapped Molecule File

MemoryMappedMoleculeFile()

MemoryMappedMoleculeFile(String filename)

Void **load**(String **filename**)

Int numMolecules()

Bool readMolecule(Int index, Molecule mol)

Void error()

## **SmirksError**

Enum Type: None, NoReaction, ReactantSmarts,

ProductSmarts, AtomClassPairWise,

ProductContainsOr, ProductContainsNot, InvalidProductBond, ProductConflict

Type type()

String what()

## MoleculeFile

MoleculeFile()

MoleculeFile(String filename)

Void load(String filename)

Int numMolecules()

Bool readMolecule (Molecule mol)

Bool readMolecule(Int index, Molecule mol)

Void close()

Void error()

# MoleculeOutputFile

MoleculeOutputFile(String filename) Bool writeMolecule (Molecule mol)

Void error()

## Free Functions

#### **HYDROGENS**

Void make hydrogens explicit(Molecule mol)

Void make hydrogens implicit(Molecule mol)

Void reset\_implicit\_hydrogens(Molecule mol)

Void <a href="reset\_implicit\_hydrogens">reset\_implicit\_hydrogens</a>(Molecule mol, Atom atom)

#### **FINGERPRINTS**

Int BitePerWord

Int bitvec num words for bits(Int bits)

Void **bitvec\_zero**(Fingerprint **fp**)

Fingerprint bitvec copy(Fingerprint fp)

Bool **bitvec\_get**(Int **index**, Fingerprint **fp**)

Void **bitvec\_set**(Int **index**, Fingerprint **fp**)

Void **bitvec\_reset**(Int **index**, Fingerprint **fp**)

Int bitvec\_count(Fingerprint fp)

Int bitvec\_count(Fingerprint fp,

Int begin, Int end)

String **bitvec\_to\_binary**(Fingerprint **fp**)

String **bitvec\_to\_hex**(Fingerprint **fp**)

Fingerprint bitvec from binary(String bin)

Fingerprint **bitvec\_from\_hex**(String **hex**)

Int bitvec union count(Fingerprint fp1, Fingerprint fp2)

Bool bitvec is subset superset(Fingerprint subset, Fingerprint superset)

Real bitvec tanimoto(Fingerprint fp1, Fingerprint fp2) Real bitvec tanimoto(Fingerprint fp1, Fingerprint fp2, Int count1, Int count2)

Real bitvec\_cosine(Fingerprint fp1, Fingerprint fp2) Real <a href="mailto:bitvec\_cosine">bitvec\_cosine</a>(Fingerprint fp1, Fingerprint fp2,

Int count1, Int count2)

Real **bitvec\_hamming**(Fingerprint **fp1**, Fingerprint **fp2**)

Real bitvec\_hamming(Fingerprint fp1, Fingerprint fp2, Int count1, Int count2)

Real bitvec forbes(Fingerprint fp1, Fingerprint fp2) Real <a href="mailto:bitvec\_forbes">bitvec\_forbes</a>(Fingerprint fp1, Fingerprint fp2,

Int count1, Int count2)

Real bitvec russell rao(Fingerprint fp1, Fingerprint fp2)

## **DFSVisitor** [base class]

Void initialize(Molecule mol)

Void component(Int component)

Void atom(Molecule mol, Atom prev, Atom atom)

Void bond(Molecule mol, Atom prev, Bond bond)

Void **backtrack**(Molecule **mol**, Atom **atom**)

Void back\_bond(Molecule mol, Bond bond)

Bool stop()

**Default implementations**: DFSAtomOrderVisitor,

DFSBondOrderVisitor, DFSDebugVisitor,

**DFSClosureRecorderVisitor** 

## AtomInvariant [base class]

Int operator()(Molecule mol, Atom atom) [C++]
Int \_\_call\_\_(Molecule mol, Atom atom) [python]

#### **DefaultAtomInvariant**

Enum Invariants: None, Element, Mass, Charge, Degree, Aromatic, All

**DefaultAtomInvariant**(Invariants invariants = All)

# Dijkstra

Dijkstra(Molecule mol, Atom source,

Bool preferSmallerIndexPaths = false)

Int infinity()

Int distance(Atom target)

List<Atom> path(Atom target)

## BFSVisitor [base class]

Void initialize(Molecule mol)

Void component(Int component)

Void depth(Int depth)

Void <a href="mailto:atom">atom</a>(Molecule mol, Atom prev, Atom atom)

Void **bond**(Molecule **mol**, Atom **prev**, Bond **bond**)

Void <a href="mailto:back\_bond">back\_bond</a>(Molecule mol, Bond bond)

Bool stop()

**Default implementations**: BFSAtomOrderVisitor,

BFSBondOrderVisitor, BFSDebugVisitor,

**BFSClosureRecorderVisitor** 

### **BondInvariant**

Int operator()(Molecule mol, Bond bond)
Int \_\_call\_\_(Molecule mol, Bond bond)

### **DefaultBondInvariant**

Enum Invariants: None, Order, Aromatic, All DefaultAtomInvariant(Invariants invariants = All)

# SubgraphCallback

Void operator()(Subgraph subgraph)
Void \_\_call\_\_(Subgraph subgraph)

# Subgraph

List<Bool> hashable()
List<Bool> atoms, bonds

# **Algorithms**

#### **DEPTH-FIRST SEARCH**

Void depth\_first\_search(Molecule mol, DFSVisitor visitor)

Void <a href="mask">depth\_first\_search\_mask</a> (Molecule mol, DFSVisitor visitor, List<Bool> atomMask)

Void depth\_first\_search\_mask(Molecule mol, DFSVisitor visitor, List<Bool> atomMask,

List<Bool> bondMask)

Void <a href="mailto:depth\_first\_search">depth\_first\_search</a> (Molecule mol, Atom atom, DFSVisitor visitor)

Void depth\_first\_search\_mask(Molecule mol, Atom atom, DFSVisitor visitor, List<Bool> atomMask)

Void <a href="mask">depth\_first\_search\_mask</a> (Molecule mol, Atom atom, DFSVisitor visitor, List<Bool> atomMask, List<Bool> bondMask)

Void ordered\_depth\_first\_search(Molecule mol, List<Int> order, DFSVisitor visitor)

Void exhaustive depth\_first\_search(Molecule mol, Atom atom, DFSVisitor visitor)

#### **BREADTH-FIRST SEARCH**

Void breadth\_first\_search(Molecule mol, BFSVisitor visitor)

Void <a href="mask">breadth\_first\_search\_mask</a> (Molecule mol, BFSVisitor visitor, List<Bool> atomMask)

Void breadth\_first\_search\_mask(Molecule mol, BFSVisitor visitor, List<Bool> atomMask,

List<Bool> bondMask)

Void breadth first search (Molecule mol, Atom atom, BFS Visitor visitor)

Void <a href="mask">breadth\_first\_search\_mask</a> (Molecule mol, Atom atom, BFSVisitor visitor, List<Bool> atomMask)

Void breadth\_first\_search\_mask(Molecule mol, Atom atom, BFSVisitor visitor, List<Bool> atomMask,

List<Bool> bondMask)

#### **COMPONENTS**

List<Int> connected\_bond\_components(Molecule mol)

List<Int> connected\_atom\_components(Molecule mol)

Int num\_connected\_components(Molecule mol)

## Algorithms (contd.)

### **CYCLES (RINGS)**

Int cyclomatic\_number(Molecule mol)

Int cyclomatic\_number(Molecule mol, Int numComponents)

(List<Int, List<Int>) cycle\_membership(Molecule mol) [python]

Void cycle\_membership(Molecule mol, List<Bool> cyclicAtoms, List<Bool> cyclicBonds) [C++]

RingSet relevant\_cycles(Molecule mol)

RingSet relevant\_cycles(Molecule mol, List<Bool> cyclicAtoms, List<Bool> cyclicBonds)

#### FLOYD-WARSHALL SHORTEST PATH

DistanceMatrix floyd warshall(Molecule mol)

#### **MORGAN'S EXTENDED CONNECTIVITIES**

List<Int> extended connectivities (Molecule mol, AtomInvariant invariant)

#### **CANONICALIZATION**

(List<Int>, List<Int>) canonicalize component(Molecule mol, List<Int> symmetry,

AtomInvariant atomInvariant, BondInvariant bondInvariant)

( List<Int>, List<Int> ) canonicalize(Molecule mol, List<Int> symmetry,

AtomInvariant atomInvariant, BondInvariant bondInvariant,

List<Int> atomComponents, List<Int> bondComponents)

#### **ENUMERATION**

List<List<Int>> enumerate\_paths(Molecule mol, Int maxSize)

Void enumerate\_subgraphs(Molecule mol, SubgraphCallback callback, Int maxSize, Bool onlyTrees)

#### **FINGERPRINTS**

Fingerprint path\_fingerprint(Molecule mol, Int maxSize = 7, Int numWords = 16, Int hashPrime = 1021)
Fingerprint tree\_fingerprint(Molecule mol, Int maxSize = 7, Int numWords = 16, Int hashPrime = 1021)
Fingerprint subgraph\_fingerprint(Molecule mol, Int maxSize = 7, Int numWords = 16,

Int hashPrime = 1021)

#### **2D COORDINATE GENERATION**

List<(Real, Real)> generate\_diagram(Molecule mol)

## **Depict**

Enum Options: BlackWhiteAtoms, NoMargin,

DrawTermC, DrawAllC, NoWedgeHashGen,

AsymmetricDoubleBond, AromaticCircle,

AromaticHash

Depict(Painter painter)

Bool drawMolecule (Molecule mol, RingSet rings,

List<(Real, Real)> coordinates)

Void **setBondLength**(Real **length**)

Real bondLength()

Void setPenWidth(Real width)

Real penWidth()

Void setBondSpacing(Real spacing)

Real bondSpacing()

Void setBondWidth(Real width)

Real bondWidth()

Void **setOption**(Int **options**)

Int options()

Void clearOptions()

Void **setFontFamily**(String **family**)

String fontFamily()

Void setFontSize(Real size)

Real fontSize()

Void setBondColor(String color)

**Painter implementations**: SVGPainter