

Sets and Dictionaries

Nanotech Example



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Molecular formula file

helium : He 1

water : H 2 0 1

hydrogen: H 2



```
# Molecular formula file
```

helium : He 1

water : H 2 0 1

hydrogen: H 2

Atom inventory file

He 1

H 4

0 3



```
# Molecular formula file # Atom inventory file

helium: He 1
Water: H 2 0 1
H 4
hydrogen: H 2

# Atom inventory file
```

Now have all the tools we need





Keys: atomic symbols



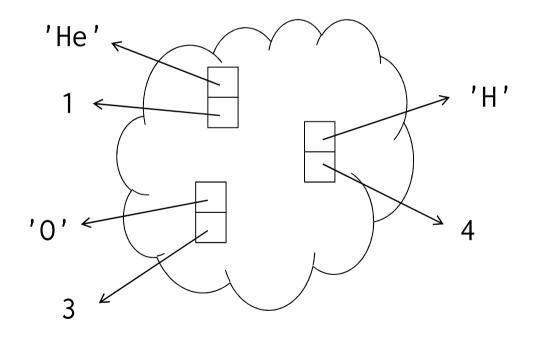
Keys: atomic symbols

Values: number of atoms available



Keys: atomic symbols

Values: number of atoms available



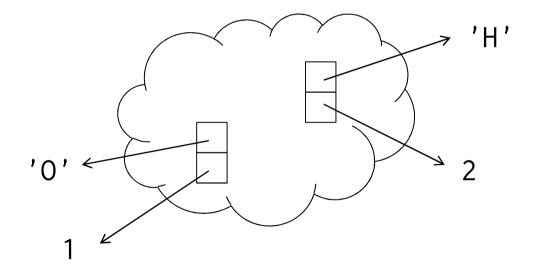


Represent individual molecules the same way



Represent individual molecules the same way

water







Keys: molecule names



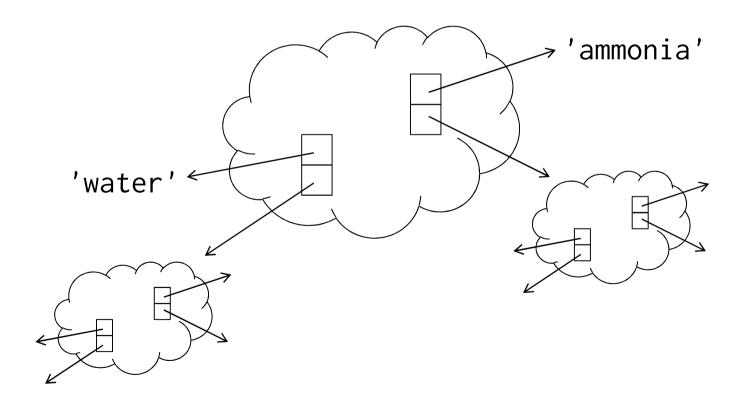
Keys: molecule names

Values: dictionaries of formulas



Keys: molecule names

Values: dictionaries of formulas



Sets and Dictionaries



min

available[atom] required[atom]

atom ∈ formula



min

available[atom] required[atom]

atom ∈ formula

If atom not in available, its count is implicitly 0



min

available[atom] required[atom]

atom ∈ formula

If atom not in available, its count is implicitly 0

Store results in yet another dictionary



min

available[atom] required[atom]

atom ∈ formula

If atom not in available, its count is implicitly 0

Store results in yet another dictionary

Keys: molecule names



min

available[atom] required[atom]

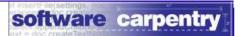
atom ∈ formula

If atom not in available, its count is implicitly 0

Store results in yet another dictionary

Keys: molecule names

Values: counts of how many can be made



'''Calculate how many molecules of each type can be made
with the atoms on hand.'''

import sys

if __name__ == '__main__':
 inventory = read_inventory(sys.argv[1])
 formulas = read_formulas(sys.argv[2])
 counts = calculate_counts(inventory, formulas)
 show_counts(counts)



```
def read_inventory(filename):
    '''Read inventory of available atoms.'''
    result = {}
    for line in read_lines(filename):
        name, count = line.split(' ')
        result[name] = int(count)
```



```
def read_lines(filename):
  '''Read lines from file, stripping out
  blank lines and comments.'''
  reader = open(filename, 'r')
  lines = []
  for line in reader:
    line = line.split('#')[0].strip()
    if line:
      lines.append(line)
  reader.close()
  return lines
```



```
def read_formulas(filename):
  '''Read molecular formulas from file.'''
  result = {}
  for line in read_lines(filename):
    name, atoms = line.split(':')
    name = name.strip()
    atoms = atoms.strip().split(' ')
    formula = {}
    for i in range(0, len(atoms), 2):
      formula[atoms[i]] = int(atoms[i+1])
    result[name] = formula
  return result
```



```
def read_formulas(filename):
  '''Read molecular formulas from file.'''
                                           Storing results
  result = {} ←
  for line in read_lines(filename):
                                          in dictionary
    name, atoms = line.split(':')
    name = name.strip()
    atoms = atoms.strip().split(' ')
    formula = {}
    for i in range(0, len(atoms), 2):
      formula[atoms[i]] = int(atoms[i+1])
    result[name] = formula
  return result
```



```
def read_formulas(filename):
  '''Read molecular formulas from file.'''
                                           For each
  result = {}
  for line in read_lines(filename): ← interesting
                                          line in the
    name, atoms = line.split(':')
    name = name.strip()
                                          input file...
    atoms = atoms.strip().split(' ')
    formula = {}
    for i in range(0, len(atoms), 2):
      formula[atoms[i]] = int(atoms[i+1])
    result[name] = formula
  return result
```



```
def read_formulas(filename):
  '''Read molecular formulas from file.'''
  result = {}
  for line in read_lines(filename):
                                          Separate the
    name, atoms = line.split(':')
                                          molecule name
    name = name.strip()
                                          and the formula
    atoms = atoms.strip().split(' ')
    formula = {}
    for i in range(0, len(atoms), 2):
      formula[atoms[i]] = int(atoms[i+1])
    result[name] = formula
  return result
```



```
def read_formulas(filename):
  '''Read molecular formulas from file.'''
  result = {}
  for line in read_lines(filename):
                                          Separate the
    name, atoms = line.split(':')
                                          atoms and
    name = name.strip()
                                          their counts
    atoms = atoms.strip().split(' ')
    formula = {}
    for i in range(0, len(atoms), 2):
      formula[atoms[i]] = int(atoms[i+1])
    result[name] = formula
  return result
```



```
def read_formulas(filename):
  '''Read molecular formulas from file.'''
  result = {}
  for line in read_lines(filename):
    name, atoms = line.split(':')
                                          Loop over pairs
    name = name.strip()
                                          of atoms and
    atoms = atoms.strip().split(' ')
                                          counts
    formula = {}
    for i in range(0, len(atoms), 2):
      formula[atoms[i]] = int(atoms[i+1])
    result[name] = formula
  return result
```



```
def read_formulas(filename):
  '''Read molecular formulas from file.'''
  result = {}
  for line in read_lines(filename):
    name, atoms = line.split(':')
    name = name.strip()
    atoms = atoms.strip().split(' ')
    formula = {}
                                          Store the count
    for i in range(0, len(atoms), 2):
      formula[atoms[i]] = int(atoms[i+1])
                                          as an integer
    result[name] = formula
                                          with the atomic
  return result
                                          symbol as key
```



```
def read_formulas(filename):
  '''Read molecular formulas from file.'''
  result = {}
  for line in read_lines(filename):
    name, atoms = line.split(':')
    name = name.strip()
    atoms = atoms.strip().split(' ')
    formula = {}
                                          And store the
    for i in range(0, len(atoms), 2):
      formula[atoms[i]] = int(atoms[i+1])
                                          molecule in
    result[name] = formula
                                          the main
  return result
                                          dictionary
```





```
def calculate_counts(inventory, formulas):
  '''Calculate how many of each molecule
  can be made with inventory.''
  counts = \{\}
  for name in formulas:
    counts[name] = dict_divide(inventory,
                               formulas[name])
  return counts
                                  Sub-dictionary holding
                                   atom counts for a
                                   particular molecule
```



Big functions: nothing is obviously wrong



Big functions: nothing is obviously wrong

Small functions: obviously, nothing is wrong



```
def dict_divide(inventory, molecule):
  '''Calculate how much of a single molecule
  can be made with inventory.'''
  number = None
  for atom in molecule:
    required = molecule[atom]
    available = inventory.get(atom, 0)
    limit = available / required
    if (number is None) or (limit < number):</pre>
      number = limit
  return number
```

Sets and Dictionaries



```
def dict_divide(inventory, molecule):
  '''Calculate how much of a single molecule
  can be made with inventory.
                                        Identical format:
  number = None
  for atom in molecule:
                                        keys are atoms,
    required = molecule[atom]
    available = inventory.get(atom, 0) values are counts
    limit = available / required
    if (number is None) or (limit < number):</pre>
      number = limit
  return number
```

Sets and Dictionaries Nanotech Example



```
def dict_divide(inventory, molecule):
  '''Calculate how much of a single molecule
  can be made with inventory.''
  number = None
  for atom in molecule:
    required = molecule[atom]
    available = inventory.get(atom, 0)
    limit = available / required
    if (number is None) or (limit < number):</pre>
      number = limit
                                   Common pattern: None
  return number
                                   means "uninitialized",
                                   so initialize the first
```

time through the loop



```
def dict_divide(inventory, molecule):
  '''Calculate how much of a single molecule
  can be made with inventory.''
  number = None
  for atom in molecule:
    required = molecule[atom]
    available = inventory.get(atom, 0)
    limit = available / required
    if (number is None) or (limit < number):</pre>
      number = limit
                                   Common pattern:
  return number
                                   stored value or default
```



```
def dict_divide(inventory, molecule):
  '''Calculate how much of a single molecule
  can be made with inventory.''
  number = None
  for atom in molecule:
    required = molecule[atom]
    available = inventory.get(atom, 0)
    limit = available / required
    if (number is None) or (limit < number):</pre>
      number = limit ←
                               Common pattern:
  return number
                               find minimum of
                               calculated values
```



```
def show_counts(counts):
    '''Show how many of each molecule can be made.'''
    counts = invert_dict(counts)
    for key in sorted(counts.keys(), reverse=True):
        for name in sorted(counts[key]):
            print key, name
```

Sets and Dictionaries Nanotech Example



```
def show_counts(counts):
    '''Show how many of each molecule can be made.'''
    counts = invert_dict(counts)
    for key in sorted(counts.keys(), reverse=True):
        for name in sorted(counts[key]):
            print key, name
```

Reverse to get greatest first



```
def invert_dict(src):
  '''Invert a dictionary, returning value->set{key}.'''
  dst = \{\}
  for key in src:
    value = src[key]
    if value not in dst:
      dst[value] = set()
    dst[value].add(key)
  return dst
```

Sets and Dictionaries Nanotech Example



```
def invert_dict(src):
    '''Invert a dictionary, returning value->set{key}.

dst = {}
  for key in src:
    value = src[key]
    if value not in dst:
        dst[value] = set()
        dst[value].add(key)

return dst
```

Common pattern:
make sure there's a
collection, then add



```
def show_counts(counts):
    '''Show how many of each molecule can be made.'''
    counts = invert_dict(counts)
    for key in sorted(counts.keys(), reverse=True):
        if key > 0:
            for name in sorted(counts[key]):
                print key, name
```

Go back and only show molecules that can actually be made



inventory-00.txt

formulas-01.txt

helium : He 1

No output, which is correct.



inventory-01.txt
He 1

formulas-01.txt

helium : He 1



```
# inventory-02.txt
He 1
H 4
```

formulas-01.txt

helium : He 1



```
# inventory-02.txt
He 1
H 4
```

formulas-02.txt

helium : He 1

water : H 2 0 1



inventory-02.txt
He 1
H 4

formulas-03.txt

helium : He 1

water : H 2 0 1

hydrogen : H 2

2 hydrogen



inventory-03.txt
He 1
H 4
O 3

formulas-03.txt

helium : He 1

water : H 2 0 1

hydrogen : H 2

2 hydrogen

2 water



```
# inventory-03.txt
He 1
H 4
O 3
```

formulas-03.txt

helium : He 1

water : H 2 0 1

hydrogen : H 2

- 2 hydrogen
- 2 water
- 1 helium

Looks good...



```
# inventory-03.txt
He 1
H 4
0 3
```

formulas-03.txt

helium : He 1

water : H 2 0 1

hydrogen: H 2

2 hydrogen

2 water

1 helium

Looks good...

Code is *much* simpler than it would be using lists of pairs



created by

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