

Java in Bioinformatics

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Outline

- 1 Object Oriented Programming in Java
- 2 GATK project
- 3 Cytoscape project

Next

1 Object Oriented Programming in Java

- Basic Ideas
- Concepts
- OOP in Java
- Reference

2 GATK project

3 Cytoscape project

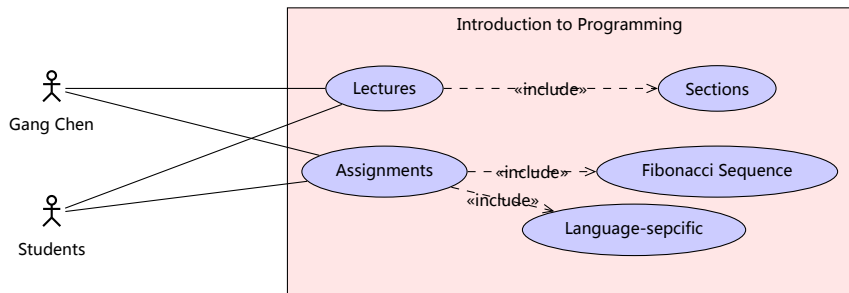
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Object-oriented Programming (OOP)

- OO is a language-independent concept
- in principle not limited to programming (OO design)
 - ⇒ databases, business plans
- improves reusability and exchangability of code
- separation of partial problems
- "real world" modelling
- representation in **Universal Markup Language (UML)**

Object-oriented Programming (OOP)



Basic ideas

- **Everything is an object**
Gang, students, lecture
project, world, spy, information
- **Objects interact by sending/receiving messages**
Gang → students: object orientation is a concept
world → map: what is the object at position X?
- **An object consists of objects**
a course consists of lectures
a world consists of land or water fields

Basic ideas

- Every object has a type
Gang is a teacher
the map is a rectangle of land / water fields
- All objects of the same type understand the same messages
all students hear the lecture
all spies can retrieve information

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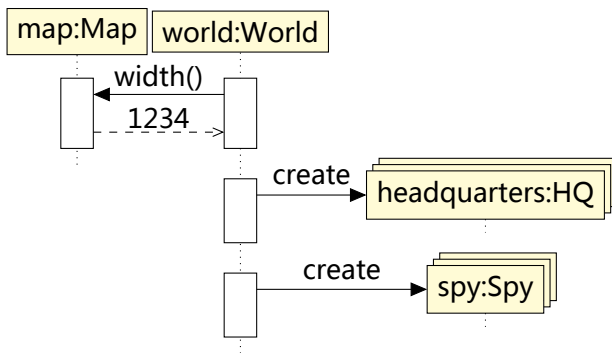
Classes, Interfaces and Methodse

World	class	Map
spies : ListOfSpies	attributes	tiles: VectorOfTiles
setSpyCount(count: int) getSpyCount() : int getMap() : Map	methods	getWidth() : int getHeight() : int at(x: int, y:int) : Tile

Classes, Interfaces and Methods

- **classes** describe the type of objects (define their **interface**)
- the interface consists of **methods** and **attributes** / properties
- methods
 - are functions that operate on objects of this class
 - can take extra arguments of arbitrary types
 - can return values of arbitrary types
- attributes are objects of arbitrary other types

Objects/Instances



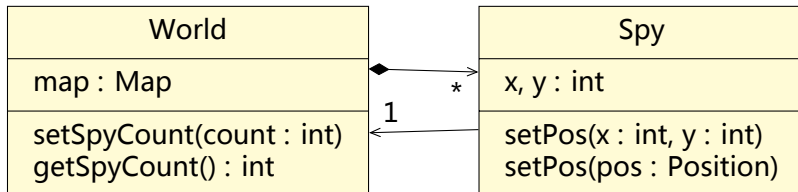
- every object has an immutable class assigned when it is created
- objects communicate via their class interfaces
- classes can communicate via static member functions

Overloading and signature

Spy
<pre>setPos(x : int, y : int) setPos(pos: Position)</pre>

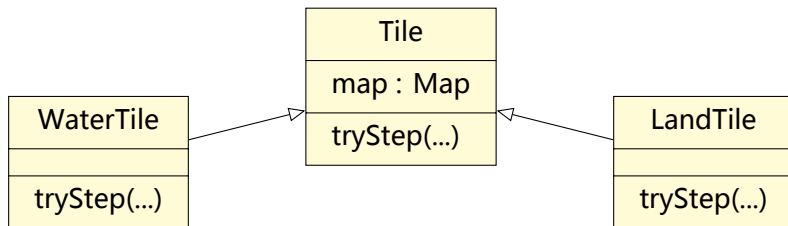
- a method is described by name and **signature**
- signature is formed by the types of all taken arguments
 - `setPos(x : int, y : int)`
 - `setPos(pos : Position)`
- methods with identical names but different arguments can exist in one class -- **overloading**
- return type is not part of the signature -- cannot always resolve overload at compile time

Composing classes



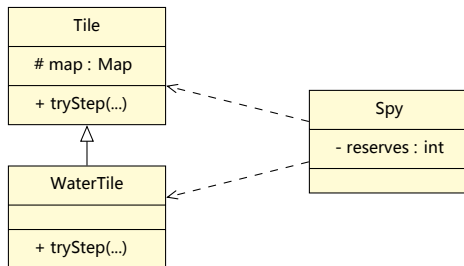
- objects are made of objects (**attributes**) --- classes declare the types of these objects
- simple attributes appear below class name
- complex classes shown as **composition**
- "has-a" or "has-many" relations:
 - a world hosts many spies,
 - a spy belongs to one world

Inheritance and class hierarchy



- subclasses of classes -- **class hierarchy**
- subclasses inherit methods and attributes of all superclasses
- no need to duplicate code
- .. but methods might behave differently (**polymorphism**)
- **abstract classes** implement only parts of the interface

Implementation hiding



- **public** (`+') elements are visible to all
- **protected** (`#') elements are only visible to derived classes
- **private** (`-') attributes or methods are not visible to other objects
- map is protected \Rightarrow visible to WaterTile, not to Spy
- Spy can access tryStep of all tiles

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Hello Java

```
public class HelloJava{  
  
    public static void main(String[] args) {  
        System.out.println("Hello Java!");  
    }  
  
}
```

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Books

Books

- Thinking in Java
- Core Java
- Martin Fowler, "UML Distilled", 3rd edition, Addison-Wesley

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GATK

The Genome Analysis Toolkit or GATK is a software package developed at the Broad Institute to analyze high-throughput sequencing data. The toolkit offers a wide variety of tools, with a primary focus on variant discovery and genotyping as well as strong emphasis on data quality assurance. Its robust architecture, powerful processing engine and high-performance computing features make it capable of taking on projects of any size.

GATK

<https://www.broadinstitute.org/gatk/>

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Cytoscape

Cytoscape is an open source software platform for visualizing complex networks and integrating these with any type of attribute data. A lot of Apps are available for various kinds of problem domains, including bioinformatics, social network analysis, and semantic web.

Cytoscape

<http://www.cytoscape.org/>

Cytoscape

- Documentation: <http://opentutorials.cgl.ucsf.edu/index.php/Portal:Cytoscape3>
- Source codes: <https://github.com/cytoscape/cytoscape-impl>
- User Manual in Chinese: <https://code.google.com/p/cytoscape-cn/>

Apps

- Developer: http://wiki.cytoscape.org/Cytoscape_3/AppDeveloper
- Example: ClusterViz