

Implémentation de concepts de DESCRIPTION de IMGT-ONTOLOGY Sous Protégé

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World Wide Web

- Créé par Tim Berners Lee en 1990
- Langage HTML

=> Pour partager des connaissances et de relier les informations partagées.

IMGT Index - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://imgt.cines.fr/textes/IMGIndex/ontology.html

Getting Started Latest Headlines tomcat Outils linguistiques

ImMunoGeneTics Information system
http://imgt.cines.fr

Here you are: IMGT Web resources > IMGT Index

Ontology (IMGT-ONTOLOGY)

An ontology is a concise and non ambiguous description of the more significant and relevant concepts in a application domain. IMGT-ONTOLOGY [1], is the first ontology which allows the management of the immunogenetics knowledge for all vertebrate species.

Citing IMGT-ONTOLOGY:

- Giudicelli, V. and Lefranc, M.-P. "Ontology for Immunogenetics: IMGT-ONTOLOGY", *Bioinformatics*, 15, 1047-1054 (1999) PMID:10745995, LIGM:221, **ESB**
- Lefranc, M.-P. et al. "IMGT-ONTOLOGY for Immunogenetics and Immunoinformatics", *http://imgt.cines.fr*, *In Silico Biology*, 2004, 4, 17-29 Epub 2003, 4, 0004, LIGM:278, PMID: 15089751
- Lefranc, M.-P. et al. "IMGT-Choreography for Immunogenetics and Immunoinformatics", *In Silico Biology*, 2005, 5, 45-60, Epub 2005, 5, 0006, 24 Dec 2004, LIGM:294, PMID: 15972004

Introduction

The molecular synthesis and genetics of the immunoglobulin (IG) and T cell receptor (TR) chains and the polymorphism of the MHC are particularly complex, and therefore one of the first tasks of IMGT-ONTOLOGY comprises a formal specification of the terms to be used in the domain of immunogenetics and bioinformatics [2-8].

IMGT-ONTOLOGY includes a controlled vocabulary and annotation rules which are indispensable to ensure accuracy, consistency and coherence in IMGT® [5]. IMGT-ONTOLOGY allows scientists and clinicians to use identical terms with the same meaning. This provides a semantic repository to be included in more general molecular biology ontologies, and will be therefore of a great help to increase interoperability between specialist and generalist databases.

IMGT-ONTOLOGY axioms and concepts

Seven IMGT-ONTOLOGY axioms have been defined [1,6-8]: **'IDENTIFICATION'**, **'DESCRIPTION'**, **'CLASSIFICATION'**, **'NUMEROTATION'**, **'LOCALIZATION'**, **'ORIENTATION'**, and **'OBTENTION'**. They constitute the Formal IMGT-ONTOLOGY or IMGT-Kaleidoscope [9,10].

The IMGT-ONTOLOGY concepts of identification, description, classification, numerotation, localization, orientation and obtention were generated from these axioms and described in ref. [1,2,6-8].

Click here for:

- [Figures illustrating some of the IMGT-ONTOLOGY axioms and concepts](#) (IMGT Education).
- [Correspondence between the IMGT-ONTOLOGY concepts and the IMGT Scientific chart rules](#) (IMGT Scientific chart).
- [Scientific chart rules and ontologies report](#) **ESB**

Marie-Paule Lefranc, François Ehrenmann, Patrice Duroux and Véronique Giudicelli (D1.2 ImmunoGrid, The European Virtual Human Immune System Project, IST-2004-028069)
Describes the IMGT-ONTOLOGY concepts of identification, description and classification at the molecular level, generated from the IDENTIFICATION, DESCRIPTION and CLASSIFICATION axioms of the Formal IMGT-ONTOLOGY (IMGT-Kaleidoscope).

http://imgt.cines.fr/textes/PDF/D1.2_ImmunoGrid.pdf

World Wide Web

- Les ressources sous forme de page HTML
- Les relations entre ses pages qui se traduisent par des liens hypertextes

The screenshot shows a Mozilla Firefox browser window with the address bar displaying `http://imgt.cines.fr/textes/IMGIndex/ontology.html`. The main content area shows the 'IMGT Index' page with a section titled 'Ontology (IMGT-ONTOLOGY)'. A smaller window titled 'Source of: http://imgt.cines.fr/textes/IMGIndex/ontology.html - Mozilla Firefox' is overlaid, showing the source code for the 'IMGT-ONTOLOGY' section. The source code includes the following HTML tags and text:

```
<h3 id="keyConcepts">IMGT-ONTOLOGY axioms and concepts</h3>
<p>
Seven IMGT-ONTOLOGY axioms have been defined <a href="#refs">[1,6-8]</a>:
<strong>'<a href="Identification.html">IDENTIFICATION</a>',
'<a href="Description.html">DESCRIPTION</a>',
'<a href="Classification.html">CLASSIFICATION</a>',
'<a href="Numerotation.html">NUMEROTATION</a>',
'LOCALIZATION',
'<a href="Orientation.html">ORIENTATION</a>', </strong>
and <strong>'<a href="Obtention.html">OBTENTION</a>'</strong>.
They constitute the Formal IMGT-ONTOLOGY or IMGT-Kaleidoscope <a href="#refs">[9,10]</a>.</p>
<p>
The IMGT-ONTOLOGY concepts of identification, description, classification,
numerotation, localization, orientation and obtention
were generated from these axioms and described in ref. <a href="#refs">[1,2,6-8]</a>.
</p>
```

The main window also shows a section titled 'IMGT-ONTOLOGY axioms and concepts' which contains the following text:

Seven IMGT-ONTOLOGY axioms have been defined [1,6-8]: 'IDENTIFICATION', 'DESCRIPTION', 'CLASSIFICATION', 'NUMEROTATION', 'LOCALIZATION', 'ORIENTATION', and 'OBTENTION'. They constitute the Formal IMGT-ONTOLOGY or IMGT-Kaleidoscope [9,10].

The IMGT-ONTOLOGY concepts of identification, description, classification, numerotation, localization, orientation and obtention were generated from these axioms and described in ref. [1,2,6-8].

Click here for:

- Figures illustrating some of the IMGT-ONTOLOGY axioms and concepts (IMGT Education).
- Correspondence between the IMGT-ONTOLOGY concepts and the IMGT Scientific chart rules (IMGT Scientific chart).
- Scientific chart rules and ontologies report [PDF]

Marie-Paule Lefranc, François Ehrenmann, Patrice Duroux and Véronique Giudicelli (D1.2 ImmunoGrid, The European Virtual Human Immune System Project, IST-2004-028069) Describes the IMGT-ONTOLOGY concepts of identification, description and classification at the molecular level, generated from the IDENTIFICATION, DESCRIPTION and CLASSIFICATION axioms of the Formal IMGT-ONTOLOGY (IMGT-Kaleidoscope).

World Wide Web

Limites

- Balises HTML: la connaissance est encapsulée dans une couche de présentation
- Introduction de balises propriétaires (Microsoft, Netscape)
- Les liens hypertexte ne permettent pas de qualifier les relations entre les informations
- La qualité des pages est très hétérogène.

=> Ces informations ne sont pas exploitables automatiquement

World Wide Web Consortium (W3C)

(créé en 1994)

- Développement de technologies, (spécifications, guides, logiciels et outils)
- Proposition des standards, pour la croissance et l'exploitation du Web

En particulier, en 1998, le langage de balisage extensible XML (Extensible Markup Language) devient une recommandation du W3C

Objectifs

- XML devrait pouvoir être utilisé sans difficulté sur Internet
- Il devrait être facile d'écrire des programmes traitant les documents XML
- Les documents XML devraient être lisibles par l'homme et raisonnablement clairs
- Il devrait être facile de créer des documents XML

Séquence EMBL AM947564

Mozilla Firefox

File Edit View History Bookmarks Yahoo! Tools Help

```
ID AM947564; SV 1; linear; genomic DNA; STD; HUM; 287 BP.
XX
AC AM947564;
XX
DT 01-APR-2008 (Rel. 95, Created)
DT 01-APR-2008 (Rel. 95, Last updated, Version 1)
XX
DE Homo sapiens partial IGHV gene for immunoglobulin heavy chain variable
DE region, patient 4
XX
KW .
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae;
OC Homo.
XX
RN [1]
RP 1-287
RA Capello D.;
RT ;
RL Submitted (13-MAR-2008) to the EMBL/GenBank/DDBJ databases.
RL Capello D., Clinical & Experimental Medicine, University of Eastern
RL Piedmont, Via Solaroli, 17 Novara, 28100, ITALY.
XX
RN [2]
RA Capello D., Martini M., Gloghini A., Cerri M., Rasi S., Deambrogi C.,
RA Rossi D., Spina M., Tirelli U., Larocca L., Carbone A., Gaidano G.;
RT "Molecular analysis of immunoglobulin variable genes in HIV-related non
RT Hodgkin lymphoma reveals implications for disease pathogenesis and
RT histogenesis";
RL Unpublished.
XX
DR IMGTL/IGM; AM947564; AM947564.
XX
FH Key Location/Qualifiers
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FT /isolate="patient 4"
FT /mol_type="genomic DNA"
FT /cell_type="B lymphocyte-derived lymphoma"
FT /tissue_type="HIV-related B-cell non-Hodgkin's lymphoma"
FT /rearranged
FT /db_xref="taxon:9606"
FT CDS <1..>287
FT /codon_start=1
FT /gene="IGHV"
FT /product="immunoglobulin heavy chain variable region"
FT /protein_id="CAQ19576.1"
FT /translation="LSLITCAVSGGSFSGYSWTWIRQTPGKGLEWIGEIKDGGTTNYNAS
FT LKSRVSIQDMSTFLLFLTLSSVTPADTAIFYCARGRSPNIGFDWFQGGTIL"
FT V_region <1..>287
FT /gene="IGHV"
FT /product="immunoglobulin heavy chain variable region"
XX
SQ Sequence 287 BP; 59 A; 80 C; 76 G; 72 T; 0 other;
ctgtccctca cctgogctgt cagtggaggg tcgttcagtg gctattogtg gacgtggatc 60
```

Done

Séquence AM947564 en format XML

Mozilla Firefox

File Edit View History Bookmarks Yahoo! Tools Help

Query Results file:///C:/D.../Temp/wgetz

This XML file does not appear to have any style information associated with it. The document tree is shown below.

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  <entry accession="AM947564" version="1" dataClass="STD" taxonomicDivision="HUM" created="2008-04-01" lastUpdated="2008-04-01" releaseCreated="95" releaseLastUpdated="95">
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      Homo sapiens partial IGHV gene for immunoglobulin heavy chain variable region, patient 4
    </description>
    <reference>
      <citation id="1" type="submission" date="2008-03-13">
        <author>Capello D.</author>
        <locator>
          Capello D., Clinical & Experimental Medicine, University of Eastern Piedmont, Via Solaroli, 17 Novara, 28100, ITALY.
        </locator>
        </citation>
        <citationLocation begin="1" end="287"/>
      </reference>
      <reference>
        <citation id="2" type="unpublished">
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            Molecular analysis of immunoglobulin variable genes in HIV-related non Hodgkin lymphoma reveals implications for disease pathogenesis and histogenesis
          </title>
          <author>Capello D.</author>
          <author>Martini M.</author>
          <author>Gloghini A.</author>
          <author>Cerri M.</author>
          <author>Rasi S.</author>
          <author>Deambrogi C.</author>
          <author>Rossi D.</author>
          <author>Spina M.</author>
          <author>Tirelli U.</author>
          <author>Larocca L.</author>
          <author>Carbone A.</author>
          <author>Gaidano G.</author>
        </citation>
      </reference>
      <dbreference db="IMGT/LIGM" primary="AM947564" secondary="AM947564">
        + <feature name="source"></feature>
        + <feature name="CDS"></feature>
        + <feature name="V_region"></feature>
        <sequence type="genomic DNA" length="287" topology="linear" version="1">
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        </sequence>
      </entry>
</EMBL_Services>
```

Done

RDF : Resource Description Framework

Créé en 1999 pour décrire les métadonnées
dans l'objectif de traiter l'information automatiquement,
de favoriser l'interopérabilité des connaissances et de structurer les
informations.

Métadonnées: information permettant d'en décrire une autre

- Les métadonnées sont habituellement comprises comme des données à propos des données.
- Un catalogue de bibliothèque contient de l'information (métadonnée) à propos de publications (données)
- Un système de fichier informatique définit des droits de lecture, écriture, etc. (métadonnées) à propos des fichiers (données).

RDF

- Standard du W3C
- Basé sur XML
- Un début vers un Web structuré
- RDF emploie les URIs comme schéma de nommage (pour éviter la confusion, entre termes de sémantique différents).
- On peut décrire n'importe quoi... même une personne
- Grande souplesse quand à l'extensibilité

RDF se base sur une description des connaissances à l'aide de phrases simples :
C'est un moyen d'exprimer des relations.

Ces relations sont décrites sous forme de graphe.

Chaque nœud du graphe est une ressource ou une valeur.

Et chaque nœud est relié à un autre par un arc "nommé"

Sujet

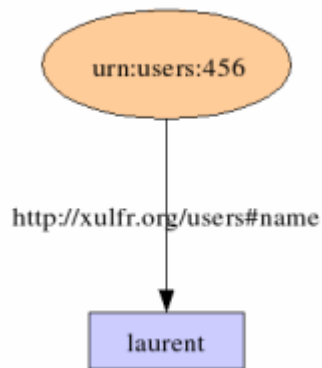
(source, ressource)

Prédicat

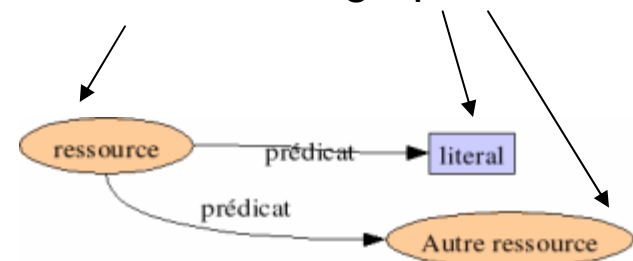
(propriété)

Objet

(cible, valeur)



nœuds du graphe



Shémas issus de <http://xulfr.org/wiki/FormatRdf/Introduction>

=> Ceci correspond à un lien qui comporte un sens : c'est du Web sémantique

Les objectifs du Web sémantique sont de partager les connaissances et de pouvoir les manipuler automatiquement.

Pour ceci, il faut qualifier le savoir (à l'aide de métadonnées), le formaliser en utilisant une syntaxe extensible (par exemple avec XML) et le structurer pour éviter les duplications).

ONTOLOGIE

Une ontologie est un ensemble structuré de connaissance dans un domaine particulier comme l'immunogénétique.

Une ontologie cherche à représenter le sens des concepts et des relations qui les lient.

Elle comprend une partie terminologique : inventaire du vocabulaire pour les métadonnées et des concepts et la déclaration des instances (valeurs) et leurs propriétés particulières (relations entre elles).

Sur le plan informatique:

Les ressources sont définies les unes par rapport aux autres selon un graphe et cette structure permet une automatisation de la manipulation des données.

Différence entre un thésaurus et une ontologie :

un thésaurus relie des concepts entre eux selon des relations précises : synonyme, homonyme, hiérarchie, terme associé.

L'ontologie ajoute des règles et des outils de comparaison sur et entre les termes, groupes de termes et relations : équivalence, symétrie, contraire, cardinalité, transitivité..

=> Dans cet objectif RDF est trop limité en particulier, il ne permet pas de donner la nature des relations (transitive inverse, ..), possède une logique trop limitée pour faire du raisonnement .

OWL (Web Ontology Language)

En 2004, OWL devient une recommandation du W3C

OWL découle de RDF et RDFS, possède des connecteurs logiques, d'exprimer des cardinalités sur les propriétés et d'en spécifier la nature

Une ontologie formalisée en OWL comprend

- Un espace de nom, :

- L'entête <owl :Ontology> pour décrire l'ontologie

- La définition des classes et des propriétés et les instances

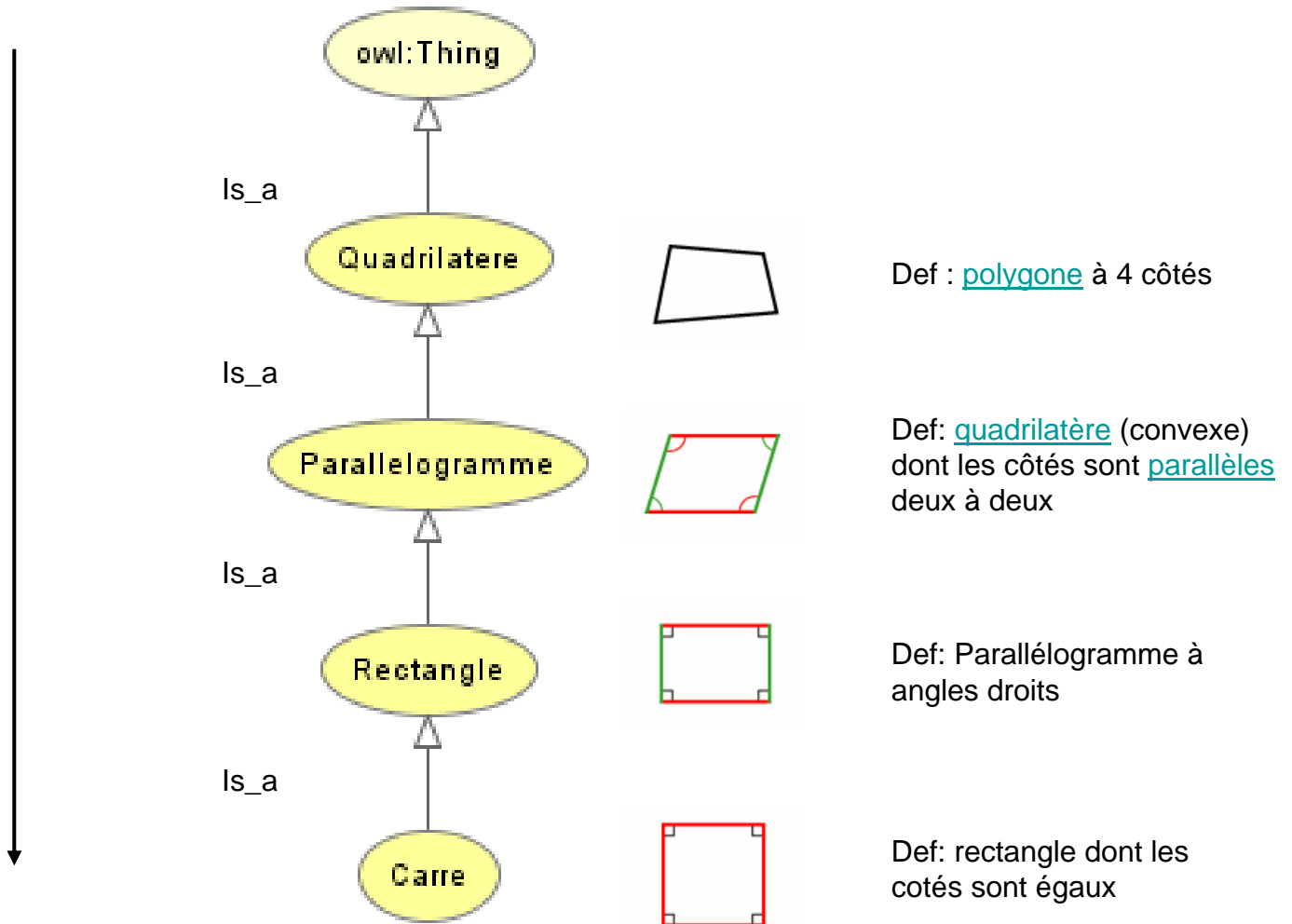
Classes, sous-classes, héritage et spécialisation

Notion de Classe :

Définit un groupe d'individus possédant des propriétés similaires.

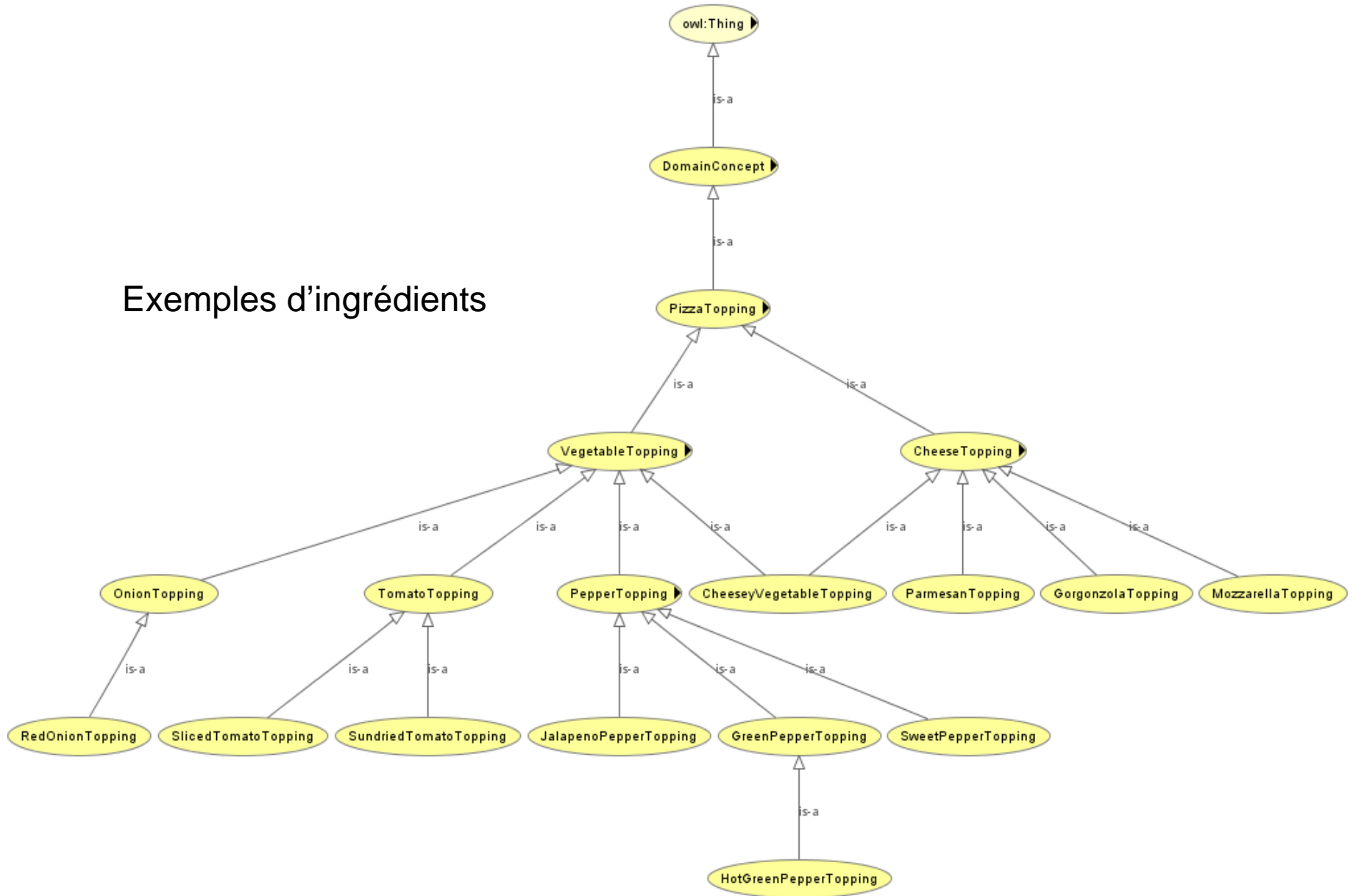
Thing est la classe mère.

spécialisation



Exemple de hiérarchie : ontologie des pizzas (exemple fournit avec Protégé)

Exemples d'ingrédients

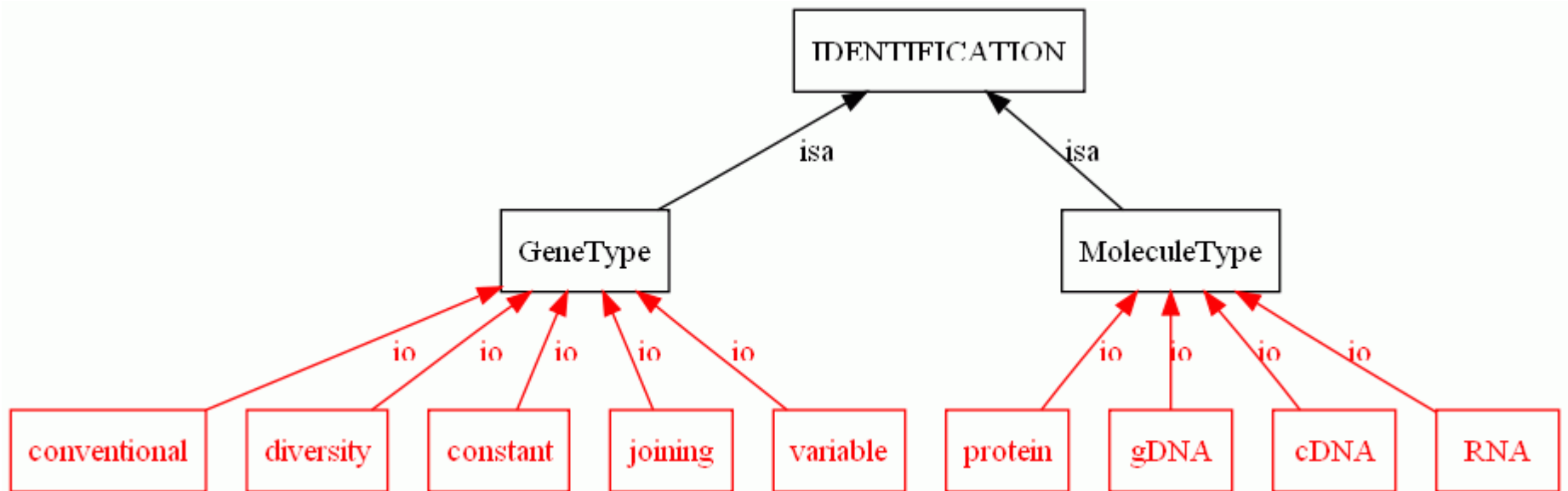


Exemples de hiérarchie : les concepts d'identification de IMGT-ONTOLOGY



Instances

Ce sont les « individus » qui peuplent les classes
Exemple des instances des concepts « GeneType » et « MoleculeType »
De IMGT-ONTOLOGY



Les 3 sous-langages OWL

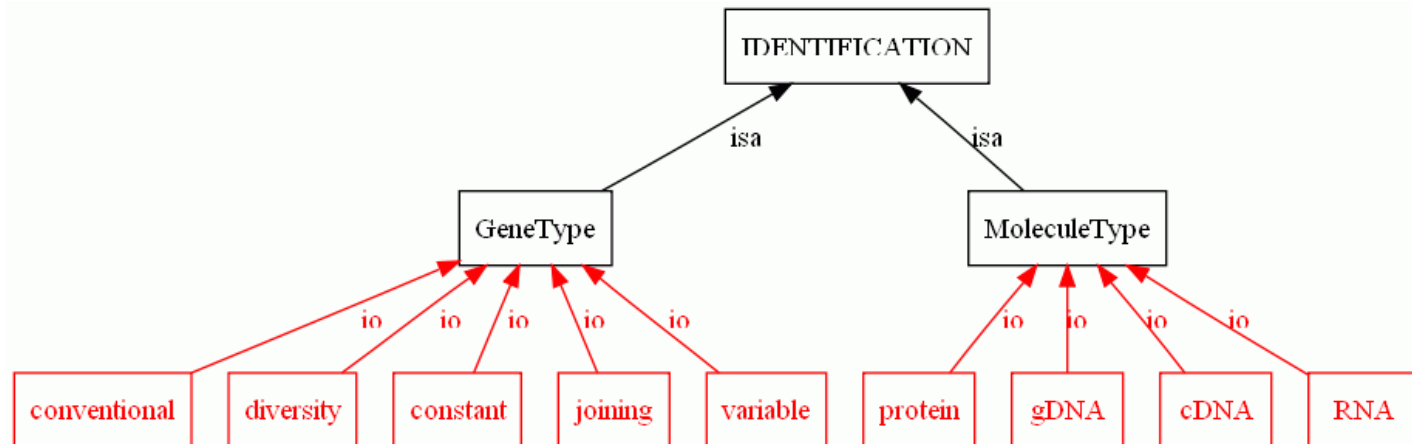
OWL LITE: permet d'établir une hiérarchie de concepts simples, contraintes simples.

OWL DL (DL pour description logic): comprend toutes les structures de OWL, possède une expressivité plus importante, avec complétude de calcul.

OWL FULL expressivité maximale, liberté syntaxique sans garantie de calcul, une classe peut aussi correspondre à l'instance d'une autre classe.

Classes équivalentes et classes disjointes

- OWL permet de déclarer que 2 classes sont équivalentes: « `equivalentClass` »
2 classes sont équivalentes lorsqu'elles ont les mêmes instances
exemple: classe « Voiture » et « Automobile »
- Inversement on peut déclarer que 2 classes sont disjointes: « `disjointWith` »
2 classes disjointes ne lorsqu'elles ont les mêmes instances
exemple: les cercles ne fait pas partie des parallogrammes.
exemple: classe « `GeneType` » et « `MoleculeType` »

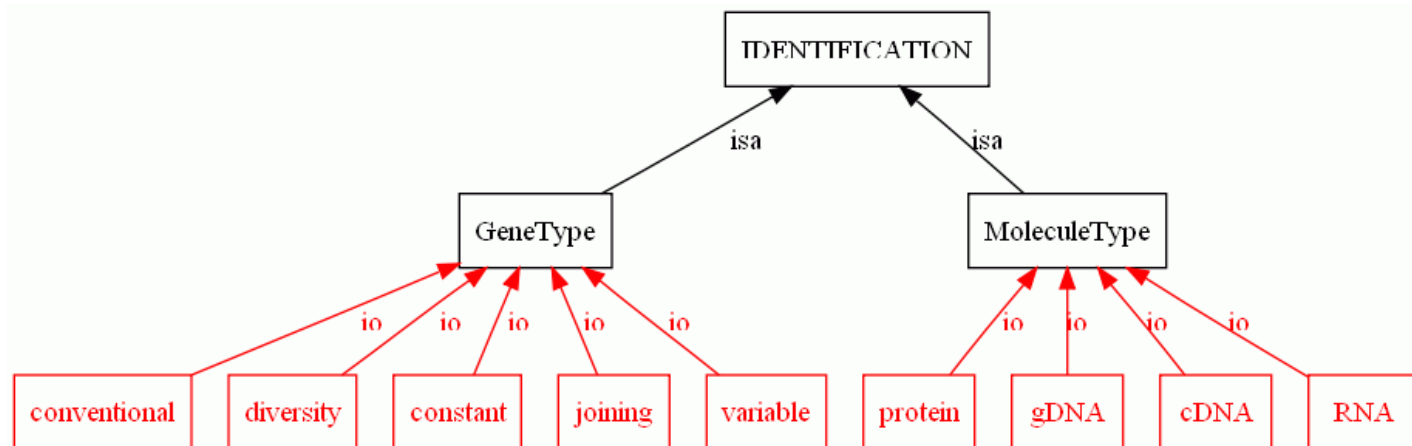


Instances identiques ou différentes

- OWL permet de déclarer que 2 instances sont les mêmes: « `sameAs` »

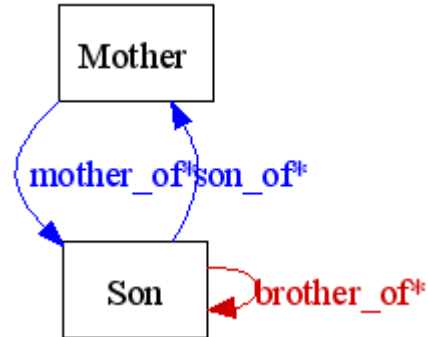
- Inversement on peut déclarer que 2 instances sont différentes: « `differentFrom` »

on peut déclarer les individus d'une même classe mutuellement différents les uns des autres: « `AllDifferent` »



Propriétés

- Propriété d'objet (Object property) : relie une instance à une autre instance



- Propriété de type de données (Datatype property): relie une instance à des valeurs.
Owl propose un héritage des propriétés (à exploiter pour les relations entre les motifs).

Son		
son_of	Instance	Mother
brother_of	Instance*	Son
age	Integer*	

Propriétés

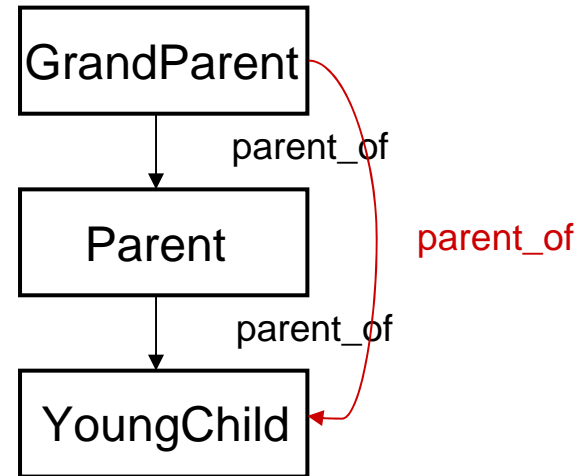
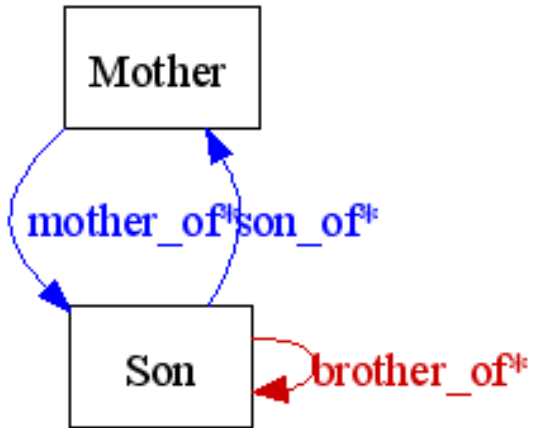
restriction globales

domain : classes pour lesquelles est définie la propriété,

range : classes reliées par la propriété au domain.

domain	relation	range
Son	brother_of	Son
Mother	mother_of	Son
Son	son_of	Mother

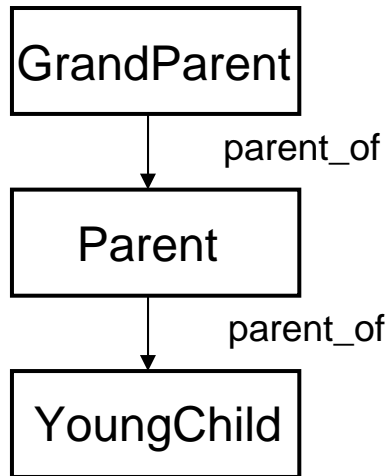
Caractéristiques des Propriétés: symétriques, transitives, inverses et fonctionnelles



(familles de 3 générations avec de jeunes enfants)

Symétrique: brother_of
Transitive: parent_of
Inverse: son_of / mother_of
Fonctionnelle : son_of

Restriction sur les Propriétés : déclaration au niveau des classes



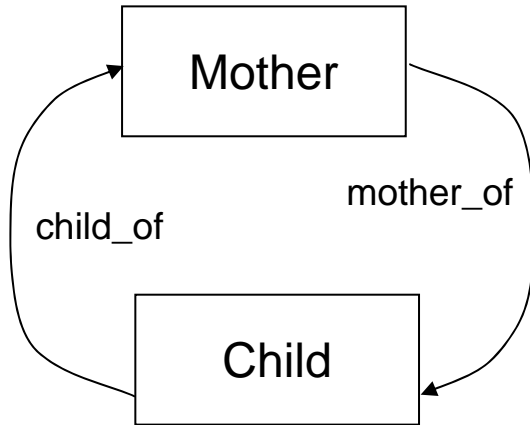
domain	relation	range
GrandParent, Parent	parent_of	Parent, YoungChild

allValuesFrom: au niveau d'une classe, permet de restreindre les classes liées par une relation. Exemple : un individu de la classe Parent ne peut être relié par la relation parent_of qu'à un individu de la classe YoungChild

someValuesFrom: au niveau d'une classe, indique qu'un individu a au moins une relation avec un individu de la classe indiquée dans la restriction
Un individu de la classe GrandParent a au moins une relation avec un individu de la classe Parent

hasValue: au niveau d'une classe, permet de restreindre la relation à un individu donné

Restriction sur les Propriétés : déclaration au niveau des classes cardinalités



Ex de familles nombreuses de moins de 10 enfants

- Une mère a au moins 3 enfants
- Une mère a au plus 10 enfants
- Un enfant a une et une seule mère

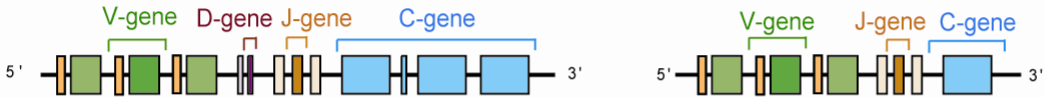
minCardinality: toute instance de la classe est liée par la propriété à au moins x individus Exemple: propriété mother_of de la classe Mother : minCardinality=3

maxCardinality: toute instance de la classe est liée par la propriété à au plus x individus Exemple: propriété mother_of de la classe Mother : maxCardinality=10

cardinality: toute instance de la classe est liée par la propriété à exactement x individus Exemple: propriété son_of de la classe Mother : cardinality=1

Synthèse des immunoglobulines et concepts d'indentification d'IMGT-ONTOLOGY

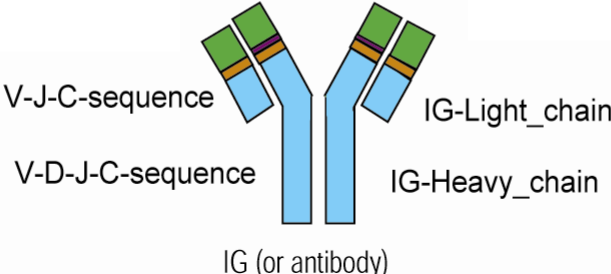
Genome



"MoleculeType"
concept

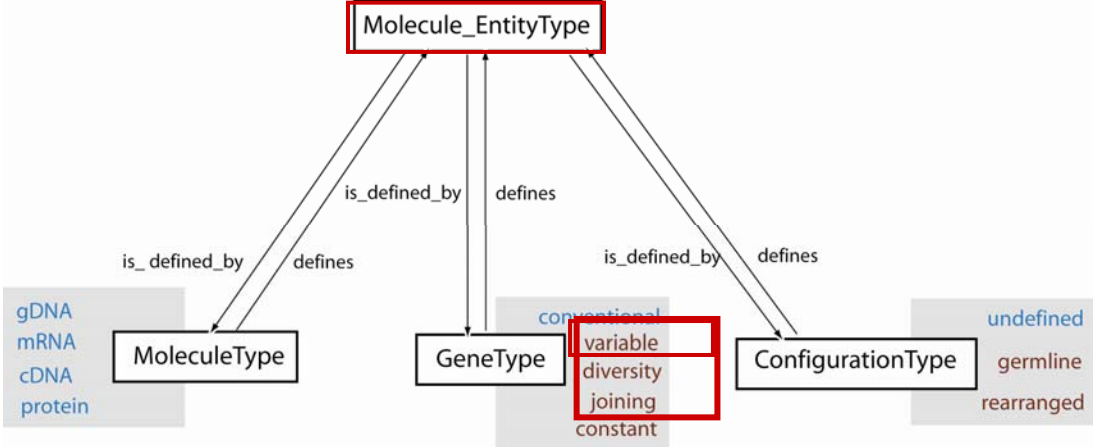
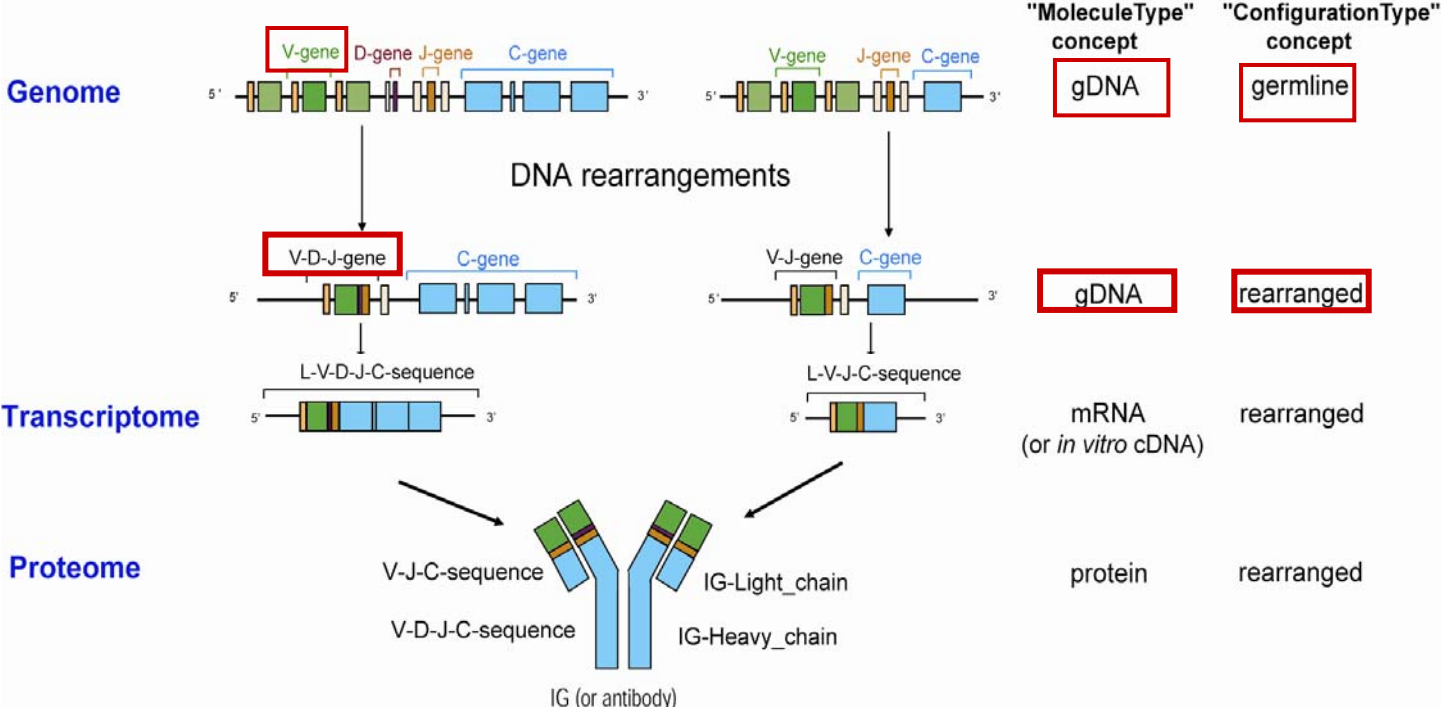
gDNA

Proteome



protein

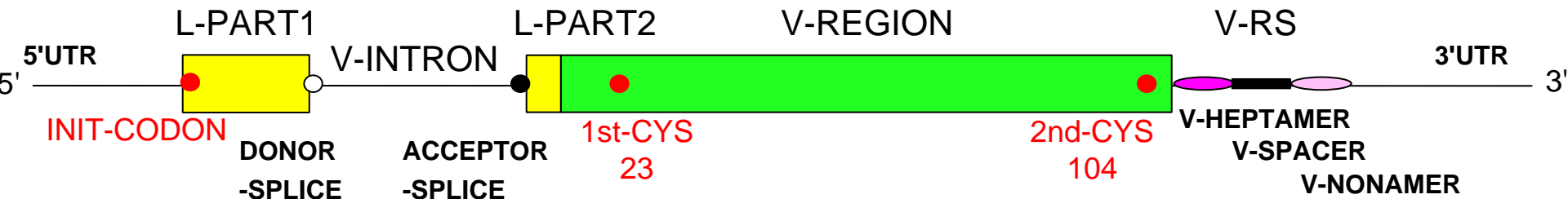
Synthèse des immunoglobulines et concepts d'indentification d'IMGT-ONTOLOGY



Les concepts de description de IMGT-ONTOLOGIE: La connaissance pour l'annotation des séquences

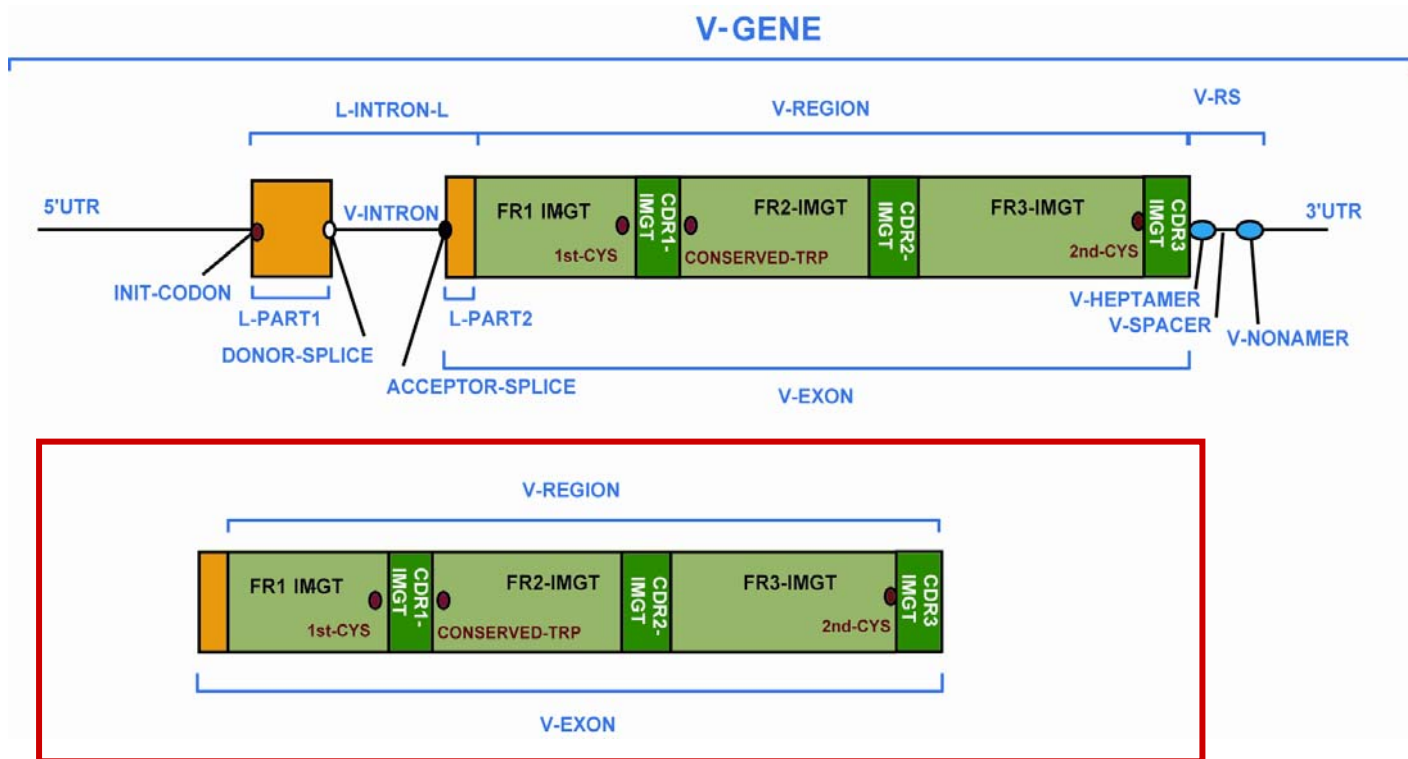
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>X62106.0|HSV12|Homo sapiens VI-2 gene for immunoglobulin heavy chain
tgagagctcc gttcctcacc atggactgga cctggaggat cctcttcttg gtggcagcag      60
ccacagggaa gaggctccct agtcccagtg atgagaaaga gattgagtcc agtccagggg      120
gatctcatcc acttctgtgt tctctccaca ggaggccact ccaggtgca gctgggtgcag      180
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agggtcacca tgaccagga cacgtccatc agcacagcct acatggagct gagcaggctg      420
agatctgacg acacggccgt gtattactgt gcgagagaca cagtggtgaaa acccacatcc      480
tgagggtgtc agaaacccaa gggaggaggc ag
  
```



Application: formalisation dans Protégé des labels qui composent Le V-EXON et de leur relations

(Source d'information: les informations de l'article de Biochimie)



Relation	Reciprocal relation (inverse)
"adjacent_at_its_5_prime_to"	"adjacent_at_its_3_prime_to"
"included_with_same_5_prime_in",	"includes_with_same_5_prime",
"included_with_same_3_prime_in",	"includes_with_same_3_prime",
"overlap_at_its_5_prime_with"	"overlap_at_its_3_prime_with"
"included_in"	"includes"

Protégé

(<http://protege.stanford.edu/>)

Protégé est un logiciel gratuit (JAVA), plate-forme open-source qui fournit une suite d'outils pour construire des bases de connaissance et des ontologies.

Protégé inclut de nombreux plugins pour la manipulation et la représentation d'ontologies dans différents formats.

L'éditeur Protégé-OWL permet aux utilisateurs de construire des ontologies pour le Web sémantique en OWL.

- Dans IMGT-ONTOLOGY, créer le concept des régions codantes de l'axiome DESCRIPTION et définir ses relations à l'aide de Protégé.
- Créer les concepts qui permettent de décrire le V-EXON, et les relations qui les lient (avec leurs caractéristiques et leurs restrictions)
- Créer une instance pour chaque concept
- Représenter graphiquement concepts, instances et relations.
- Générer le code RDF/XML.

Creation d'une nouvelle ontologie avec Protege_3.4_beta

The image shows three sequential screenshots of the Protege 'Create New Project' dialog box, connected by curved arrows indicating the flow of the process.

Step 1: Select a Project Type
The dialog box has a checkbox for 'Create from Existing Sources' which is unchecked. Under 'Select a Project Type:', several options are listed: 'Protégé Files (.port and .pins)', 'Protégé Database', 'Experimental XML File (.xml)', 'OWL / RDF Database', 'OWL / RDF Files' (which is selected and highlighted), and 'RDF Files'. Navigation buttons at the bottom include '< Back', 'Next >', 'Finish', and 'Cancel'.

Step 2: Specify Ontology URI
The 'Ontology URI (Usually a URL starting with http://)' field contains the text 'http://www.owl-ontologies.com/Ontology1211044726.owl'. A 'Default settings...' button is located to the right of the text field. Below the field is a yellow informational box with an owl icon and the text: 'Please specify a URI for this ontology. This URI will be used by other ontologies that wish to import this ontology. In general, it is recommended that a URI which corresponds to the location of the ontology on the web should be used. The URI should therefore resemble a HTTP URL, for example http://www.mydomain.com/myontology'. Navigation buttons at the bottom include '< Back', 'Next >', 'Finish', and 'Cancel'.

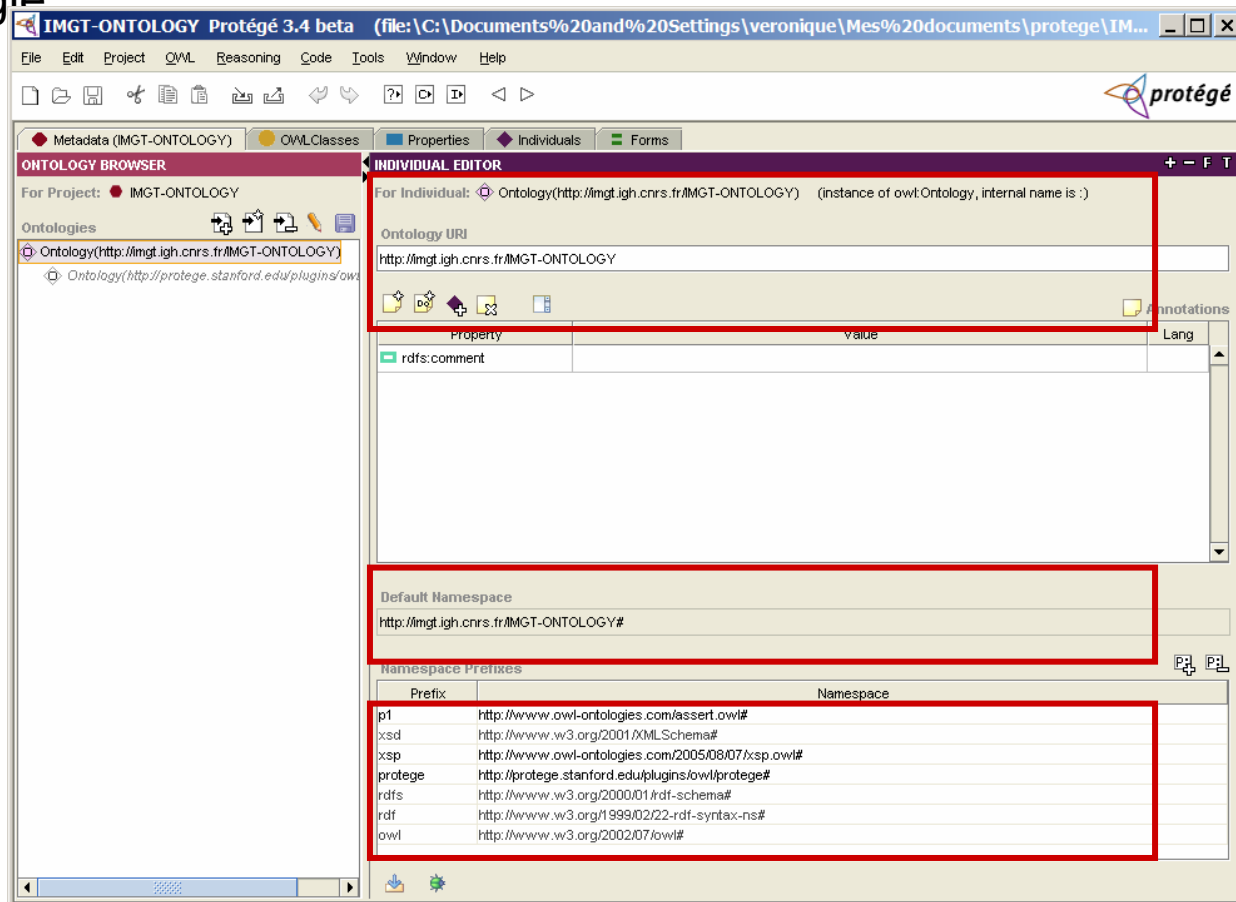
Step 3: Language Profile
The 'Language Profile' section contains four radio button options: 'RDF Schema and OWL', 'Pure RDF Schema without OWL', 'OWL Full' (which is selected), 'OWL DL', and 'OWL Lite'. Below this is another yellow informational box with an owl icon and the text: 'Which OWL/RDF dialect do you want to use? You can select which elements of OWL and RDF you want to use in your project. You can change these settings later at any time, using OWL/Preferences. For example, if you select OWL Lite, then you cannot create owl:unionOf classes, and if you select pure RDF then you can only create rdf:Properties and rdfs:Classes.'. Navigation buttons at the bottom include '< Back', 'Next >', 'Finish', and 'Cancel'.

Espace de nom

Chaque ontologie éditée avec protégé a son propre espace de nom:
C'est le « default namespace »

C'est une chaîne de caractères qui préfixe les noms des classes, propriétés, instances afin d'assurer leur unicité (Unique Resource Identifiers URI).

=> Evite la confusion en cas de termes identiques utilisés avec des significations différentes en fonction du domaine de connaissance de l'ontologie



Création de nouvelles classes avec Protégé (1)

The screenshot displays the Protégé 3.4 interface for editing an ontology. The main window is titled "CLASS EDITOR for owl:Thing (instance of owl:Class)". The "Asserted Hierarchy" panel on the left is highlighted with a red box, showing a tree structure with "owl:Thing" selected. A tooltip "Create subclass" is visible over the "owl:Thing" class. The "For Class" field is set to "http://www.w3.org/2002/07/owl#Thing". The "Properties" table is empty. The "Asserted Conditions" panel shows "NECESSARY & SUFFICIENT" and "NECESSARY" options. The "Disjoints" panel is also empty. The bottom status bar shows "Logic View" selected.

Metadata(IMGT-ONTOLOGY20090105.owl) | OWLClasses | Properties | Individuals | Forms | Classes & Instances | Jambalaya * | Ontoviz | OWLViz | Instances

SUBCLASS EXPLORER | CLASS EDITOR for owl:Thing (instance of owl:Class)

For Project: IMGT-ONTOLOGY | For Class: http://www.w3.org/2002/07/owl#Thing | Inferred View

Asserted Hierarchy

- owl:Thing (Create subclass)
- rdfs:Class
- IDENTIFICATION

Property	Value	Lang
rdfs:comment		

Asserted Conditions

- NECESSARY & SUFFICIENT
- NECESSARY

Disjoints

Logic View | Properties View

Création de nouvelles classes avec Protégé (2)

The screenshot displays the Protégé 3.4 interface for editing the 'DESCRIPTION' class. The main window is titled 'CLASS EDITOR for DESCRIPTION (instance of owl:Class)'. The 'For Class' field shows the URI: `http://www.imgt.org/IMG-ONTOLOGY1.owl#DESCRIPTION`. A red box highlights the 'Annotations' table, which contains one entry:

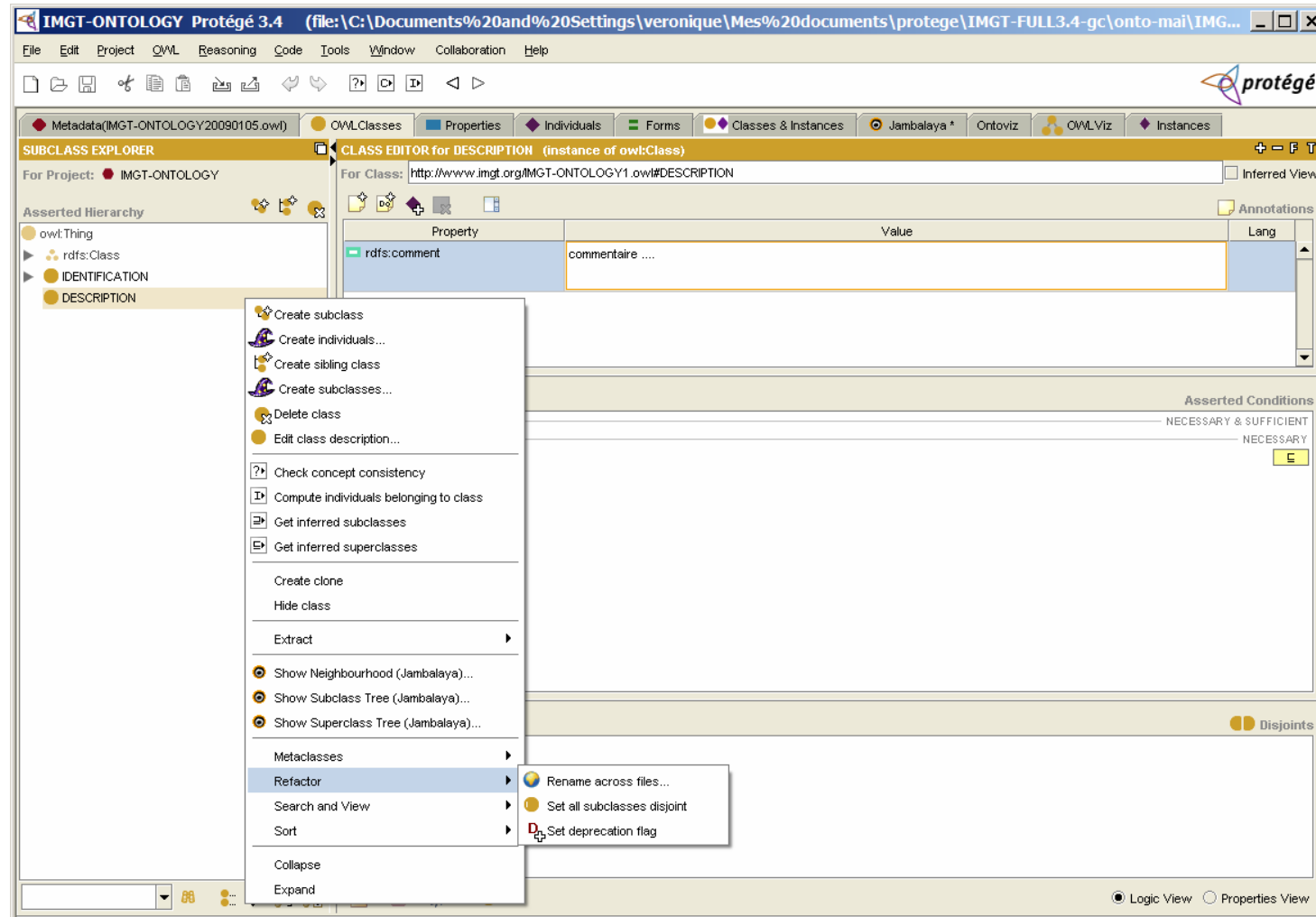
Property	Value	Lang
<code>rdfs:comment</code>	commentaire	

Below the annotations table is the 'Asserted Conditions' section, which is currently empty. At the bottom of the interface, there are icons for 'Disjoints' and a view selector showing 'Logic View' selected and 'Properties View' unselected.

Classes disjointes

On peut soit exprimer que les sous classes d'une classe sont toutes disjointes

Click droit =>



Soit expliciter quelles sont les classes disjointes

The screenshot shows the Protégé 3.4 interface for editing the **MoleculeType** class. The **Subclass Explorer** on the left shows the hierarchy: **owl:Thing** > **rdfs:Class** > **IDENTIFICATION** > **MoleculeType**. The **Class Editor** in the center shows the class **MoleculeType** with the URI <http://www.imgt.org/IMG-ONTOLOGY1.owl#MoleculeType>. The **Annotations** table shows a single entry for **rdfs:comment**. The **Asserted Conditions** panel shows the following conditions:

- IDENTIFICATION
- defines **only** Molecule_EntityType
- defines **some** Molecule_EntityType

The **Disjoints** panel at the bottom, highlighted with a red box, lists the following classes as disjoint:

- EntityType
- GeneType
- ConfigurationType

The interface also includes a menu bar (File, Edit, Project, OWL, Reasoning, Code, Tools, Window, Collaboration, Help), a toolbar, and a status bar at the bottom with **Logic View** and **Properties View** options.

Création de sous-classes avec Protégé

The screenshot displays the Protégé 3.4 beta interface for editing the IMGT-ONTOLOGY. The main window is titled "IMGT-ONTOLOGY Protégé 3.4 beta" and shows the "CLASS EDITOR" for the class "CodingRegion".

Subclass Explorer: On the left, the "Subclass Explorer" shows the ontology hierarchy. Under "DESCRIPTION", the class "CodingRegion" is selected. A tooltip "Create subclass" is visible over the "Create subclass" icon.

Class Editor: The "CLASS EDITOR" is set to "CodingRegion". It features a table for defining properties:

Property	Value	Lang
rdfs:comment		

Below the table, the "Asserted Conditions" section shows "NECESSARY & SUFFICIENT" and "NECESSARY" options. The "DESCRIPTION" section is currently empty.

The bottom of the interface includes a status bar with "Logic View" selected and "Properties View" unselected.

Création d'une nouvelle propriété avec Protégé de type ObjectProperty

The screenshot displays the Protégé 3.4 interface for creating a new property. The main window is titled "PROPERTY EDITOR for includes (instance of owl:ObjectProperty)". The "For Property:" field is set to "http://www.imgt.org/IMG-ONTOLOGY1.owl#includes".

The "PROPERTY EDITOR" window is divided into several sections:

- Property Editor Table:** A table with columns "Property", "Value", and "Lang". The "Property" column contains "rdfs:comment" and the "Value" column contains "commentaire ...".
- Domain and Range:** Both the "Domain" and "Range" fields are set to "DESCRIPTION".
- Property Characteristics:** A list of checkboxes for property characteristics: Functional, InverseFunctional, Symmetric, and Transitive. All are currently unchecked.
- Inverse:** A section for defining inverse properties, currently empty.

The "PROPERTY BROWSER" on the left shows the "includes" property selected under "Object properties". The "Super Properties" section at the bottom is also visible.

Création d'une nouvelle propriété avec Protégé de type ObjectProperty

The screenshot displays the Protégé 3.4 interface for creating a new ObjectProperty. The main window is titled "PROPERTY EDITOR for includes (instance of owl:ObjectProperty)". Below this, the "PROPERTY EDITOR for inverse_of_includes (instance of owl:ObjectProperty)" is open, showing the following details:

- For Property:** `http://www.imgt.org/IMGT-ONTOLOGY1.owl#inverse_of_includes`
- Annotations:** A table with columns "Property", "Value", and "Lang". The first row contains `rdfs:comment`, `commentaire ...`, and an empty cell.
- Domain:** `owl:Thing`
- Range:** (Empty)
- Properties:** A list of checkboxes for `Functional`, `InverseFunctional`, `Symmetric`, and `Transitive`, all of which are currently unchecked.
- Inverse:** A list containing the property `includes`.

In the background, another window titled "PROPERTY EDITOR for includes" is visible, showing the same property editor for the `includes` property. A red box highlights a small icon in the bottom right corner of the background window, which is used to add super-properties.

Création d'une nouvelle propriété avec Protégé de type ObjectProperty

The screenshot shows the Protégé 3.4 interface for creating a new property. The main window is titled "PROPERTY EDITOR for defines (instance of owl:ObjectProperty)". The "For Property:" field contains the URI "http://www.imgt.org/IMGT-ONTOLOGY1.owl#defines".

The "PROPERTY BROWSER" on the left shows a list of object properties, with "defines ↔ is_defined_by" selected. The "Domain" and "Range" fields are both set to "IDENTIFICATION". The "Inverse" checkbox is checked, and the "Inverse" field contains "is_defined_by".

The "PROPERTY EDITOR" window has a table with the following columns: Property, Value, and Lang. The table contains one row: rdfs:comment.

The "Domain" and "Range" fields are both set to "IDENTIFICATION". The "Inverse" checkbox is checked, and the "Inverse" field contains "is_defined_by".

The "Super Properties" field is empty.

Property	Value	Lang
rdfs:comment		

Domain: IDENTIFICATION

Range: IDENTIFICATION

Functional:

InverseFunctional:

Symmetric:

Transitive:

Inverse: is_defined_by

Création d'une nouvelle propriété avec Protégé de type DataTypeProperty

The screenshot shows the Protégé 3.4 interface with the 'PROPERTY EDITOR for length' window open. The 'length' property is selected in the 'Datatype Properties' list on the left. The 'Domain' is set to 'DESCRIPTION' and the 'Range' is set to 'int'. The 'Functional' checkbox is unchecked.

PROPERTY BROWSER
For Project: IMGT-ONTOLOGY

Datatype Properties

- length
- EntrezGene_identifier
- HGNC_identifier
- IMGT_gene_symbol
- NCBI_taxonomy_identifier
- number

PROPERTY EDITOR for length (instance of owl:DatatypeProperty)
For Property: <http://www.imgt.org/IMGT-ONTOLOGY1.owl#length>

Property	Value	Lang
rdfs:comment		

Domain DESCRIPTION

Range int

Functional

Allowed values

Restrictions sur les propriétés

The screenshot shows the Protégé 3.4 interface for editing the `MoleculeType` class. The left pane shows the class hierarchy, and the right pane shows the class editor with asserted conditions.

Subclass Explorer:

- owl:Thing
 - rdfs:Class
 - IDENTIFICATION
 - ConfigurationType
 - EntityType
 - Molecule_EntityType
 - MoleculeType**
 - GeneType

CLASS EDITOR for MoleculeType (instance of owl:Class)

For Class: `http://www.imgt.org/IMG-ONTOLOGY1.owl#MoleculeType` Inferred View

Property	Value	Lang
rdfs:comment		

Asserted Conditions

Condition	Restriction
IDENTIFICATION	NECESSARY & SUFFICIENT
defines only Molecule_EntityType	NECESSARY
defines some Molecule_EntityType	NECESSARY

Disjoints

- EntityType
- GeneType
- ConfigurationType

Logic View Properties View

Restrictions sur les propriétés

The screenshot shows the Protégé 3.4 interface. The main window is titled "CLASS EDITOR for Molecule_EntityType (instance of owl:Class)". The "For Class" field contains the URI "http://www.imgt.org/IMG-ONTOLOGY1.owl#Molecule_EntityType".

The "Asserted Conditions" section displays the following conditions:

- EntityType
- is_defined_by **only** (ConfigurationType or MoleculeType or GeneType)
- is_defined_by **some** ConfigurationType
- is_defined_by **some** MoleculeType
- is_defined_by **some** GeneType

The "Disjoints" section is currently empty.

The "Subclass Explorer" on the left shows the hierarchy:

- owl:Thing
 - rdfs:Class
 - IDENTIFICATION
 - ConfigurationType
 - EntityType
 - Molecule_EntityType
 - MoleculeType
 - GeneType

- DESCRIPTION

Restrictions sur les propriétés

The screenshot displays the Protégé 3.4 interface for editing the `ConfigurationType` class. The main window is titled "CLASS EDITOR for ConfigurationType (instance of owl:Class)".

Subclass Explorer: Shows the hierarchy starting from `owl:Thing`, through `IDENTIFICATION`, `ConfigurationType`, `EntityType`, and `Molecule_EntityType`. Other classes like `AA-sequence`, `C-sequence`, `J-sequence`, `J-gene`, `V-gene`, `J-C-sequence`, `C-gene`, `V-J-C-sequence`, `D-J-gene`, `D-sequence`, `V-D-J-gene`, `gene`, `V-J-gene`, `L-V-sequence`, `nt-sequence`, `L-V-J-C-sequence`, `L-V-D-J-C-sequence`, `D-gene`, `V-D-J-C-sequence`, and `MoleculeType` are also visible.

Class Editor: The "For Class:" field is set to `http://www.imgt.org/IMGT-ONTOLOGY1.owl#ConfigurationType`. The "Property" table is empty.

Property	Value	Lang
<code>rdfs:comment</code>		

Asserted Conditions: Shows the following conditions for `ConfigurationType`:

- `IDENTIFICATION` (NECESSARY & SUFFICIENT)
- `defines only Molecule_EntityType` (NECESSARY)
- `defines some Molecule_EntityType` (NECESSARY)

Disjoints: Shows the following disjoint classes:

- `EntityType`
- `MoleculeType`
- `GeneType`

The interface includes a menu bar (File, Edit, Project, OWL, Reasoning, Code, Tools, Window, Collaboration, Help), a toolbar, and a status bar at the bottom with "Logic View" and "Properties View" options.

Tests et verifications

The screenshot displays the Protégé 3.4 ontology editor interface. The main window is titled "CLASS EDITOR for V-D-J-gene (instance of owl:Class)". The left sidebar shows the "Subclass Explorer" with a tree view of the ontology hierarchy, including classes like "Molecule_EntityType" and "V-D-J-gene". The top menu bar includes "File", "Edit", "Project", "OWL", "Reasoning", "Code", "Tools", "Window", "Collaboration", and "Help". A dropdown menu is open under "OWL", showing options like "Ontology repositories...", "Edit owl:AIDifferents...", "Run ontology tests...", "Show TODO list...", and "Preferences...". The main workspace is divided into several panes: "Properties" (showing "rdfs:comment"), "Annotations", "Asserted Conditions" (listing various "is_defined_by" constraints), and "Disjoints". The "Asserted Conditions" pane shows constraints such as "is_defined_by has variable", "is_defined_by has joining", "is_defined_by has diversity", "is_defined_by has rearranged", "is_defined_by has gDNA", and "is_defined_by exactly 5". The "Disjoints" pane shows a list of classes including "L-V-sequence", "J-C-sequence", "V-gene", "V-D-J-C-sequence", "J-gene", "nt-sequence", "L-V-J-C-sequence", and "D-J-gene". The bottom status bar indicates "Logic View" is selected.

Tests et verifications

The screenshot displays the Protégé 3.4 ontology editor interface. The main window is titled "IMGT-ONTOLOGY Protégé 3.4" and shows the "CLASS EDITOR for intron" for the class `http://www.imgt.org/IMGT-ONTOLOGY1.owl#intron`. The left sidebar shows the "SUBCLASS EXPLORER" with an "Asserted Hierarchy" tree. The main editor area is divided into several sections: a table for "Property" and "Value", a section for "Asserted Conditions" with a "DESCRIPTION" entry, and a "Disjoints" section. At the bottom, a "Test Results" panel shows a warning icon and the message: "Missing disjoints on primitive subclasses: CodingRegion intron".

Subclass Explorer (Asserted Hierarchy):

- owl:Thing
 - rdfs:Class
 - IDENTIFICATION
 - ConfigurationType
 - EntityType
 - MoleculeType
 - GeneType
 - DESCRIPTION
 - CodingRegion
 - intron

Class Editor (For Class: `http://www.imgt.org/IMGT-ONTOLOGY1.owl#intron`):

Property	Value	Lang
rdfs:comment		

Asserted Conditions:

- DESCRIPTION
 - NECESSARY & SUFFICIENT
 - NECESSARY

Disjoints:

Test Results:

Type	Source	Test Result
DESCRIPTION		Missing disjoints on primitive subclasses: CodingRegion intron

Tests et verifications

The screenshot displays the Protégé 3.4 interface with the 'Reasoning' menu open. The menu options are:

- None
- DIG Reasoner
 - Pellet 1.5.2 (direct)
 - Check consistency...
 - Classify taxonomy...
 - Compute inferred types...
 - Reasoner inspector...
 - Open SPARQL Query panel
 - Open SWRL Tab

The main window shows the 'SUBCLASS EXPLORER' for the project 'IMG-ONTOLOGY'. The 'Asserted Hierarchy' is expanded to show the class 'Molecule_EntityType' with its subclasses: AA-sequence, C-sequence, J-sequence, J-gene, V-gene, J-C-sequence, C-gene, V-J-C-sequence, D-J-gene, D-sequence, V-D-J-gene, gene, V-J-gene, L-V-sequence, nt-sequence, L-V-J-C-sequence, D-gene, L-V-D-J-C-sequence, and V-D-J-C-sequence.

The 'Properties' tab is active, showing the instance 'OR for V-D-J-gene' with the URI 'http://www.imgt.org/IMG-ONTOLOGY1.owl#V-D-J-gene'. The 'Annotations' table is empty.

The 'Asserted Conditions' panel shows the following conditions for 'Molecule_EntityType':

- is_defined_by **has** variable
- is_defined_by **has** joining
- is_defined_by **has** diversity
- is_defined_by **has** rearranged
- is_defined_by **has** gDNA
- is_defined_by **exactly** 5

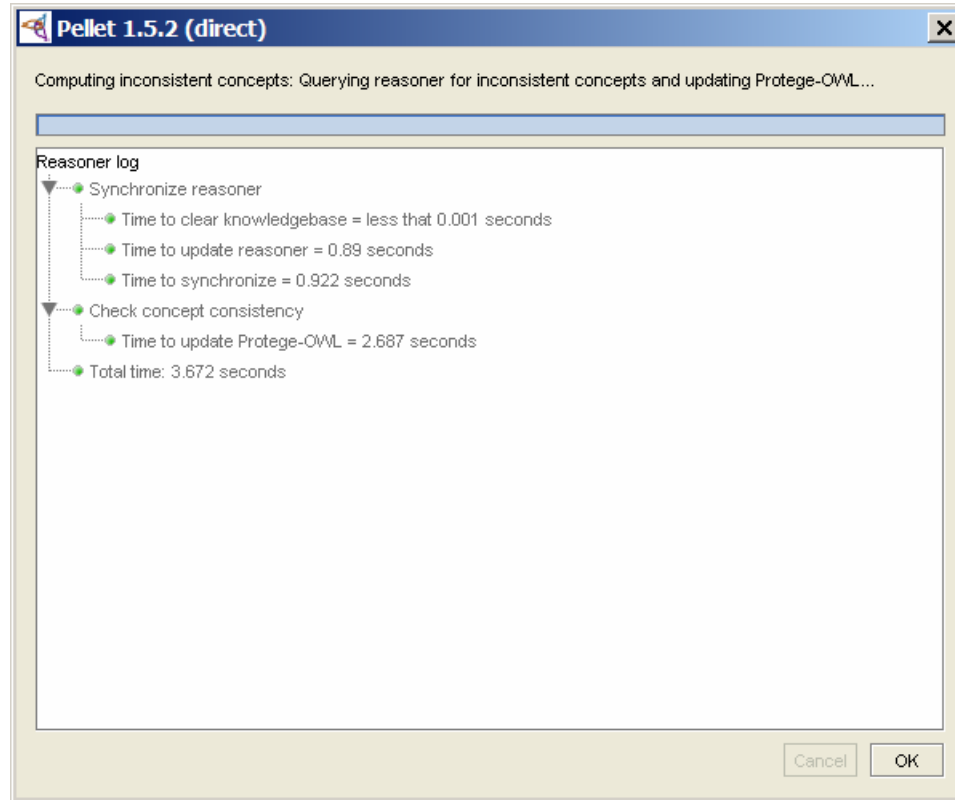
The 'Disjoints' panel shows the following disjoints:

- is_defined_by **only** (ConfigurationType or MoleculeType or GeneType)
- is_defined_by **some** ConfigurationType
- is_defined_by **some** MoleculeType
- is_defined_by **some** GeneType

The interface also includes a 'Metadata' section, a 'SUBCLASS EXPLORER' section, and a 'Properties' section. The 'Properties' section shows the instance 'OR for V-D-J-gene' with the URI 'http://www.imgt.org/IMG-ONTOLOGY1.owl#V-D-J-gene'. The 'Annotations' section is empty.

The interface also includes a 'Metadata' section, a 'SUBCLASS EXPLORER' section, and a 'Properties' section. The 'Properties' section shows the instance 'OR for V-D-J-gene' with the URI 'http://www.imgt.org/IMG-ONTOLOGY1.owl#V-D-J-gene'. The 'Annotations' section is empty.

Tests et verifications



Création d'instances avec Protégé

The screenshot displays the Protégé 3.4 interface with the following components:

- Window Title:** IMGT-ONTOLOGY Protégé 3.4 (file: \C:\Documents%20and%20Settings\veronique\Mes%20documents\protege\IMGT-FULL3.4-gc\onto-mai\IMG...
- Menu Bar:** File, Edit, Project, OWL, Reasoning, Code, Tools, Window, Collaboration, Help
- Toolbar:** Standard Protégé icons for file operations and navigation.
- Tab Bar:** Metadata(IMGT-ONTOLOGY20090105.owl), OWLClasses, Properties, Individuals, Forms, Classes & Instances, Jambalaya *, Ontoviz, OWLViz, Instances.
- CLASS BROWSER:** For Project: IMGT-ONTOLOGY. Class Hierarchy showing: owl:Thing, rdfs:Class (31), IDENTIFICATION, EntityType, Molecule_EntityType, ConfigurationType (3), MoleculeType (4), GeneType (5), DESCRIPTION.
- INSTANCE BROWSER:** For Class: GeneType. Asserted Instances list: constant, conventional, diversity, **joining** (highlighted), variable.
- INDIVIDUAL EDITOR for joining (instance of GeneType):** For Individual: <http://www.imgt.org/IMGT-ONTOLOGY1.owl#joining>. Annotations table:

Property	Value	Lang
rdfs:comment		

defines list: D-J-gene, J-C-sequence, J-gene, J-sequence, L-V-D-J-C-sequence.

Représentation graphique de l'ontologie

The screenshot displays the Protégé 3.4 beta application window. The title bar reads "IMG-T-ONTOLOGY Protégé 3.4 beta (file: \\C:\\Documents%20and%20Settings\\veronique\\Mes%20documents\\protege\\IMG-T-ONTOLOGY\\IMG-T-O...". The menu bar includes File, Edit, Project, OWL, Reasoning, Code, Tools, Window, and Help. The toolbar contains various icons for file operations and editing. The main interface is divided into several panes:

- ONTOLGY BROWSER:** Shows the project "IMG-T-ONTOLOGY" and a list of ontologies, including "Ontology(http://imgt.igh.cnrs.fr/IMG-T-ONTOLOGY)".
- INDIVIDUAL EDITOR:** The active pane, showing the "Ontology URI" as "http://imgt.igh.cnrs.fr/IMG-T-ONTOLOGY". It features a table for annotations with columns for Property, Value, and Lang. The table currently contains one row: "rdfs:comment".
- Default Namespace:** Set to "http://imgt.igh.cnrs.fr/IMG-T-ONTOLOGY#".
- Namespace Prefixes:** A table listing various prefixes and their corresponding namespaces.

The "Ontoviz" and "OWL Viz" buttons in the top toolbar are highlighted with a red box, indicating the focus of the presentation.

Property	Value	Lang
rdfs:comment		

Prefix	Namespace
p1	http://www.owl-ontologies.com/assert.owl#
xsd	http://www.w3.org/2001/XMLSchema#
xsp	http://www.owl-ontologies.com/2005/08/07/xsp.owl#
protege	http://protege.stanford.edu/plugins/owl/protege#
rdfs	http://www.w3.org/2000/01/rdf-schema#
rdf	http://www.w3.org/1999/02/22-rdf-syntax-ns#
koala	http://www.domain3.com#
owl	http://www.w3.org/2002/07/owl#

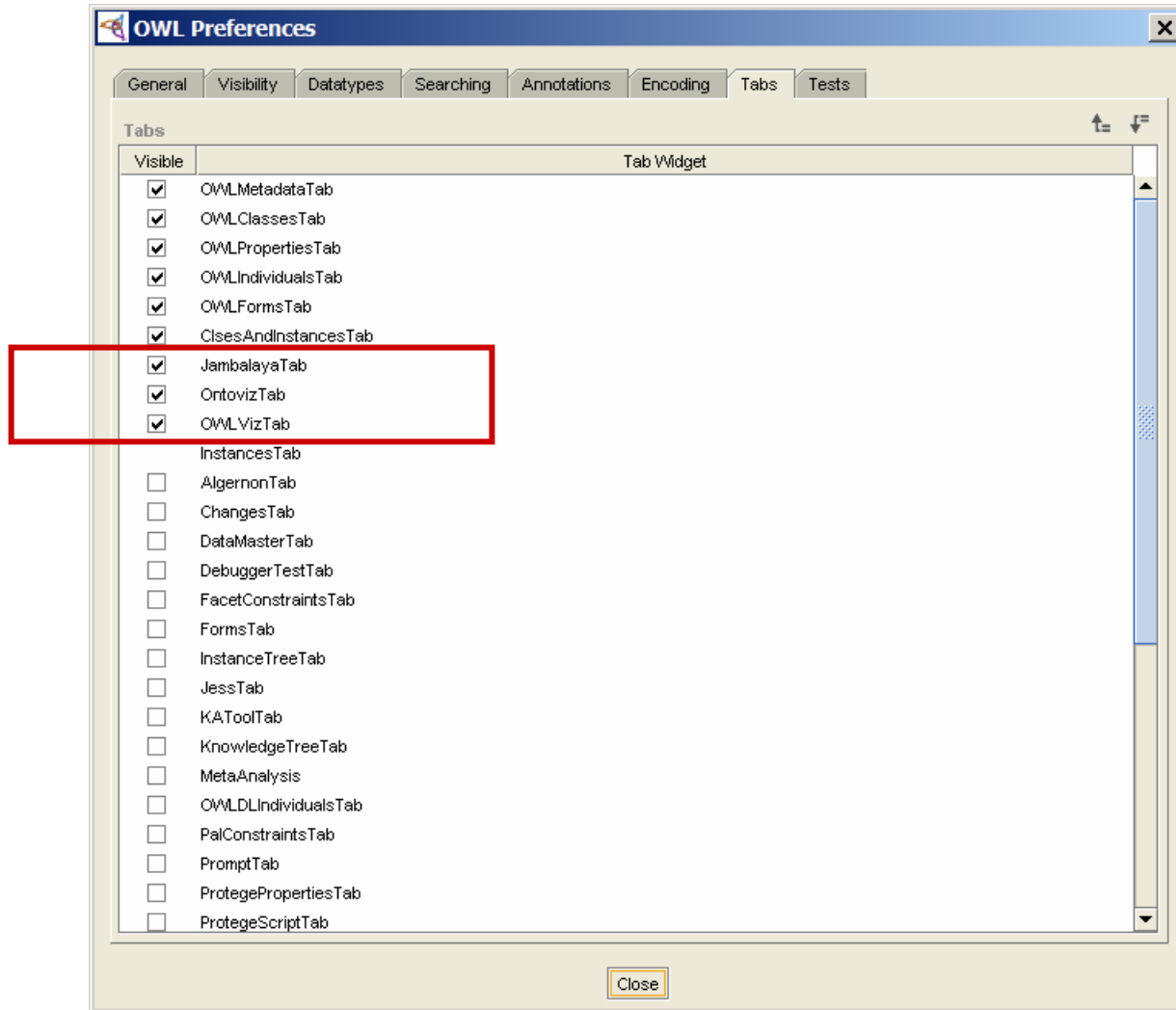
Représentation graphique de l'ontologie

The screenshot displays the Protégé 3.4 OWL editor interface. The title bar reads "IMG-T ONTOLOGY Protégé 3.4 (file: \C:\Documents%20and%20Settings\veronique\Mes%20documents\protege\IMG-T-FULL3.4-gc\onto-mai\IMG...". The menu bar includes File, Edit, Project, OWL, Reasoning, Code, Tools, Window, Collaboration, and Help. The toolbar contains icons for file operations and navigation. The main window is divided into several panes:

- Left Pane:** "Subclass Explorer" showing the hierarchy: owl:Thing > rdfs:Class > IDENTIFICATION > DESCRIPTION.
- Top Pane:** "CLASS EDITOR for DESCRIPTION (instance of owl:Class)". It shows the class URI: `http://www.imgt.org/IMG-T-ONTOLOGY1.owl#DESCRIPTION`.
- Table:** A table with columns "Property", "Value", and "Lang". It contains one row: `rdfs:comment` with the value `commentaire`.
- Bottom Pane:** "Asserted Conditions" and "Disjoints". The "Asserted Conditions" section shows "owl:Thing" with a "NECESSARY & SUFFICIENT" condition. The "Disjoints" section shows "IDENTIFICATION".

The bottom status bar indicates "Logic View" is selected over "Properties View".

Représentation graphique de l'ontologie



Représentation graphique de l'ontologie: OWLviz

The screenshot shows the Protégé 3.4 beta interface with the OWLviz tab selected. The main visualization area displays a hierarchical tree of classes. The root class is `owl:Thing`, which is a subclass of `IDENTIFICATION`. `IDENTIFICATION` is further divided into several subclasses: `Function`, `Specificity`, `ChainType`, `Taxon`, `DomainType`, `MoleculeType`, `StructureType`, `GeneType`, `Functionality`, `ReceptorType`, `ConfigurationType`, and `EntityType`. The `Taxon` class has several subclasses: `Strain`, `species`, `Breed`, and `EthnicGroup`. The `species` class has a subclass `subspecies`. The `ReceptorType` class has a subclass `Molecule_ReceptorType`. The `EntityType` class has a subclass `Molecule_EntityType`. The `IDENTIFICATION` class is highlighted with a blue box. The `CLASS BROWSER` on the left shows the hierarchy, with `IDENTIFICATION` selected. A legend in the bottom right corner provides controls for showing/hiding classes and their children/parents.

CLASS BROWSER
For Project ● IMGT-ONTOLOGY

Asserted Hierarchy

- owl:Thing
- CLASSIFICATION
- IDENTIFICATION**

Legend:

- Show class
- Show children
- Show parents
- Hide class
- Hide children
- Hide all classes
- Show Info

Représentation graphique de l'ontologie:Ontoviz

The screenshot displays the Protégé 3.4 beta interface for the 'IMGT-ONTOLOGY'. The main window title is 'IMGT-ONTOLOGY Protégé 3.4 beta (file: \\C:\\Documents%20and%20Settings\\veronique\\Mes%20documents\\protege\\IMGT-ONTOLOGY\\IMGT-O...'. The menu bar includes File, Edit, Project, OWL, Reasoning, Code, Tools, Window, and Help. The toolbar contains various icons for file operations and navigation. The main workspace is divided into several tabs: Metadata (IMGT-ONTOLOGY), OWLClasses, Properties, Individuals, Forms, Ontoviz, and OWLViz. The OWLClasses tab is active, showing a configuration table for the 'IDENTIFICATION' class. A red box highlights the 'add class' button in the configuration table. Below the configuration table, the 'Classes' list shows a hierarchy: owl:Thing, CLASSIFICATION, and IDENTIFICATION. A red box highlights the 'IDENTIFICATION' class in the list.

File Edit Project OWL Reasoning Code Tools Window Help

Metadata (IMGT-ONTOLOGY) OWLClasses Properties Individuals Forms Ontoviz OWLViz

Config

frame	sub	sup	obj	inv	st	sl	ins	sy
IDENTIFICATION	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Classes

- owl:Thing
- CLASSIFICATION
- IDENTIFICATION

Représentation graphique de l'ontologie: Ontoviz

The screenshot shows the Protégé 3.4 beta interface for the IGMT-ONTOLOGY. The main window has several tabs: Metadata (IGMT-ONTOLOGY), OWLClasses, Properties, Individuals, Forms, Ontoviz, and OWLViz. The Ontoviz tab is active, showing a configuration panel with a 'Config' section and a 'Classes' section. The 'Config' section has a 'slot' column with a dropdown menu open, showing 'edit global options'. The 'Classes' section shows a tree view with 'owl:Thing', 'CLASSIFICATION', and 'IDENTIFICATION'.

Two configuration windows are open:

- Ontoviz Slot Configuration**: A window with a checkbox 'hide slots as default' and a table of slot configurations.
- Ontoviz Global Options**: A window with two tabs: 'general' and 'colors'. The 'general' tab is active, showing various options and dropdown menus.

slot	config
for	default
has	default
defines	default
is_defined_by	default
NCBITaxon	default
protege:abstract	default
protege:allowedParent	default
protege:defaultLanguage	default
protege:excludedTest	default
protege:isCommentedOut	default
protege:probeClass	default

Ontoviz Global Options (general tab):

- save as gif
- show io :STANDARD-CLASS edges
- show system own slots
- slot edges dashed
- show instances only
- 3 maximum depth for slot extension (instances)
- 1 maximum depth for slot extension (classes)
- 3 maximum displayed values per slot
- 5 maximum displayed slots per node

Représentation graphique de l'ontologie: Ontoviz

The screenshot shows the Protégé 3.4 interface with the IMGT-ONTOLOGY loaded. The main visualization area displays the following ontology structure:

- IDENTIFICATION** (Root Class)
 - GeneType** (Subclass)
 - joining
 - diversity
 - variable
 - conventional
 - constant
 - MoleculeType** (Subclass)
 - cDNA
 - protein
 - mRNA
 - gDNA
 - ConfigurationType** (Subclass)
 - undefined
 - germline
 - rearranged
- V-gene** (Class)
 - Defined by: variable, gDNA, germline

The left sidebar shows the class hierarchy, and the top menu includes File, Edit, Project, OWL, Reasoning, Code, Tools, Window, Collaboration, and Help.

Représentation graphique de l'ontologie: Jambalaya

The screenshot displays the Protégé 3.4 interface for editing the 'Jambalaya' ontology. The main workspace shows a class hierarchy starting with 'owl:Thing' at the top. 'owl:Thing' is a subclass of 'IDENTIFICATION' and 'DESCRIPTION'. 'IDENTIFICATION' is a subclass of 'EntityType', which is further specialized into 'Molecule_EntityType'. 'DESCRIPTION' is a subclass of 'Entity', 'EntityType', 'Class', and 'Region'. 'Molecule_EntityType' has numerous instances listed at the bottom, including 'AA', 'Environ', 'Chem', 'Prot', 'Des', 'Vid', 'O', 'M', 'D', 'Ch', 'E', 'P', 'g', 'L', 'y', 'e', 'C', 'P', 'D', 'B', 'J', 'g', 'e', 'n', 'e'. The left sidebar contains the 'CLASS BROWSER' showing the class hierarchy and the 'INSTANCE BROWSER'. A red box highlights the 'Custom Views' icon in the bottom-left corner of the interface.

Protégé 3.4 (file: \\C:\Documents%20and%20Settings\veronique\Mes%20documents\protege\IMGT-FULL3.4-gc\onto-mai\IMGT-ONTOLOGY.pprj, O...)

File Edit Project QWL Reasoning Code Tools Window Collaboration Jambalaya Help

Metadata(IMGT-ONTOLOGY20090105.owl) OWLClasses Properties Individuals Forms Jambalaya

CLASS BROWSER For Project: IMGT-ONTOLOGY

Class Hierarchy

- owl:Thing
 - rdfs:Class (31)
 - IDENTIFICATION
 - DESCRIPTION

owl:Thing

IDENTIFICATION

DESCRIPTION

EntityType

Entity

Class

Region

Molecule_EntityType

AA Environ Chem Prot Des Vid O M D Ch E P g L y e C P D B J g e n e

Custom Views

No Hierarchy Root: owl:Thing Node Labels: Above Node (fixed) Arc Labels: Navigation: Magnify

Nested View (Default)

Nested Treemap

Nested Composite View

Class & Individual Tree

Class Tree


Domain/Range

test

test Details

Name: **Display?**

Layout:

Label mode: Icon: 

Node & Arc Types Nesting Hierarchy Composite Arcs

Select the node types of interest: [Check All](#) [Check None](#)

- Defined Class
- Enumeration
- Individual
- Logical Operation
- Primitive Class
- RDFS Class
- Restriction

Select the arc types of interest: [Check All](#) [Check None](#)

- defines
- defines (Domain>Range)
- defines (Necessary and Sufficient)
- defines (Necessary)
- describes
- describes (Domain>Range)
- describes (Necessary and Sufficient)
- describes (Necessary)
- has instance
- has subclass
- includes
- includes (Domain>Range)
- includes (Necessary and Sufficient)
- includes (Necessary)
- is_defined_by
- is_defined_by (Domain>Range)
- is_defined_by (Necessary and Sufficient)
- is_defined_by (Necessary)
- is_described_by
- is_described_by (Domain>Range)
- is_described_by (Necessary and Sufficient)
- is_described_by (Necessary)
- is_included_in
- is_included_in (Domain>Range)
- is_included_in (Necessary and Sufficient)
- is_included_in (Necessary)

New Quick Vi...

Name: **New Quick**

Nested Quick View

Flat Quick View

OK Cancel

IMGT-ONTOLOGY Protégé 3.4 (file: C:\Documents%20and%20Settings\veronique\Mes%20documents\protege\IMGT-FULL3.4-gc\onto-mai\IMGT-ONTOLOGY.pprj, O...

File Edit Project OWL Reasoning Code Tools Window Collaboration Jambalaya Help

Metadata(IMGT-ONTOLOGY20090105.owl) OWLClasses Properties Individuals Forms Jambalaya

CLASS BROWSER
For Project: IMGT-ONTOLOGY

Class Hierarchy

- V-gene
- V-J-gene
- V-D-J-C-sequence
- AA-sequence
- C-sequence
- J-sequence
- J-gene
- J-C-sequence
- V-J-C-sequence
- C-gene
- D-sequence
- D-J-gene
- V-D-J-gene
- gene
- L-V-sequence
- L-V-J-C-sequence
- nt-sequence
- L-V-D-J-C-sequence
- D-gene

Quick Views

Search: contains Search Clear

INSTANCE BROWSER
For Class: <http://www.imgt.org/IMGT-ONTOLOG...>

:NAME

Custom Views

No Hierarchy Root: owl:Thing Node Labels: Above Node (fixed) Arc Labels: Navigation: Magnify

The diagram illustrates an ontology structure. At the top level, **GeneType**, **MoleculeType**, and **ConfigurationType** are interconnected. **GeneType** is a subclass of **GeneType** and includes instances: conventional, variable, diversity, joining, and constant. **MoleculeType** is a subclass of **MoleculeType** and includes instances: gDNA, mRNA, cDNA, and protein. **ConfigurationType** is a subclass of **ConfigurationType** and includes instances: rearranged, undefined, and germline. Additionally, **GeneType** is related to **MoleculeType** and **ConfigurationType**. **MoleculeType** is related to **ConfigurationType**. **ConfigurationType** is related to **ConfigurationType**. The diagram also shows a large number of subclasses of **MoleculeType** and **ConfigurationType**, including: L-V-D-J-C-sequence, V-J-gene, V-D-J-gene, J-sequence, L-V-J-C-sequence, J-C-sequence, D-gene, gene, C-sequence, D-sequence, V-D-J-C-sequence, D-J-gene, V-J-C-sequence, AA-sequence, V-gene, C-gene, L-V-sequence, nt-sequence, and J-gene.

Restriction sur les cardinalités Properties View

The screenshot displays the Protégé 3.4 beta interface. The main window shows the 'CLASS EDITOR' for the class 'Molecule_EntityType'. The 'Properties View' is active, showing a table of properties:

Property	
protege:subclassesDisjoint	true
rdfs:comment	If the object is a molecule, the "EntityType" concept is "MoleculeType", "GeneType" and "ConfigurationType", "Functionality" and "StructureType" concepts.

Below the table, the class hierarchy is visible, showing 'Molecule_EntityType' as a subclass of 'EntityType'. The 'Create Restriction' dialog box is open, showing the 'Restricted Property' list with 'is_defined_by' selected. The 'Restriction' list includes 'allValuesFrom', 'someValuesFrom', 'hasValue', 'cardinality', 'minCardinality', and 'maxCardinality'. The 'Filler' field is empty, and an error message at the bottom reads: "Error: Please enter a filler. at """.

The 'SUBCLASS EXPLORER' on the left shows the following hierarchy:

- owl:Thing
 - CLASSIFICATION
 - IDENTIFICATION
 - ChainType
 - ConfigurationType
 - DomainType
 - EntityType
 - Molecule_EntityType
 - Function
 - Functionality
 - GeneType
 - MoleculeType
 - ReceptorType
 - Molecule_ReceptorType
 - Specificity
 - StructureType
 - Taxon

Restriction sur les cardinalités Logic View

The screenshot shows the Protégé 3.4 beta interface in Logic View. The main window displays the class editor for `Molecule_EntityType`. The left pane shows the asserted hierarchy, and the right pane shows the asserted conditions for the class.

Subclass Explorer (Left Pane):

- owl:Thing
 - CLASSIFICATION
 - IDENTIFICATION
 - ChainType
 - ConfigurationType
 - DomainType
 - EntityType
 - Molecule_EntityType**
 - Function
 - Functionality
 - GeneType
 - MoleculeType
 - ReceptorType
 - Molecule_ReceptorType
 - Specificity
 - StructureType
 - Taxon

Class Editor (Right Pane):

For Class: `Molecule_EntityType` (instance of owl:Class) Inferred View

Property	Value	Lang
<code>protege:subclassesDisjoint</code>	true	
<code>rdfs:comment</code>	If the object is a molecule, the "EntityType" concept is designated as "Molecule_EntityType", which is defined by the "MoleculeType", "GeneType" and "ConfigurationType" concepts of identification and has properties identified in the "Functionality" and "StructureType" concepts.	

Asserted Conditions (Right Pane):

NECESSARY & SUFFICIENT

NECESSARY

- EntityType
- `_has_max 1` Functionality
- `_has_max 1` StructureType
- `is_defined_by some` GeneType
- `is_defined_by some` MoleculeType
- `is_defined_by exactly 1` ConfigurationType

Disjoints (Bottom Right):

Logic View Properties View

Importation d'ontologies

Il est possible d'utiliser les classes les propriétés et les instances de L'ontologie importée, d'en étendre la description

⇒ Attention, la référence aux classes, propriétés et individus d'une autre Ontologie en utilisant l'espace de nom est différent de l'importation complète D'ontologies.

