

References of the papers used to populate the OncoCardio database
with their accessible URLs and search strategies used
Supplementary material 1 to the paper
"OncoCardioDB: A Public and Curated Database of Molecular Information in
Onco-cardiology/Cardio-oncology"

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Supplementary Table 1: Search strategies used to retrieve the articles from bibliographic databases.

| Database | Field | Query |
|----------|-----------------------------|--|
| | onco-cardiology | (onco-cardiology[All Fields] OR oncocardiology[All Fields]) AND ("gene"[All Fields] OR "target"[All Fields] OR "protein"[All Fields] OR "biomarker"[All Fields] OR "RNA"[All Fields] OR "methylation"[All Fields] OR "review"[Publication Type] OR "in vivo"[All Fields] OR "rats"[All Fields] OR "mice"[All Fields] OR "cell line"[All Fields]) NOT ("review"[Title/Abstract]) AND English[lang] NOT ("in vitro"[All Fields] OR "in vivo"[All Fields] OR "rats"[All Fields] OR "mice"[All Fields] OR "cell line"[All Fields]) |
| | cardio-oncology | (cardio-oncology[All Fields] OR cardiooncology[All Fields]) AND ("gene"[All Fields] OR "target"[All Fields] OR "protein"[All Fields] OR "biomarker"[All Fields] OR "RNA"[All Fields] OR "methylation"[All Fields] OR "review"[Publication Type] OR "in vivo"[All Fields] OR "rats"[All Fields] OR "mice"[All Fields] OR "cell line"[All Fields]) |
| Pubmed | oncology AND cardiotoxicity | ("oncology"[All Fields] OR "cancer"[All Fields] AND ("cardiotoxicity"[All Fields] OR "cancer therapeutics-related cardiac dysfunction" [All Fields]) AND ("gene"[All Fields] OR "target"[All Fields] OR "protein"[All Fields] OR "biomarker"[All Fields] OR "RNA"[All Fields] OR "methylation"[All Fields]) NOT ("review"[Publication Type] OR "in vivo"[All Fields] OR "rats"[All Fields] OR "mice"[All Fields] OR "cell line"[All Fields]) |
| | Cancer AND Cardio | ("oncology"[Title/Abstract] OR "cancer"[Title/Abstract]) AND ("cardio"[Title/Abstract] OR "atherosclerosis"[Title/Abstract]) AND ("gene"[All Fields] OR "target"[All Fields] OR "protein"[All Fields] OR "biomarker"[All Fields] OR "RNA"[All Fields] OR "methylation"[All Fields]) NOT ("review"[Publication Type] OR "in vivo"[All Fields] OR "rats"[All Fields] OR "mice"[All Fields] OR "cell line"[All Fields]) |
| | Onco-cardiology | SU="Life Sciences & Biomedicine" AND TS=(onco-cardiology OR oncocardiology) AND TS=(gene OR target OR protein OR RNA OR biomarker OR methylation OR pathway) NOT SO="review" NOT SO="letter" NOT SO="correspondence as topic" NOT SO="comments" NOT SO="opinion" NOT TS=("in vitro" OR "in vivo" OR rats OR mice OR "cell line") |
| | Cardio-oncology | SU="Life Sciences & Biomedicine" AND TS=(cardio-oncology OR cardiooncology) AND TS=(gene OR target OR protein OR RNA OR biomarker OR methylation OR pathway) NOT SO="review" NOT SO="letter" NOT SO="correspondence as topic" NOT SO="comments" NOT SO="opinion" NOT TS=("in vitro" OR "in vivo" OR rats OR mice OR "cell line") |
| WoS | Onco AND cardiotoxicity | SU="Life Sciences & Biomedicine" AND TS=(cancer OR oncology) AND TS=(cardiotoxicity OR "cancer therapeutics related cardiac dysfunction") AND TS=(gene OR target OR protein OR RNA OR biomarker OR methylation OR pathway) NOT SO="review" NOT SO="letter" NOT SO="correspondence as topic" NOT SO="comments" NOT SO="opinion" NOT TS=("in vitro" OR "in vivo" OR rats OR mice OR "cell line") |
| | Onco AND Cardio | SU="Life Sciences & Biomedicine" AND TS=("cancer" OR oncology) AND TS=(cardio OR "atherosclerosis") AND TS=(gene OR target OR protein OR RNA OR biomarker OR methylation OR pathway) NOT SO="review" NOT SO="letter" NOT SO="correspondence as topic" NOT SO="comments" NOT SO="opinion" NOT TS=("in vitro" OR "in vivo" OR rats OR mice OR "cell line") |

| Database | Field | Query | |
|----------|-------------------------|---|--|
| Scopus | Onco-cardiology | TITLE-ABS(onco-cardiology OR oncocardiology) AND (gene OR target OR protein OR rna OR biomarker OR methylation OR pathway) AND NOT ("in vitro" OR "in vivo" OR rat OR mice OR "cell line*" OR culture) AND (LIMIT-TO(DOCTYPE, "ar")) AND (LIMIT-TO(LANGUAGE, "English")) | |
| | Cardio-oncology | TITLE-ABS(cardio-oncology OR cardiooncology) AND (gene OR target OR protein OR rna OR biomarker OR methylation OR pathway) AND NOT ("in vitro" OR "in vivo" OR rat OR mice OR "cell line*" OR culture) AND (LIMIT-TO(DOCTYPE, "ar")) AND (LIMIT-TO(LANGUAGE, "English")) | |
| | Onco AND cardiotoxicity | TITLE-ABS(onco OR cancer) AND TITLE-ABS(cardiotoxicity OR "cancer therapeutics-related cardiac dysfunction") AND (gene OR target OR protein OR rna OR biomarker OR methylation OR pathway) AND NOT ("in vitro" OR "in vivo" OR rat OR mice OR "cell line*" OR culture) AND (LIMIT-TO(DOCTYPE, "ar")) AND (LIMIT-TO(LANGUAGE, "English")) | |
| | Onco AND Cardio | TITLE-ABS(oncology OR cancer) AND TITLE-ABS(cardio OR atherosclerosis) AND (gene OR target OR protein OR rna OR biomarker OR methylation OR pathway) AND NOT ("in vitro" OR "in vivo" OR rat OR mice OR "cell line*" OR culture) AND (LIMIT-TO(DOCTYPE, "ar")) AND (LIMIT-TO(LANGUAGE, "English")) | |
| | Onco-cardiology | ('onco-cardiology':ab,ti OR 'oncocardiology':ab,ti) AND ('protein' OR 'gene' OR 'rna' OR 'methylation' OR 'biomarker' OR 'pathway') NOT ('letter:it' OR 'editor:it' OR 'hypothesis:it' OR comment:it OR opinion:it OR review:it) NOT ('in vitro study' OR 'in vivo study' OR 'mouse' OR 'mice' OR 'rat' OR 'cell\$ line\$' OR culture) AND [article]/lim AND [humans]/lim AND [embase]/lim | |
| | Cardio-oncology | ('cardio-oncology':ab,ti OR 'cardiooncology':ab,ti) AND ('protein' OR 'gene' OR 'rna' OR 'methylation' OR 'biomarker' OR 'pathway') NOT ('letter:it' OR 'editor:it' OR 'hypothesis:it' OR comment:it OR opinion:it OR review:it) NOT ('in vitro study' OR 'in vivo study' OR 'mouse' OR 'mice' OR 'rat' OR 'cell\$ line\$' OR culture) AND [article]/lim AND [humans]/lim AND [embase]/lim | |
| | Onco AND cardiotoxicity | ('cancer':ab,ti OR 'oncology':ab,ti) AND ('cardiotoxicity':ab,ti OR 'cancer therapeutics related cardiac dysfunction':ab,ti) AND ('protein' OR 'gene' OR 'rna' OR 'methylation' OR 'biomarker' OR 'pathway') NOT ('letter:it' OR 'editor:it' OR 'hypothesis:it' OR opinion:it OR review:it) NOT ('in vitro study' OR 'in vivo study' OR 'mouse' OR 'mice' OR 'rat' OR 'cell line' OR culture) AND [article]/lim AND [humans]/lim AND [embase]/lim | |
| | Onco AND Cardio | ('cancer':ab,ti OR 'oncology':ab,ti) AND ('cardio':ab,ti OR 'atherosclerosis':ab,ti) AND ('protein' OR 'gene' OR 'rna' OR 'methylation' OR 'biomarker' OR 'pathway') NOT ('letter:it' OR 'editor:it' OR 'hypothesis:it' OR review:it) NOT ('in vitro study' OR 'in vivo study' OR 'mouse' OR 'mice' OR 'rat' OR 'cell\$ line\$' OR culture) AND [article]/lim AND [humans]/lim AND [embase]/lim | |
| | | | |
| | Embase | | |

Objects and fields used in the OncoCardio database

Supplementary material 2 to the paper

”OncoCardioDB: A Public and Curated Database of Molecular Information in Onco-cardiology/Cardio-oncology”

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Abstract

This document is an explanation of the terms (objects and fields) used for the construction and internal organization of a database for onco-cardiology and their associated genes. Also, it explains some details about data curation and choice of standards. It is delivered as appendix/additional material of the paper about the design, implementation and population of such database.

1 Data curation

The information to fill this database comes essentially from two types of sources: lists of items or standard classifications of items already available and concrete biomedical studies done on a population of human subjects. In our case, the lists and standards are Entrez for genes, International Classification of Diseases (ICD10) for pathologies and Anatomical Therapeutic Chemical Classification (ATC) for drugs. On the other hand, relevant fields of each medical study are collected from the medical literature. Therefore, some information does not depend on the consulted studies, neither it is specific for onco-cardiology. It is to be stored in tables that from now on will be called generic tables. These are:

- Tables 'Gene', 'GeneTranscript', 'Synonym', 'GeneInEnsemble', 'Variation' and 'GenomeFullPosition' as long as those which relate them ('transcribes_as' and 'has_ensemble_id') were filled from the information provided by the R package `org.Hs.eg.db` included in Bioconductor ([1, 3]). This time a R script instead of a Perl macro was used to generate the SQL sentences.
- Table 'Drug' was filled from the classification of the Anatomical Therapeutic Chemical classification (ATC) as provided by the WHO Collaborating Centre for Drug Statistics Methodology of Norway ([4]) first, extracting it as an ASCII text file and then processing it with a Perl macro.
- Table 'Pathology' was filled from the International Classification of Diseases (ICD10) as provided by the Web's Free 2022 ICD-10-CM/PCS Medical Coding Reference ([2]). Again, the information was obtained as an ASCII table and processed by a Perl macro.

The rest of the tables were populated from the fields present in the spreadsheet filled from the published studies; they will be called specific tables. As stated before, such spreadsheet was filled by experts in the area. This time the Perl macro makes a careful check before generating the SQL sentences. Indeed, a list of constraints must be met:

- Values for numeric fields are really numbers and they are in the appropriate interval.
- Strings of characters do not exceed the intended lengths, as designed in the database tables.
- Unknown values are stored always with the same mark.
- Dates follow a standardized format (yyyy-mm-dd).
- Country codes are taken for the known list of countries (ISO country codes).
- Some fields, namely therapies, detection methods and validation methods must belong to a predefined list.

- Statistical significance must be provided as one of a predefined list of known possibilities for its meaning.
- Values for items already stored in the previously filled generic tables (i.e.: all those related with genes, drugs and pathologies) really correspond to an existing value.
- No value is introduced as a duplicate row (for instance: panel kit names are incorporated only when they are mentioned for the first time, as long as drug codes, pathology codes, etc).

2 Naming conventions

The following conventions have been used:

- Tables that represent objects (entities) will be named after the name of the entity, first letter in upper case. The different words in the name (and, in general, in all names of fields) will be capitalized.
- The primary key for each table will in most cases be called 'IdName', being Name the name of the object (table), with a few exceptions.
- The foreign keys will be named as the name of the key they refer to.
- There are two reasons by which a key cannot be NULL: either we know it represents important information that should not be omitted (marked as 'not NULL by choice') or it is a foreign key which refers to the primary key of another table (marked as 'not NULL by design').
- Tables that represent relationships between objects (arising from an N:M cardinality) will have a significant name all in lower case with words separated by the underscore character.
- Fields containing a Digital Object Identifier (DOI) representing different publications will be stored as URLs in the form `https://doi.org/<the_doi>`

With respect to gene denotation, we have used the R Bioconductor package `org.Hs.eg.db` which according to its documentation is primarily based on mapping using Entrez Gene identifiers. Therefore, we have used the Entrez identifier as primary key, since it is unique in this database. Also, analyzing it we can observe that each of the (currently) 61547 different Entrez id's has exactly one gene symbol associated, even though a few symbols are associated to two different Entrez id's (and even one it is associated to three Entrez id's). With respect to Ensembl identifiers, many Entrez id's have no an associated Ensembl id and some Ensembl identifiers have more than one associated Entrez. This has forced the introduction of a new table to store genes by their Ensembl identifiers and relate it with the first gene table with a suitable relation. The same situation happens between Entrez identifiers and transcripts which gives rise to a secondary relation table, too.

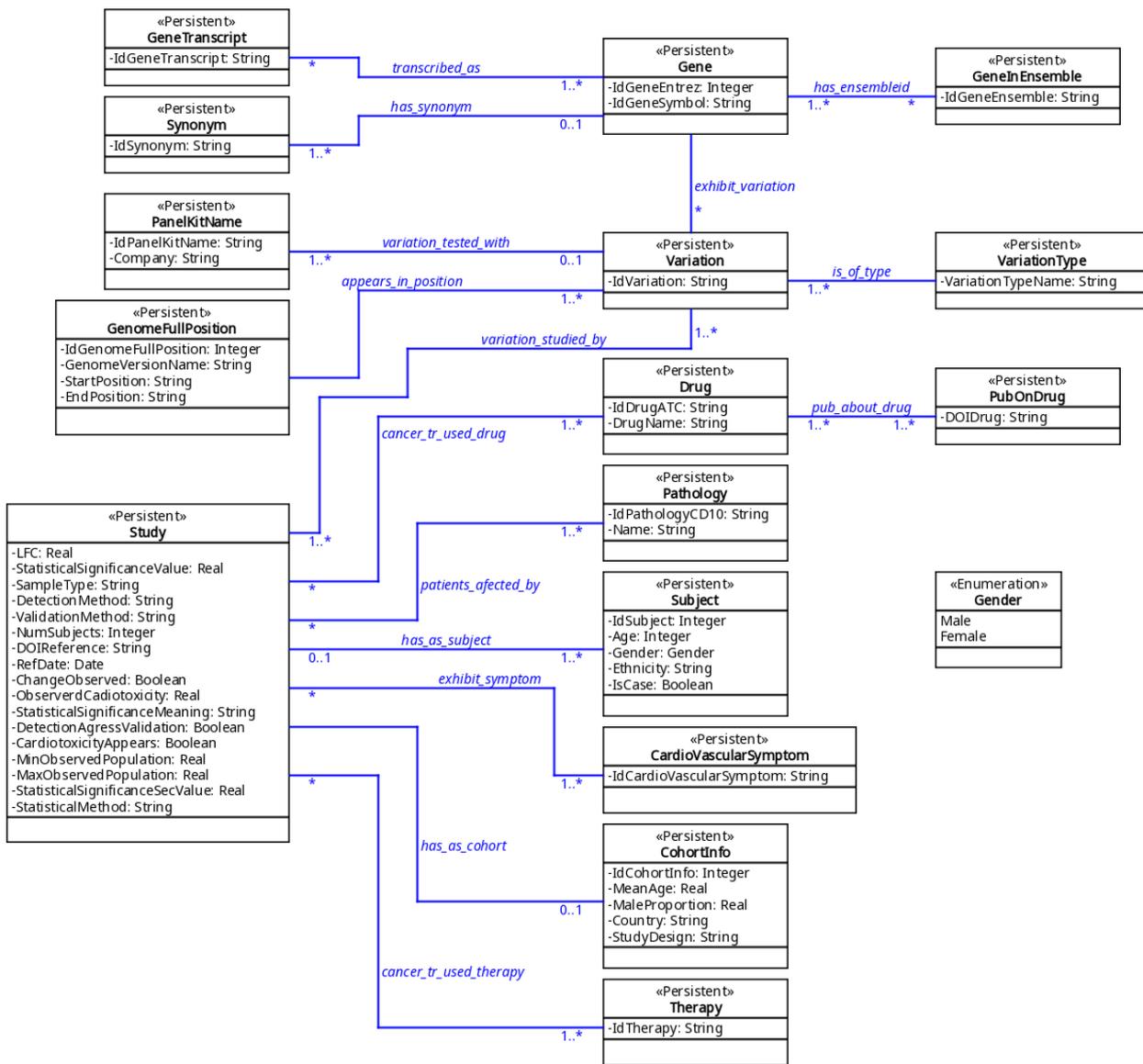


Figure 1: UML diagram of the database.

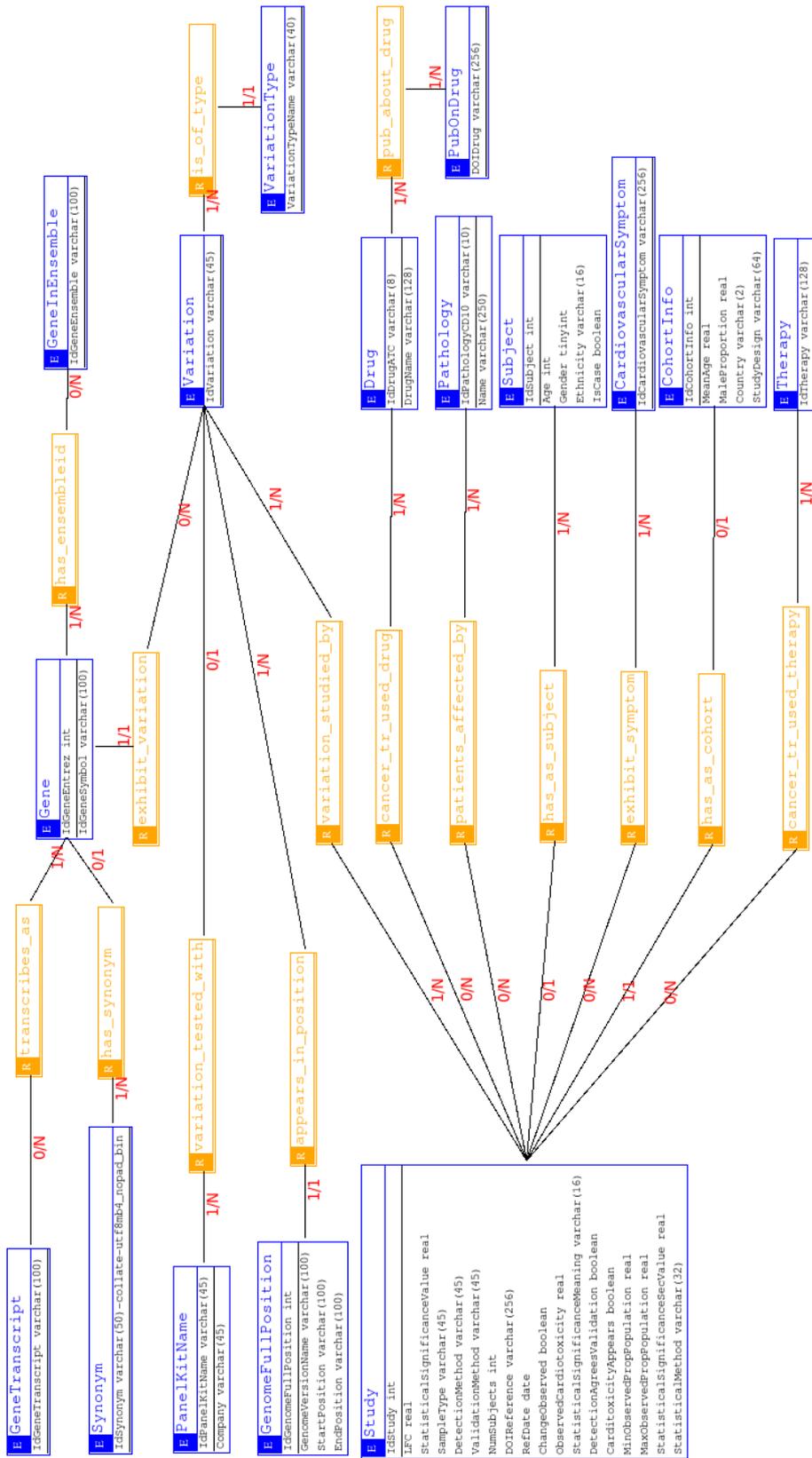


Figure 2: Proposed entity/relationship model.

3 Tables corresponding to entities

Object: **Gene**

| Identifier | Type | Meaning |
|--|--------------|---|
| IdGeneEntrez Primary key (NOT NULL). | INT | The gene identifier in the Entrez gene database (see Entrez). |
| IdGeneSymbol NOT NULL by choice. | VARCHAR(100) | The symbol used in the genetic notation for the gene. This field will always have a value since it has been tested that every Entrez identifier has an associated symbol. |

Object: **GeneInEnsemble**

| Identifier | Type | Meaning |
|--|--------------|--|
| IdGeneEnsemble Primary key (NOT NULL). | VARCHAR(100) | The gene identifier in the Ensemble gene database (see Ensemble). |

Object: **GeneTranscript**

| Identifier | Type | Meaning |
|--|--------------|--|
| IdGeneTranscript Primary key (NOT NULL). | VARCHAR(100) | The identifier of this transcript. It uses to be similar to the Ensemble designation for a gene, but with some letters changed and/or added. |

Object: **Synonym**

| Identifier | Type | Meaning |
|---|-------------|---|
| IdSynonym Primary key (NOT NULL). | VARCHAR(50) | The name of the synonym. |
| IdGeneEntrez NOT NULL by design. | INT | A reference to the Entrez id of the gene of which this object is a synonym. Notice that several synonyms can designate the same gene (i.e.: the same Entrez id) so this field may take repeated values in several rows. |

Object: **Variation**

| Identifier | Type | Meaning |
|---|-------------|--|
| IdVariation Primary key (NOT NULL). | VARCHAR(45) | The name used to designate this variation. It is standard, depending on the nature of the variation. |
| IdGeneEntrez Can be NULL | INT | The reference to the primary key of the gene this variation refers to. We assume that a variation manifests itself in only one gene, but it might be an intergenic variation, too, not associated to a particular gene. In that case this field would be NULL. |

| | | |
|--|-------------|---|
| VariationTypeName NOT NULL by design. | VARCHAR(40) | The reference to the variation type this variation belongs to. |
| IdGenomeFullPosition NOT NULL by design. | INT | The reference to the GenomeFullPosition object that contains the position in the genome at which this variation occurs. |

Object: **VariationType**

| Identifier | Type | Meaning |
|---|-------------|--|
| VariationTypeName Primary key (NOT NULL). | VARCHAR(40) | The type of the variation. Variants have a type which refers to its role in biological processes. Currently, 11 types are admitted: SNV, SNP, InDel, CNV, abundance proteins, differential expression, DNA methylation, RNA methylation, histone modifications, Post-translational modification and metabolites. Others could be added, if needed. |

Object: **PanelKitName**

| Identifier | Type | Meaning |
|--|-------------|---|
| IdPanelKitName Primary key (NOT NULL). | VARCHAR(45) | The name of the panel kit, as given by the company that manufactures it. |
| Company NOT NULL by choice. | VARCHAR(45) | The name of the company that manufactures this panel. |
| IdVariation NOT NULL by design. | VARCHAR(45) | The identifier of the variation whose expression is tested with this panel kit. |

Object: **GenomeFullPosition**

| Identifier | Type | Meaning |
|---|--------------|---|
| IdGnomeFullPosition Primary key (NOT NULL). | INT | A unique identifier for this position object. Unfortunately, it has to be arbitrary, since this table needs a primary key and none of its components can play such role. |
| GenomeVersionName NOT NULL by choice. | VARCHAR(100) | The name of this genome version, like GRCh37, as obtained either from USC or from Ensembl . There are consortia that update the human genome regularly. |
| StartPosition NOT NULL by choice. | VARCHAR(100) | The place in the sequence where this genome version starts in the version of reference genome expressed in the former field, like chr6:76,573,879. |
| EndPosition NOT NULL by choice. | VARCHAR(100) | The place in the sequence where this genome version ends in the version of reference genome expressed in the former field, as before. |

Object: **Pathology**

| Identifier | Type | Meaning |
|---|--------------|--|
| IdPathologyCD10 Primary key (NOT NULL). | VARCHAR(10) | The identifier for the pathology, as given by the ICD10 classification of 2021 (see IDC10). |
| Name NOT NULL by choice. | VARCHAR(200) | The CD10 name of the pathology. All codes in the CD10 table have a name, so this field will not be NULL. It can be ambiguous, so pathologies should be primarily identified by their CD10 codes. |

Object: **Drug**

| Identifier | Type | Meaning |
|---|--------------|---|
| IdDrugATC Primary key (NOT NULL). | VARCHAR(8) | A unique identifier for the drug according to the ATC (Anatomical Therapeutic Chemical Classification System). See ATC . |
| DrugName NOT NULL by choice. | VARCHAR(128) | The ATC drug name. All codes in the ATC table have a name, so this field will not be NULL. It can be ambiguous, so drugs should be primarily identified by their ATC codes. |

Object: **Study**

| Identifier | Type | Meaning |
|--|--------------|--|
| IdStudy Primary key (NOT NULL). | INT | A unique arbitrary identifier for an study. Differently to the other primary keys, this is completely arbitrary, since there is no standard or accepted way to give something like a “reference number” to the studies a research group decides to make. |
| StatisticalMethod NOT NULL by choice. | VARCHAR(32) | It refers to the statistical method with which the “StatisticalSignificanceMeaning” is obtained. For instance, t-test, Cox elastic net regression, general linear model, etc. When the method is not specified, the field takes as value “unspecified”. |
| StatisticalSignificanceMeaning NOT NULL by choice. | VARCHAR(16) | The way in which statistical significance of the experiment is expressed. It can only be one of these strings: BH (also incorrectly denoted as FDR), Bonferroni, OddsRatio or pVal. |
| StatisticalSignificanceValue NOT NULL by choice. | REAL | The value of the significance, expressed as stated in the field ‘StatisticalSignificanceMeaning’. |
| SampleType NOT NULL by choice. | VARCHAR(45) | The type of sample, such as blood, tissue, plaque, saliva, etc. |
| DetectionMethod NOT NULL by choice. | VARCHAR(45) | The detection method used. There includes all the massive ones like arrays and sequencing and also the specific ones like PCR, etc. as long as new methods when available. |
| ValidationMethod Can be NULL | VARCHAR(45) | The validation method used, that is, if a different technique is used to confirm that the results will be the same regardless of the biological technique used to obtain the data. If not used, this field takes as value “None”. |
| NumSubjects NOT NULL by choice. | INT | The number of subjects used for this study. |
| DOIReference NOT NULL by choice. | VARCHAR(256) | The DOI of the publication that reported this study. WARNING: Notice that this publication is not the same as those used in the PubOnDrug table. |
| RefDate NOT NULL by choice. | DATE | The date of the publication that reported this study, in format yyyy-mm-dd. |

| | | |
|--|---------|--|
| ChangeObserved NOT NULL by choice. | BOOLEAN | Boolean value to mark if the study has shown any change in the expression of affected cases vs. controls. |
| CarditoxicityAppears NOT NULL by design. | BOOLEAN | A mark to indicate if the drug analyzed in this study showed cardiotoxicity effects (TRUE) or not (FALSE). |
| ObservedCarditoxicity Can be NULL | REAL | The proportion (as a number in 0..1) of the total participants who manifested cardiotoxic effects. It can be NULL if either the former field is FALSE (no cardiotoxic effects have been observed) or the study does not give any value for this parameter. |
| DetectionAgreesValidation Can be NULL | BOOLEAN | In the case that a validation of the results (ValidationMethod) has been carried out, it is included if the results were concordant between both biological techniques, taking the value of TRUE. If the result was not in agreement or in the case that a validation has not been carried out, then the field takes the value of FALSE. |
| MinObservedPropPopulation Can be NULL | FLOAT | The lowest value of the proportion of the general population in which the effects associated to this study has been observed. Restriction: must be in [0..1]. NULL value means unknown or unspecified. |
| MaxObservedPropPopulation Can be NULL | FLOAT | The highest value of the proportion of the general population in which the effects associated to this study has been observed. If the available datum is not an interval but a single value both of these fields will have to be filled with the same value. Restriction: must be in [0..1] and must be \geq MinObservedPropPopulation. NULL value means unknown or unspecified. |

Object: **PubOnDrug**

| Identifier | Type | Meaning |
|---|--------------|---|
| DOIDrug Primary key (NOT NULL). | VARCHAR(256) | The DOI that points to a significant publication about a drug (the first of most important one about this drug and/or its use in this context). WARNING: This is not the same as the field used in the Variation and 'cancer_tr_used_drug' tables. Currently, this table is empty; to be filled in the future, if possible. |

Object: **Subject**

| Identifier | Type | Meaning |
|--|-------------|---|
| NumSubject Primary key (NOT NULL). | INT | An arbitrary integer number to designate each of the subjects that participated in the study. WARNING: Currently, this table is empty since studies do not use to provide detailed (disaggregated) information about each subject of the cohort. Nevertheless, is kept for the case any study would have done or would do it. |
| Age Can be NULL | INT | The age of this subject. |
| Gender Can be NULL | TINYINT | A number to identify the gender of this subject. |
| Ethnicity Can be NULL | VARCHAR(16) | An identifier of the race of this subject. |

| | | |
|---------------------------------------|---------|---|
| IsCase Can be NULL | BOOLEAN | A mark to indicate if this subject participated in the study as case (TRUE) or control (FALSE). |
| IdStudy NOT NULL by design. | INT | A reference to the identifier of the study this subject was part of. |

Object: **CohortInfo**

| Identifier | Type | Meaning |
|--|-------------|---|
| IdCohortInfo Primary key (NOT NULL). | INT | An arbitrary integer number to designate each of the cohorts associated to any study. |
| MeanAge Can be NULL | REAL | The mean age of the subjects who participated in the study. |
| MaleProportion Can be NULL | REAL | The proportion (as a number in 0..1) of the total participants who were males. Female proportion can be obtained as 1 minus this value. |
| StudyDesign Can be NULL | VARCHAR(64) | The study design used for the experiment. This field can take values such as: prospective cohort study, case-control study, etc. If it is not specified in the study, "Not included" is included. |
| Country Can be NULL | VARCHAR(2) | The country in which the study took place, using the international standard for country designation ISO 3166-1 |
| IdStudy NOT NULL by design. | INT | A reference to the identifier of the study this subject was part of. |

Object: **CardiovascularSymptom**

| Identifier | Type | Meaning |
|---|--------------|---|
| IdCardiovascularSymptom Primary key (NOT NULL). | VARCHAR(256) | The clinical denomination of a symptom that can be observed in the cardiovascular system due to the administration of a drug. |

Object: **Therapy**

| Identifier | Type | Meaning |
|---|--------------|---|
| IdTherapy Primary key (NOT NULL). | VARCHAR(128) | The name of a therapy used to treat a cancer. It can be one of these: chemotherapy,radiotherapy,targeted therapy,immunotherapy,surgery and hormonal, or any combination of them (so there will be up to 64 possibilities). It can also be none, indicating that no therapy was applied. |

4 Tables corresponding to relations between entities

Object: **has_ensembleid**

| Identifier | Type | Meaning |
|--|--------------|---|
| IdGeneEntrez Primary key (NOT NULL). | INT | An Entrez identifier for a gene (points to the homonymous field of table Gene). |
| IdGeneEnsemble Primary key (NOT NULL). | VARCHAR(100) | An Ensemble identifier for a gene (points to the homonymous field of table GeneInEnsemble). |

Object: **transcribes_as**

| Identifier | Type | Meaning |
|--|--------------|--|
| IdGeneTranscript Primary key (NOT NULL). | VARCHAR(100) | A reference to the transcript name (points to the homonymous field of table GeneTranscript). |
| IdGeneEntrez NOT NULL by design. | INT | A reference to the Entrez id of the transcript (points to the homonymous field of table Gene). |

Object: **pub_about_drug**

| Identifier | Type | Meaning |
|---|--------------|--|
| IdDrugATC Primary key (NOT NULL). | VARCHAR(8) | The identifier of a drug that is mentioned in a publication (points to the homonymous field of table Drug). |
| DOIDRUG Primary key (NOT NULL). | VARCHAR(256) | The DOI of the publication that first or most importantly mentions the drug whose ATC code is in this table. This relation arises from the fact that the Drugbank database contains multiple publications about each drug, and also a publication might appear in it repeated (i.e.: associated to more than one drug). |

Object: **variation_studied_by**

| Identifier | Type | Meaning |
|---|-------------|--|
| IdVariation Primary key (NOT NULL). | VARCHAR(45) | The identifier of a variation that is discovered by a study (points to the homonymous field of table Variation). |
| IdStudy Primary key (NOT NULL). | INT | The identifier of an study that has discovered a variation (points to the homonymous field of table Study). |

Object: **patients_affected_by**

| Identifier | Type | Meaning |
|---|------|---|
| IdStudy Primary key (NOT NULL). | INT | The identifier of a study that reports the patients to suffer from one or more pathologies (points to the homonymous field of table Study). |

| | | |
|---|-------------|---|
| IdPathologyCD10 Primary key (NOT NULL). | VARCHAR(10) | The ICD10 code of each of the pathologies that the study reports to have been observed in its cohort of subjects (points to the homonymous field of table Pathology). |
|---|-------------|---|

Object: **exhibit_symptom**

| Identifier | Type | Meaning |
|---|--------------|---|
| IdStudy Primary key (NOT NULL). | INT | The identifier of a study that reports the patients to exhibit one or more cardiovascular symptoms (points to the homonymous field of table Study). |
| IdCardiovascularSymptom Primary key (NOT NULL). | VARCHAR(256) | The identifier of each of the cardiovascular symptoms that the study reports to have been observed in its cohort of subjects (points to the homonymous field of table CardioVascularSymptom). |

Object: **cancer_tr_used_drug**

| Identifier | Type | Meaning |
|---|------------|---|
| IdStudy Primary key (NOT NULL). | INT | The identifier of a study that reports that the patients have suffered cancer and have been treated with some drug (points to the homonymous field of table Study). |
| IdDrugATC Primary key (NOT NULL). | VARCHAR(8) | The ATC identifier of a drug that was used to treat the cancer of the patients in the related study (points to the homonymous field of table Drug). |

Object: **cancer_tr_used_therapy**

| Identifier | Type | Meaning |
|---|--------------|---|
| IdStudy Primary key (NOT NULL). | INT | The identifier of a study that reports that the patients have suffered cancer and have been treated by the application of some therapy (points to the homonymous field of table Study). |
| IdTherapy Primary key (NOT NULL). | VARCHAR(128) | The therapy identifier (the therapy name) that was used to treat the cancer of the patients in the related study (points to the homonymous field of table Therapy). |

References

- [1] Marc Carlson. *org.Hs.eg.db: Genome wide annotation for Human*. R package version 3.13.0. 2021.
- [2] ICD10Data. *The Web's Free 2022 ICD-10-CM/PCS Medical Coding Reference*. 2021. URL: <https://www.icd10data.com/>.

- [3] Martin Morgan. *BiocManager: Access the Bioconductor Project Package Repository*. R package version 1.30.16. 2021. URL: <https://CRAN.R-project.org/package=BiocManager>.
- [4] WHO Collaborating Centre for Drug Statistics Methodology of Norway. *Guidelines for ATC classification and DDD assignment, 2021. Oslo, 2020*. 2021. URL: https://www.whocc.no/atc_ddd_index/.

Data on content of the OncoCardio database

Supplementary material 3 to the paper

”OncoCardioDB: A Public and Curated Database of Molecular Information in Onco-cardiology/Cardio-oncology”

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Total number of Entrez identifiers:

Asked query: SELECT COUNT(IdGeneEntrez) FROM Gene;

Result table:

| COUNT) |
|--------|
| 61548 |

Number of different Entrez identifiers that appear in any study:

Asked query: SELECT COUNT(DISTINCT Gene.IdGeneEntrez) FROM Gene,Variation,variation_studied_by WHERE Gene.IdGeneEntrez=Variation.IdGeneEntrez AND variation_studied_by.IdVariation=Variation.IdVariation;

Result table:

| COUNT |
|-------|
| 93 |

Gene Entrez identifiers that appear and their names ordered by number of occurrences

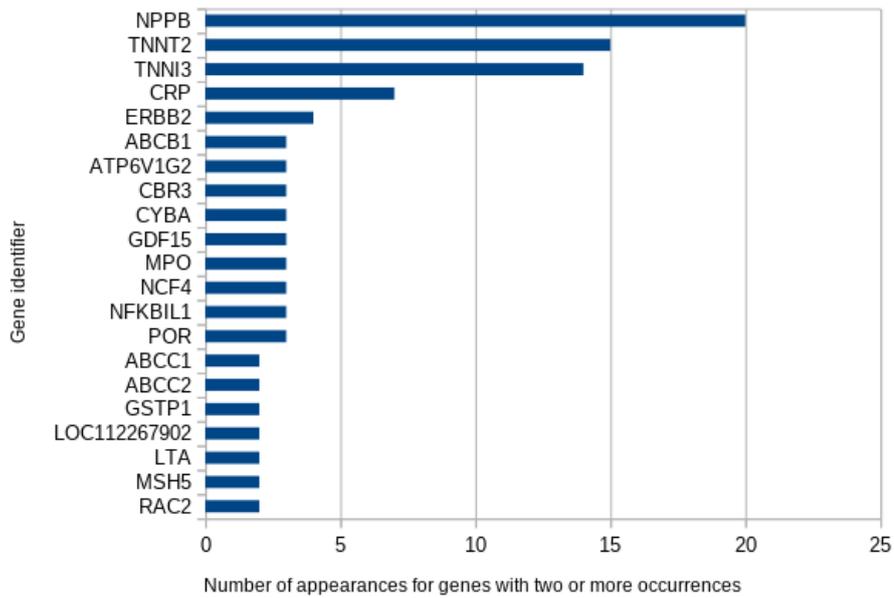
Asked query: SELECT Gene.IdGeneEntrez, Gene.IdGeneSymbol, COUNT(Gene.IdGeneEntrez) FROM Gene,Variation,variation_studied_by WHERE Gene.IdGeneEntrez=Variation.IdGeneEntrez AND variation_studied_by.IdVariation=Variation.IdVariation GROUP BY Gene.IdGeneEntrez ORDER BY COUNT(Gene.IdGeneEntrez) DESC;

Result table:

| IdGeneEntrez | IdGeneSymbol | COUNT) |
|--------------|--------------|--------|
| 4879 | NPPB | 20 |
| 7139 | TNNT2 | 15 |
| 7137 | TNNI3 | 14 |
| 1401 | CRP | 7 |
| 2064 | ERBB2 | 4 |
| 874 | CBR3 | 3 |

| IdGeneEntrez | IdGeneSymbol | COUNT) |
|---------------------|---------------------|---------------|
| 1535 | CYBA | 3 |
| 4689 | NCF4 | 3 |
| 5243 | ABCB1 | 3 |
| 9518 | GDF15 | 3 |
| 534 | ATP6V1G2 | 3 |
| 4353 | MPO | 3 |
| 4795 | NFKBIL1 | 3 |
| 5447 | POR | 3 |
| 1244 | ABCC2 | 2 |
| 2950 | GSTP1 | 2 |
| 4049 | LTA | 2 |
| 4363 | ABCC1 | 2 |
| 112267902 | LOC112267902 | 2 |
| 4439 | MSH5 | 2 |
| 5880 | RAC2 | 2 |
| 212 | ALAS2 | 1 |
| 355 | FAS | 1 |
| 383 | ARG1 | 1 |
| 1158 | CKM | 1 |
| 1668 | DEFA3 | 1 |
| 2167 | FABP4 | 1 |
| 2244 | FGB | 1 |
| 3106 | HLA-B | 1 |
| 3490 | IGFBP7 | 1 |
| 3569 | IL6 | 1 |
| 4282 | MIF | 1 |
| 4878 | NPPA | 1 |
| 5155 | PDGFB | 1 |
| 5327 | PLAT | 1 |
| 5834 | PYGB | 1 |
| 5919 | RARRES2 | 1 |
| 6347 | CCL2 | 1 |
| 6647 | SOD1 | 1 |
| 7035 | TFPI | 1 |
| 7097 | TLR2 | 1 |
| 7124 | TNF | 1 |
| 7364 | UGT2B7 | 1 |
| 7799 | PRDM2 | 1 |
| 10673 | TNFSF13B | 1 |
| 25794 | FSCN2 | 1 |
| 255738 | PCSK9 | 1 |
| 406904 | MIR1-1 | 1 |
| 406938 | MIR146A | 1 |
| 406967 | MIR192 | 1 |
| 406984 | MIR200B | 1 |
| 407040 | MIR34A | 1 |
| 693159 | MIR574 | 1 |
| 100126334 | MIR885 | 1 |
| 100507436 | MICA | 1 |

| IdGeneEntrez | IdGeneSymbol | COUNT) |
|---------------------|---------------------|---------------|
| 106480086 | RNU6-1186P | 1 |
| 240 | ALOX5 | 1 |
| 356 | FASLG | 1 |
| 1088 | CEACAM8 | 1 |
| 1241 | LTB4R | 1 |
| 1577 | CYP3A5 | 1 |
| 1669 | DEFA4 | 1 |
| 2109 | ETFB | 1 |
| 2214 | FCGR3A | 1 |
| 2246 | FGF1 | 1 |
| 3084 | NRG1 | 1 |
| 3339 | HSPG2 | 1 |
| 3497 | IGHE | 1 |
| 4000 | LMNA | 1 |
| 4151 | MB | 1 |
| 5228 | PGF | 1 |
| 5266 | PI3 | 1 |
| 6288 | SAA1 | 1 |
| 6368 | CCL23 | 1 |
| 6696 | SPP1 | 1 |
| 7040 | TGFB1 | 1 |
| 7099 | TLR4 | 1 |
| 7273 | TTN | 1 |
| 7450 | VWF | 1 |
| 9173 | IL1RL1 | 1 |
| 10665 | TSBP1 | 1 |
| 10850 | CCL27 | 1 |
| 58191 | CXCL16 | 1 |
| 406885 | MIRLET7C | 1 |
| 406913 | MIR126 | 1 |
| 406952 | MIR17 | 1 |
| 406982 | MIR20A | 1 |
| 406992 | MIR210 | 1 |
| 494327 | MIR378A | 1 |
| 693164 | MIR579 | 1 |
| 100507428 | LINC00458 | 1 |
| 105377364 | LOC105377364 | 1 |
| 107984727 | LOC107984727 | 1 |



Number of different variations that appear in any study

Asked query: SELECT COUNT(DISTINCT IdVariation) FROM variation_studied_by;

Result table:

| COUNT |
|-------|
| 107 |

Different variations that appear ordered by number of occurrences

Asked query: SELECT IdVariation, COUNT(IdVariation) from variation_studied_by GROUP BY IdVariation ORDER BY COUNT(IdVariation) DESC;

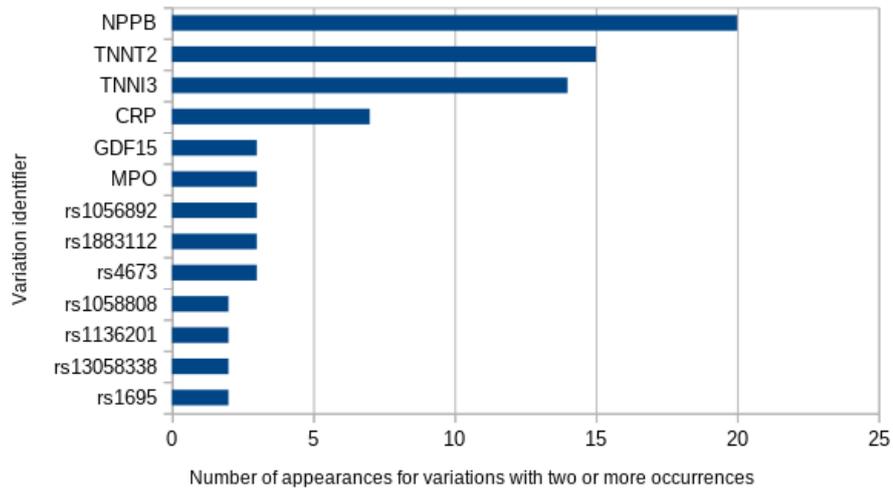
Result table:

| IdVariation | COUNT |
|-------------|-------|
| NPPB | 20 |
| TNNT2 | 15 |
| TNNI3 | 14 |
| CRP | 7 |
| rs1056892 | 3 |
| rs4673 | 3 |
| MPO | 3 |

| IdVariation | COUNT |
|--------------------|--------------|
| GDF15 | 3 |
| rs1883112 | 3 |
| rs1695 | 2 |
| rs1058808 | 2 |
| rs13058338 | 2 |
| rs1136201 | 2 |
| CCL2 | 1 |
| CKM | 1 |
| DEFA4 | 1 |
| FGB | 1 |
| IGFBP7 | 1 |
| let-7c | 1 |
| miR-146a-5p | 1 |
| miR-34a-5p | 1 |
| MIR1-1 | 1 |
| MIR579 | 1 |
| PCSK9 | 1 |
| PLAT | 1 |
| rs10127939 | 1 |
| rs11932853 | 1 |
| rs2050190 | 1 |
| rs2229109 | 1 |
| rs2523619 | 1 |
| rs3130059 | 1 |
| rs7668258 | 1 |
| rs8187710 | 1 |
| SAA1 | 1 |
| TGFB1 | 1 |
| ALAS2 | 1 |
| CCL23 | 1 |
| FABP4 | 1 |
| FGF1 | 1 |
| IGHE | 1 |
| LTB4R | 1 |
| miR-17-5p | 1 |
| MiR-378 | 1 |
| MIR126 | 1 |
| PDGFB | 1 |
| proANP | 1 |
| rs1041981 | 1 |
| rs17222723 | 1 |
| rs2071591 | 1 |
| rs2235047 | 1 |
| rs28415722 | 1 |
| rs3131378 | 1 |
| rs4732513 | 1 |
| rs776746 | 1 |
| rs909253 | 1 |
| SOD1 | 1 |

| IdVariation | COUNT |
|-------------------------------|--------------|
| TLR2 | 1 |
| ALOX5 | 1 |
| CCL27 | 1 |
| CXCL16 | 1 |
| FAS | 1 |
| IL1RL1 | 1 |
| MB | 1 |
| miR-192-5p | 1 |
| miR-574-3p | 1 |
| MIR20A | 1 |
| PGF | 1 |
| PYGB | 1 |
| rs1045642 | 1 |
| rs13240755 | 1 |
| rs1800629 | 1 |
| rs2071592 | 1 |
| rs246221 | 1 |
| rs2868177 | 1 |
| rs3131379 | 1 |
| rs7406710 | 1 |
| rs79338777 | 1 |
| rs9264942 | 1 |
| SPP1 | 1 |
| TLR4 | 1 |
| TTN:c.53918del (p.Gly17973fs) | 1 |
| ARG1 | 1 |
| CEACAM8 | 1 |
| DEFA3 | 1 |
| FASLG | 1 |
| HSPG2 | 1 |
| IL6 | 1 |
| MIF | 1 |
| miR-200b-3p | 1 |
| miR-885-5p | 1 |
| MIR210 | 1 |
| NRG1 | 1 |
| PI3 | 1 |
| RARRES2 | 1 |
| rs10484554 | 1 |
| rs11796 | 1 |
| rs1553265328 | 1 |
| rs2071594 | 1 |
| rs2523451 | 1 |
| rs3093949 | 1 |
| rs45511401 | 1 |
| rs7542939 | 1 |
| rs8032978 | 1 |
| rs9316695 | 1 |
| TFPI | 1 |

| IdVariation | COUNT |
|-------------|-------|
| TNFSF13B | 1 |
| VWF | 1 |



Total number of drugs stored in the database (by its ATC code and name)

Asked query: `SELECT COUNT(IdDrugATC) FROM Drug;`

Result table:

| COUNT |
|-------|
| 6460 |

Number of drugs which appear in any study

Asked query: `SELECT COUNT(IdDrugATC) FROM cancer.tr.used.drug`

Result table:

| COUNT |
|-------|
| 259 |

Number of different drugs which appear in any study

(This is different from the former one, since some studies mention many drugs).

Asked query: SELECT COUNT(distinct IdDrugATC) FROM cancer_tr_used_drug;

Result table:

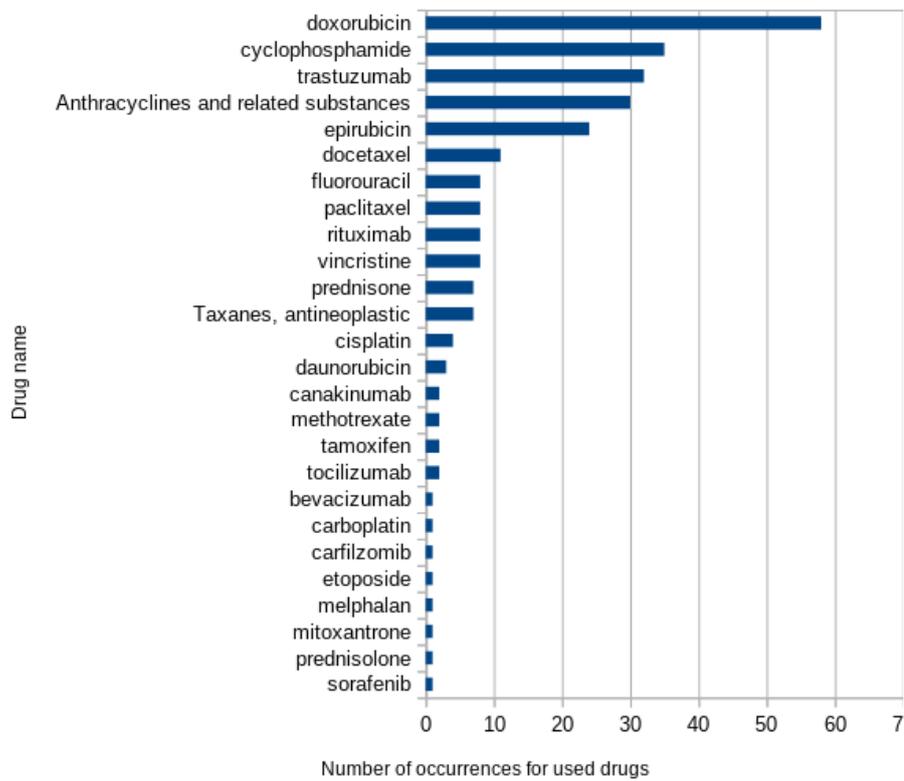
| COUNT |
|-------|
| 26 |

ATC codes and names of the drugs which are mentioned in any study, ordered by number of occurrences

Asked query: SELECT cancer_tr_used_drug.IdDrugATC,Drug.DrugName,COUNT(cancer_tr_used_drug.IdDrugATC) FROM cancer_tr_used_drug,Drug WHERE cancer_tr_used_drug.IdDrugATC=Drug.IdDrugATC GROUP BY cancer_tr_used_drug.IdDrugATC ORDER BY COUNT(cancer_tr_used_drug.IdDrugATC) DESC;

Result table:

| IdDrugATC | DrugName | COUNT |
|---|------------------|-------|
| L01DB01 | doxorubicin | 58 |
| L01AA01 | cyclophosphamide | 35 |
| L01XC03 | trastuzumab | 32 |
| L01DB Anthracyclines and related substances | | 30 |
| L01DB03 | epirubicin | 24 |
| L01CD02 | docetaxel | 11 |
| L01BC02 | fluorouracil | 8 |
| L01XC02 | rituximab | 8 |
| L01CD01 | paclitaxel | 8 |
| L01CA02 | vincristine | 8 |
| L01CD Taxanes, antineoplastic | | 7 |
| H02AB07 | prednisone | 7 |
| L01XA01 | cisplatin | 4 |
| L01DB02 | daunorubicin | 3 |
| L04AC07 | tocilizumab | 2 |
| L04AX03 | methotrexate | 2 |
| L02BA01 | tamoxifen | 2 |
| L04AC08 | canakinumab | 2 |
| L01XE05 | sorafenib | 1 |
| L01CB01 | etoposide | 1 |
| L01DB07 | mitoxantrone | 1 |
| L01AA03 | melphalan | 1 |
| L01XC07 | bevacizumab | 1 |
| L01XA02 | carboplatin | 1 |
| L01XX45 | carfilzomib | 1 |
| S03BA02 | prednisolone | 1 |



Total number of diseases (pathologies) stored in the data base (by its ICD10 code and name)

Asked query: `SELECT COUNT(IdPathologyCD10) FROM Pathology;`
 Result table:

| COUNT |
|-------|
| 46564 |

Number of different pathologies mentioned in any study

Asked query: `SELECT COUNT(IdPathologyCD10) FROM patients_affected_by;`
 Result table:

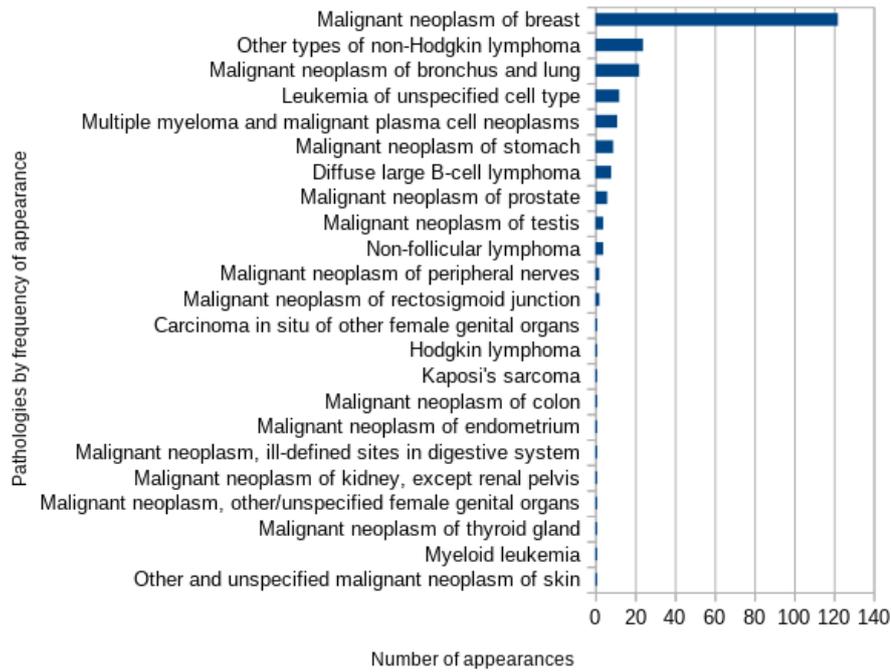
| COUNT |
|-------|
| 237 |

Pathologies that appear in any study, ordered by its number of occurrences

Asked query: SELECT patients_affected_by.IdPathologyCD10,Pathology.Name,COUNT(patients_affected_by.IdPathologyCD10)
 FROM patients_affected_by,Pathology WHERE patients_affected_by.IdPathologyCD10=Pathology.IdPathologyCD10
 GROUP BY patients_affected_by.IdPathologyCD10 ORDER BY COUNT(patients_affected_by.IdPathologyCD10)
 DESC;

Result table:

| IdPathologyCD10 | Name | COUNT |
|-----------------|--|-------|
| C50 | Malignant neoplasm of breast | 122 |
| C85 | Other specified and unspecified types of non-Hodgkin lymphoma | 24 |
| C34 | Malignant neoplasm of bronchus and lung | 22 |
| C95 | Leukemia of unspecified cell type | 12 |
| C90 | Multiple myeloma and malignant plasma cell neoplasms | 11 |
| C16 | Malignant neoplasm of stomach | 9 |
| C83.3 | Diffuse large B-cell lymphoma | 8 |
| C61 | Malignant neoplasm of prostate | 6 |
| C62 | Malignant neoplasm of testis | 4 |
| C83 | Non-follicular lymphoma | 4 |
| C19 | Malignant neoplasm of rectosigmoid junction | 2 |
| C47 | Malignant neoplasm of peripheral nerves and autonomic nervous system | 2 |
| C57 | Malignant neoplasm of other and unspecified female genital organs | 1 |
| C26.9 | Malignant neoplasm of ill-defined sites within the digestive system | 1 |
| C92 | Myeloid leukemia | 1 |
| C44 | Other and unspecified malignant neoplasm of skin | 1 |
| C64 | Malignant neoplasm of kidney, except renal pelvis | 1 |
| C46 | Kaposi's sarcoma | 1 |
| C73 | Malignant neoplasm of thyroid gland | 1 |
| D07.3 | Carcinoma in situ of other and unspecified female genital organs | 1 |
| C81 | Hodgkin lymphoma | 1 |
| C18 | Malignant neoplasm of colon | 1 |
| C54.1 | Malignant neoplasm of endometrium | 1 |



Number of different cardiovascular symptoms which appear in any study

Asked query: `SELECT COUNT(DISTINCT IdCardiovascularSymptom) FROM exhibit_symptom;`
 Result table:

| COUNT |
|-------|
| 42 |

Number of different cardiovascular symptoms which appear in any study ordered by number of occurrences

Asked query: `SELECT IdCardiovascularSymptom,COUNT(IdCardiovascularSymptom) FROM exhibit_symptom GROUP BY IdCardiovascularSymptom ORDER BY COUNT(IdCardiovascularSymptom) DESC;`
 Result table:

| IdCardiovascularSymptom | COUNT |
|--|-------|
| decline in left ventricular ejection fraction (LVEF) | 125 |
| heart failure | 30 |
| arrhythmia | 15 |
| congestive hearth failure | 13 |
| congestive heart failure | 11 |

| | IdCardiovascularSymptom | COUNT |
|---|--|--------------|
| | cardiac arrest | 7 |
| | fatal arrhythmia | 7 |
| | acute coronary artery syndrome | 7 |
| | coronary syndrome | 7 |
| | myocardial injury | 5 |
| | hypertension | 4 |
| | atherosclerosis | 4 |
| | atrial fibrillation | 3 |
| | systolic dysfunction | 3 |
| | myocardial fibrosis | 2 |
| | decline in peak filling rate | 2 |
| | myocardial infarction | 2 |
| | cardiac failure | 2 |
| tricuspid annular plane systolic excursion (TAPSE) decrease greater or equal than 15% | cardiovascular death | 2 |
| | myocytolysis | 2 |
| | nonfatal myocardial infarction | 2 |
| | nonfatal stroke | 2 |
| | patched myocardial necrosis | 2 |
| | coronary heart disease | 2 |
| | cancer therapy-related cardiac dysfunction (CTRCD) | 2 |
| | myocardial damage | 2 |
| | target lesion revascularization | 1 |
| | cardiac biomarkers | 1 |
| | total cardiovascular events | 1 |
| | dilated cardiomyopathy | 1 |
| abnormal values of parameters of heart and left ventricle | change in left ventricular diastolic diameter (LVDD) | 1 |
| | change in ventricular mass | 1 |
| | high diastolic and systolic diameter | 1 |
| | higher systolic diameter | 1 |
| | arterial hypertension | 1 |
| | subclinical myocardial damage | 1 |
| | coronary artery disease | 1 |
| | left ventricular dysfunction | 1 |
| | symptomatic congestive hearth failure | 1 |
| | lower fractional shortening | 1 |

Number of different therapies (considering combined therapies) that appear in any study

Asked query: SELECT COUNT(DISTINCT IdTherapy) FROM cancer_tr_used_therapy;

Result table:

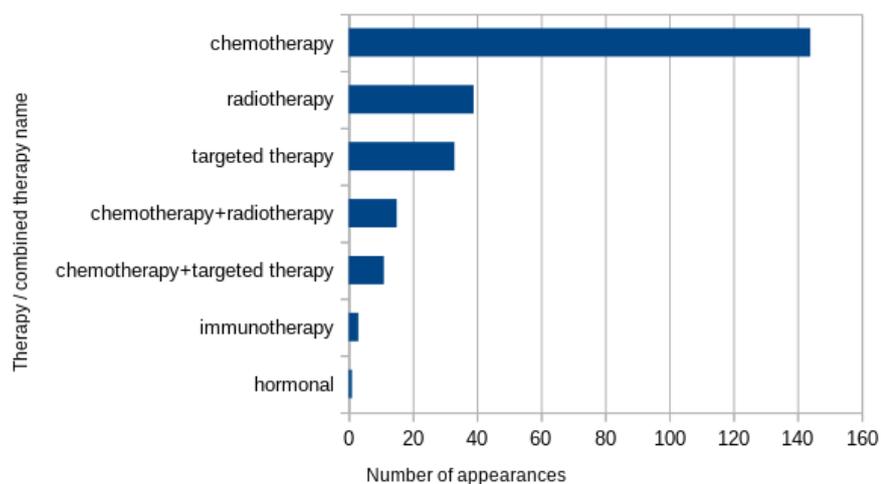
| COUNT |
|-------|
| 7 |

Number of different therapies (considering combined therapies) that appear, ordered by number of occurrences

Asked query: SELECT IdTherapy,COUNT(Idtherapy) FROM cancer_tr_used_therapy GROUP BY IdTherapy ORDER BY COUNT(IdTherapy) DESC;

Result table:

| IdTherapy | COUNT |
|-------------------------------|-------|
| chemotherapy | 144 |
| radiotherapy | 39 |
| targeted therapy | 33 |
| chemotherapy+radiotherapy | 15 |
| chemotherapy+targeted therapy | 11 |
| immunotherapy | 3 |
| hormonal | 1 |



SQL generation and data curation of Oncocardio DB. Page 1 of 3

This is the basic workflow to create the SQL tables for Oncocardio, as long as the SQL sentences to populate them from appropriately curated information.

Directory BASIC_SQL contains the SQL macro for the creation of the tables. This may have been created manually or generated with any program from the entity/relationship diagram. In our case it will be called DBOnco.sql.

The next of the steps described here is done automatically by the script recreate.sh. Nevertheless, it is described here for anyone interested in reproducing the methodology with a different database

From now on, -> is the Unix/Linux prompt so

```
-> ./recreate.sh
```

does everything. Nevertheless, and to explain each step:

0) This script needs to have some software installed. Namely:

- *) R with package stringr and package org.Hs.eg.db from Bioconductor. To install it, from the R prompt do:

```
install.packages(stringr)
```

```
if (!require("BiocManager", quietly = TRUE))
```

```
  install.packages("BiocManager")
```

```
BiocManager::install("org.Hs.eg.db")
```

- *) A recent Perl version with packages perl-List-MoreUtils, perl-Scalar-Util-LooksLikeNumber and perl-Algorithm-Combinatorics

1) Remove all the .sql files in the current folder to be sure all will be reconstructed

```
-> rm -f *.sql
```

2) The file generated automatically by your program to build the SQL script from the table diagrams or E/R diagram may need some minimal corrections related with SQL dialects. In our case this is done by the macro CorrectTable.pl applied as

```
-> ./CorrectTable.pl BASIC_SQL/DBOnco.sql
```

3) Generate the .sql to drop tables (dropall.sql) based on the .sql to create them using the script DB2drop.pl. This script needs the files doall.sql and delete_all_studies.sql

```
-> ./DB2drop.pl DBOnco.sql
```

4) Other two .sql files will be needed. These are static and only have to be copied from the BASIC_SQL folder:

```
cp BASIC_SQL/doall.sql .
```

```
cp BASIC_SQL/delete_all_studies.sql .
```

5) Clean all the database and fill the part of it that depends on "static" knowledge. This will be done by the SQL script doall.sql, which:

- + Calls to dropall.sql to erase the relevant tables (if any)

- + Calls to DBOncol.sql to create the empty tables

- + Calls to ten .sql scripts of the form Fill...sql that must be generated. To do so:

5.1) Go to directory EXTRACT and execute ./dogenotables.sh to generate .sql related with tables of genes (Gene, Transcript, Synonym, etc.)

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```
-> cd EXTRACT
-> rm -f *.sql
-> R --no-save < dogenatables.R
-> mv -f *.sql ../
-> cd ..
```

Since the information for the gene databases is taken from public databases using R packages, R must be installed in your system including the packages `org.Hs.eg.db` and `stringr` (used by the R macro `FillTables.R`). The first of them, in turn, requires packages `AnnotationDbi`, `stats4`, `BiocGenerics` and `parallel` which in turn need `Biobase`, `IRanges` and `S4Vectors`.

5.2) Go to directory `GENSQL` and execute `./dotables.sh` to generate `.sql` related with the tables `Drug`, `Pahtologies` and `Therapies`. They need the text files `ATCsimp.csv` and `icd10cm_order_2021.txt`, extracted or downloaded from the corresponding sites, and the perl macros build to generate the correct SQL sentences:

```
-> cd GENSQL
-> rm -f *.sql
-> ./FillDrug.pl ATCsimp.csv
-> ./FillTherapy.pl
-> ./FillPathology.pl icd10cm_order_2021.txt
-> ./FillVariationType.pl
-> mv -f *.sql ../
-> cd ..
```

5.3) Fill all tables which contain the actual data from studies by creating the `.sql` scripts from the `.csv` file filled manually from the papers describing the studies. This file is `data.csv` in directory `FILL_FROM_CSV`

Since most people prefer to work with spreadsheets in Excel format, `.xlsx` can be used too to contain the information but must be exported to `.csv` at the end. If you do so from LibreOffice the parameters for `.csv` export should be:

```
Character set: Unicode (TUF-8)
Field delimiter: (a blank space)
String delimiter: " (the double quote)
Save cell content as show: UNmarked
Save cell formulas instead of calculated values: UNmarked
Quote all text cells: Marked <--
Fixed column width: UNmarked
```

The perl macro `FILL_FROM_CSV/FillFromPapers.pl` will generate the `.sql` scripts from `data.csv`. It needs the text file `fields.csv` to check field names. The rationale for data curation and actual algorithm to generate the `.sql` sentences are described in file `FILL_FROM_CSV/filling_algorithm.txt`. Actual generation must be done as:

```
-> cd FILL_FROM_PAPERS
-> ./FillFromPapers.pl data.csv fill_all_studies.sql > inform.txt
-> mv -f *.sql ../
```

This generates a file (`inform.txt`) which contains two parts: the syntactic analysis (to verify that each field has a legal data type: number, boolean, string..) and that fields with restricted values have legal values (for instance: all pathologies are listed in the ICD10 list, all drugs are included in the ATC list, and so on).

6) Next we need to create the database and introduce all the information in it. According to your configuration you should run MySQL and have access to the database prompt. Assuming you have created a database named `oncocardio` you should be able to access the SQL console as

```
mysql --silent -u oncocardio -p oncocardio
```

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At the SQL prompt execute:

```
MariaDB [oncocardio]> source doall.sql;  
MariaDB [oncocardio]> source fill_all_studies.sql;
```

If, later on, you want to keep the static tables and fill only the variable part (studies), for example when you have added more studies, just do

```
MariaDB [oncocardio]> source delete_all_studies.sql;  
MariaDB [oncocardio]> source fill_all_studies.sql;
```

Using the OncoCardio database with a different domain

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This guide is intended for system administrators who want to run the oncoCardio database with the purpose of reproducibility or to get inspiration to build a similar system with a different database.

The simplest way to test the system is to use it by running the virtual machine we provide. It is a .vmdk disk image file that can be run with VMWare (either Player or Workstation) or with qemu/KVM. From now on, the virtual machine that is run in that way will be called the 'virtual server'.

Step 1 : Choose and register a machine name.

First, you will have to choose a virtual host name (in our case it was 'biodb') so the virtual server will be `yourname.your.domain` (in our case, `biodb.uv.es`). Ask your system administrators for an IP to be assigned to it. If you plan to configure the network of the virtual server by DHCP, generate randomly a MAC (but take note of it) and deliver it to your network administrators that will associate it to the new IP.

Step 2 : Prepare network in real host.

Network configuration has been thought to run the virtual server in a real machine with two or more network cards using one of them as a dedicated network interface for the virtual server. This is to prevent conflicts and to assign more easily a different IP number and domain to the virtual server.

The network interface intended to be used for the virtual server must be left untouched by the host (the real machine). To do so:

If you use NetworkManager : prevent NetworkManager from using such card. Directions to do so can be found for example in <https://support.qacafe.com/knowledge-base/how-do-i-prevent-network-manager-from-controlling-an-interface/>

If you do not use NetworkManager :

- a) In Fedora/Rocky Linux/Redhat: do not add a `/etc/sysconfig/ifcfg-<interface>` for that interface.
- b) In Debian/Ubuntu: Alter the `/etc/network/interfaces` according to the directions in <https://wiki.debian.org/NetworkConfiguration>

Step 3 : Create a virtual machine.

Now create a virtual machine with VMPlayer or qemu/KVM (with `virt-manager`). We recommend to assign it either one or two virtual CPUs, and about 2GB of RAM. The operating system obviously must not be installed since it is already installed, together with all the needed software, in the .vmdk image we provide (if VMWare asks for the version, it is a Fedora 32). This virtual disk is to be set as primary (and probably only) disk of the first virtual SATA interface.

The only detail to be specially changed in the creation of the virtual machines is the network configuration:

For creation with virt-manager : set as network source a "Macvtap device" and as device name, the name the host gives to the dedicated network card (in our case, it was `enp3s0` but find it with command `ip link show` or `ifconfig -a`). If you plan to boot the virtual server with dhcp, edit the XML and alter the MAC of this virtual interface to match the one your DHCP server expects. More information on this can be found in <https://linuxconfig.org/how-to-use-bridged-networking-with-libvirt-and-kvm>

For creation using VMWare : mark the network adapter of the virtual machine as 'Connect at power on' and 'Bridged' and, in the 'Advanced' part of the network configuration, set the MAC to the one expected by your DHCP server if you plan to use dhcp.

Step 4 : Virtual machine boot configuration (change of name and domain).

Now, boot the virtual server. It boots in multi-user mode (runlevel 3, no graphical interface). Log in as `root`, with password `oncocardiopwd`. Change the root password if you wish with command `passwd`.

From now on, all commands must be executed as the superuser (`root`).

Step 4a : Virtual DHCP network configuration.

The virtual server is currently prepared to boot and start the network using DHCP, so if you have used that and asked for a new IP, the IP should have been assigned as long as the machine name.

Step 4b : Alternative manual network configuration

If you do not use DHCP and prefer to configure the virtual host network manually, execute these commands:

```
cd /etc/sysconfig/network-scripts/  
cp ./tmp/ifcfg-ens1 ./  
nano ifcfg-ens1
```

This will open an editor to change the network configuration file. Only the values for `HWADDR`, `IPADDR`, `NETMASK` and `GATEWAY` should be altered with the correct values that you will have to ask to your network administrator (except the `HWADDR`, that must be the one you chose as MAC when creating the virtual machine). Finally, edit the file `/etc/hostname` and write there your machine name and domain.

After this, execute

```
systemctl stop NetworkManager  
systemctl disable NetworkManager  
systemctl restart network
```

Step 5 : Network check.

Whatever the way you have configured the network, you can check that it is working with commands

```
systemctl status network (which should inform of 'running' status)
systemctl status NetworkManager (as the previous)
ip addr show (which should show the MAC and IP address assigned to the network interface)
hostname (which should show the name of the machine)
hostname -d (which should show the domain of the machine)
hostname -i (which should show the IP address that must coincide with the one shown by the
ip command before)
```

Step 6 : Acquisition of certificates.

To be able to operate in secure mode (encrypted hypertext transfer protocol, or https) you need to obtain the TLS certificates recognized by an external validation authority. Currently, Let's Encrypt (a nonprofit certificate authority ruled by the Internet Security Research Group) provides such certificates for free. Details on the procedure to set up can be found in <https://certbot.eff.org/instructions>.

Nevertheless, the provided virtual server has already installed the software to get and update such certificates. You only have to execute command

```
certbot certonly --nginx
```

and answer the questions about your server name, domain and organization. This will create the folder `/etc/letsencrypt/live/<your-server-name>` containing four files (in fact, symbolic links to files with the same name in `/etc/letsencrypt/archive/<your-server-name>`) named `cert.pem`, `chain.pem`, `fullchain.pem` and `privkey.pem`.

Step 7 : Setting up the server.

Now, edit the file `/etc/nginx/nginx.conf` and replace all references to `biodb.uv.es` by your virtual server name-domain. It appears five times, in lines which currently say

```
server_name biodb.uv.es;
ssl_certificate /etc/letsencrypt/live/biodb.uv.es/fullchain.pem; # managed by Certbot
ssl_certificate_key /etc/letsencrypt/live/biodb.uv.es/privkey.pem; # managed by Certbot
if ($host = biodb.uv.es)
server_name biodb.uv.es;
```

Step 8 : Generate internal certificates.

Use the newly obtained certificates to generate the certificates for the internal tomcat server. To do so, the commands are (substitute `yourserver.your.domain` by you particular value and `oncardiopwd` by any password you choose. We suggest to use the same as for the root password of the virtual server):

```
cd /etc/certs/yourserver.your.domain
openssl pkcs12 -export -in fullchain.pem -inkey privkey.pem -out server.p12 \
-name tomcat
```

```
keytool -importkeystore -deststorepass oncardiopwd -destkeypass oncardiopwd \  
-destkeystore /etc/tomcat/fkeystore.jks -srckeystore server.p12 \  
-srcstoretype PKCS12 -srcstorepass oncardiopwd -alias tomcat \  
rm server.p12
```

where the symbol \`\` at the end of a line means 'follows in the same line'.

Step 9 : Update references to new server name.

Some configuration files must be changed to refer to your new host/domain name. In particular:

Substitute the references to `biodb.uv.es` by your server and domain in the following files:

```
/home/dist/ocserv.js (several references)  
/etc/tomcat/server.xml (just one reference in line keystoreFile="/etc/tomcat/biodb.jks")
```

and change appropriately according to your preferences the file

```
/etc/oncardio/mailtext
```

which is the text sent by mail to the user when they receive their results attached.

Also, change and the file

```
background.png
```

which is the background the users see in the oncardio screen.

Step 10 : Reboot

Just reboot the virtual machine with command `reboot`. Then you should be able to use a browser to access by `https` to your domain. The oncardio database should work in your domain.