UBC01 Transformation Documentation

UBC01 has two transformations, one for case centric data (enrollment) and one for sample data. The input files for these transformations can be found in Box at <https://nih.app.box.com/folder/117852979155>.

The transformations map the columns from the input files to node.properties in the database. Mappings can be one-to-one (i.e., one column in the input file maps to a single node.property), or many-to-one (i.e., two or more columns in the input file are concatenated to map to a single node.property). In addition some columns map the values in the input file to a set of accepted values in the database for the given node.property.

# Case Transformation

## Case Node Mappings

|  |  |  |  |
| --- | --- | --- | --- |
| **PROPERTY** | **MAPPING** | **VALUE MAPPING FROM** | **VALUE MAPPING TO** |
| case\_id | Study Code + "-" + Patient ID |  |  |
| patient\_id | Patient ID |  |  |

## Demographic Node Mappings

|  |  |  |  |
| --- | --- | --- | --- |
| **PROPERTY** | **MAPPING** | **VALUE MAPPING FROM** | **VALUE MAPPING TO** |
| breed | Breed |  |  |
| patient\_age\_at\_enrollment | Age at Registration |  |  |
| date\_of\_birth | Date of Birth |  |  |
| sex | Sex (M,F, or U) |  |  |
| weight | Body Weight at Start of Vemurafenib (kg) |  |  |
| neutered\_indicator | Neutered Status Indicator (Y,N, U) |  |  |

## Diagnosis Node Mappings

|  |  |  |  |
| --- | --- | --- | --- |
| **PROPERTY** | **MAPPING** | **VALUE MAPPING FROM** | **VALUE MAPPING TO** |
| disease\_term | Diagnosis |  |  |
| primary\_disease\_site | Disease Site General Location |  |  |
| stage\_of\_disease | Stage of Disease at Start of Vemurafenib |  |  |
| date\_of\_diagnosis | Date of Diagnosis |  |  |
| best\_response | Best Tumor Response |  |  |
| treatment\_data | Treatment Outcome Available |  |  |
| follow\_up\_data | Follow-up Available |  |  |
| concurrent\_disease | Concurrent Disease |  |  |
| concurrent\_disease\_type | Concurrent Disease Type |  |  |

## Enrollment Node Mappings

|  |  |  |  |
| --- | --- | --- | --- |
| **PROPERTY** | **MAPPING** | **VALUE MAPPING FROM** | **VALUE MAPPING TO** |
| date\_of\_registration | Date of Registration |  |  |
| site\_short\_name | Study site |  |  |
| cohort\_description | Cohort Description |  |  |

## Additional Mappings

In addition, we include some extra columns to the transformed files. These columns are used by the data loader.

|  |  |
| --- | --- |
| **NODE.PROPERTY** | **MAPPING** |
| study.clinical\_study\_designation | Study Code |
| cohort.cohort\_description | Cohort Description |
| enrollment\_id | Study Code + "-" + Patient ID |
| diagnosis\_id | Study Code + "-" + Patient ID |

## Input Columns Not Used

Submitters sometimes include columns with data that are not going to be included in our database. We leave these columns in the input file, but the transformation ignores them. For the case input file, these columns include:

* Study Arm
* Cohort (Dose Group - 1=25mg/kg; 2=50mg/kg; 3=37.5mg/kg
* Actual Dose (mg/kg)
* Stage of Disease at Diagnosis
* More Specific Tumor Location
* Tumor Size (cm3)
* Age at Diagnosis
* Supplementary Data Files

# Sample Transformation

## Sample Node Mappings

|  |  |  |  |
| --- | --- | --- | --- |
| **PROPERTY** | **MAPPING** | **VALUE MAPPING FROM** | **VALUE MAPPING TO** |
| sample\_id | Study Code + “-“ + Sample ID |  |  |
| sample\_site | Sample Site |  |  |
| physical\_sample\_type | Sample Type |  |  |
| general\_sample\_pathology | General Sample Pathology |  |  |
| tumor\_sample\_origin | Tumor Sample Origin |  |  |
| summarized\_sample\_type | Sample Type + “;” + General Sample Pathology + “;” + Tumor Sample Origin |  |  |
|  |  | Tissue;Normal;Not Applicable | Normal Tissue |
|  |  | Tissue;Malignant;Primary | Primary Malignant Tumor Tissue |
| specific\_sample\_pathology | Specific Sample Pathology |  |  |
| date\_of\_sample\_collection | Sample Collection Date |  |  |
| sample\_chronology | Sample Aquisition Timing (Before Treatment, During Treatment, Upon Relapse in Vemurafenib Trial) |  |  |
| necropsy\_sample | Necropsy Sample: N=NO, Y=YES |  |  |
| percentage\_tumor | Percent Tumor |  |  |
| tumor\_grade | Grade (1-4 With 4 Being Highest Grade) |  |  |
| sample\_preservation | Sample Preservation Method |  |  |

## Additional Mappings

In addition, we include some extra columns to the transformed files. These columns are used by the data loader.

|  |  |
| --- | --- |
| **NODE.PROPERTY** | **MAPPING** |
| case.case\_id | Study Code + "-" + Patient ID |

## Input Columns Not Used

All input columns were used in UCB01.