# TCGA2BED

## User Guide

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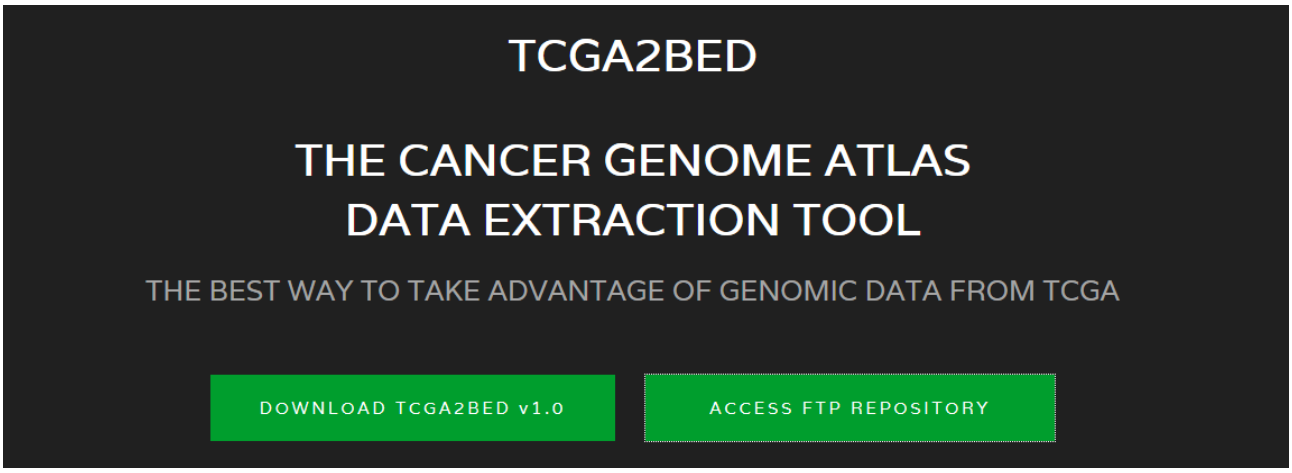


# Contents

# Introduction

This user guide is intended for all the users that want to learn how to use the TCGA2BED tool for downloading and converting TCGA data into the BED format. Please refer also to the `TCGA2BED_readme.txt` file (that is included in the software package) for additional details.

# TCGA2BED procedure steps

The following steps are necessary to perform the download of public TCGA data and their conversion into the BED format. These steps are thoroughly explained in the following sections of this tutorial:

1. Meta data download;
2. Experimental data download;
3. Conversion into the BED format.

# Installation

## JAVA

The TCGA2BED tool requires a working JAVA Virtual Machine (VM) installed. Thus, if not done yet, first download and install the free Oracle JAVA Runtime Environment from http://www.java.com/getjava/.
Several versions for the most common operating systems are available (e.g., Windows x86 for Windows 32 bit, Windows x64 for Windows 64 bit, MacOsX, or Linux). Please choose the right version according to your operating system.

## TCGA2BED

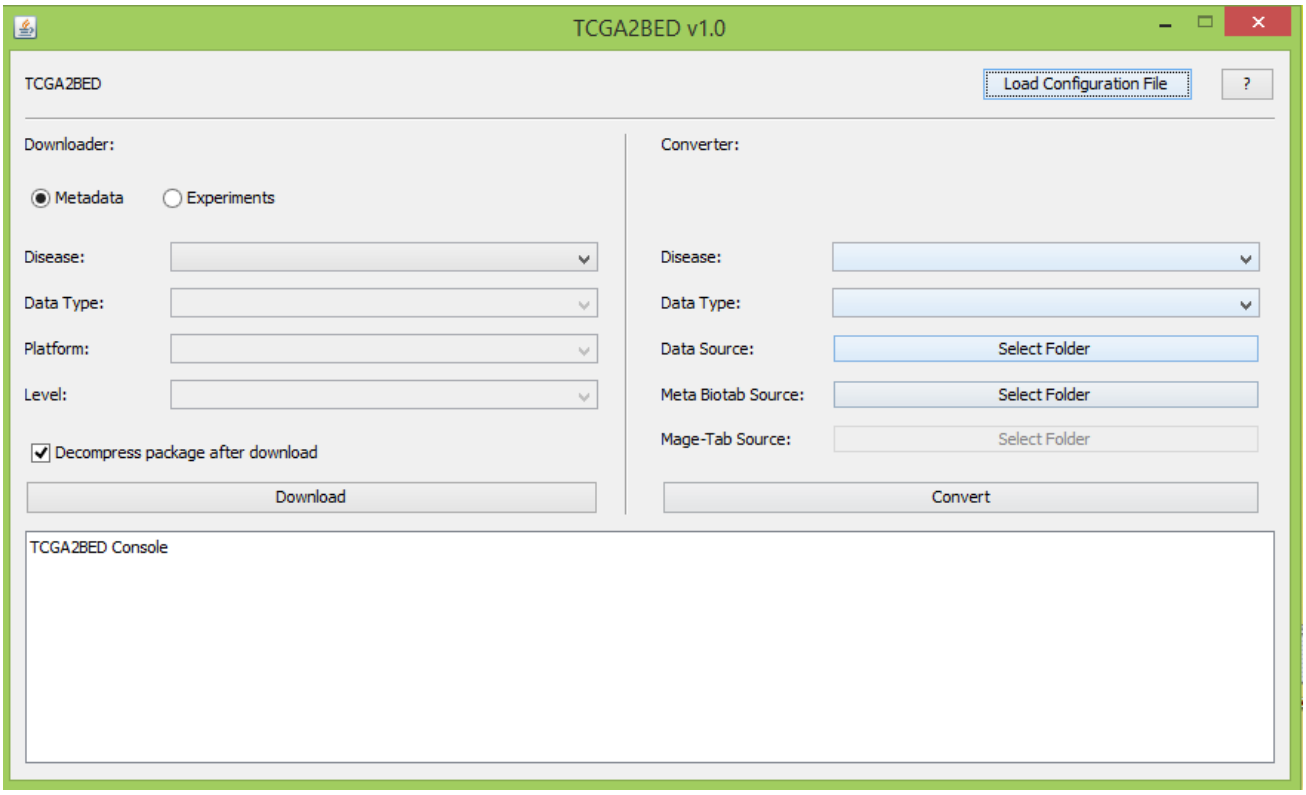
You can download and unzip the multi-platform (Windows, Linux and MacOS) Java software TCGA2BED from http://bioinf.iasi.cnr.it/tcga2bed/ ("TCGA2BED-v1.0.zip"), that allows to retrieve TCGA data and convert them into the BED format.

# Executing TCGA2BED

Go to the directory where you extracted the TCGA2BED archive and execute TCGA2BED.jar by double clicking it (for supported operating systems) or by executing the following command from a prompt: `java -jar TCGA2BED.jar`

## Start screen

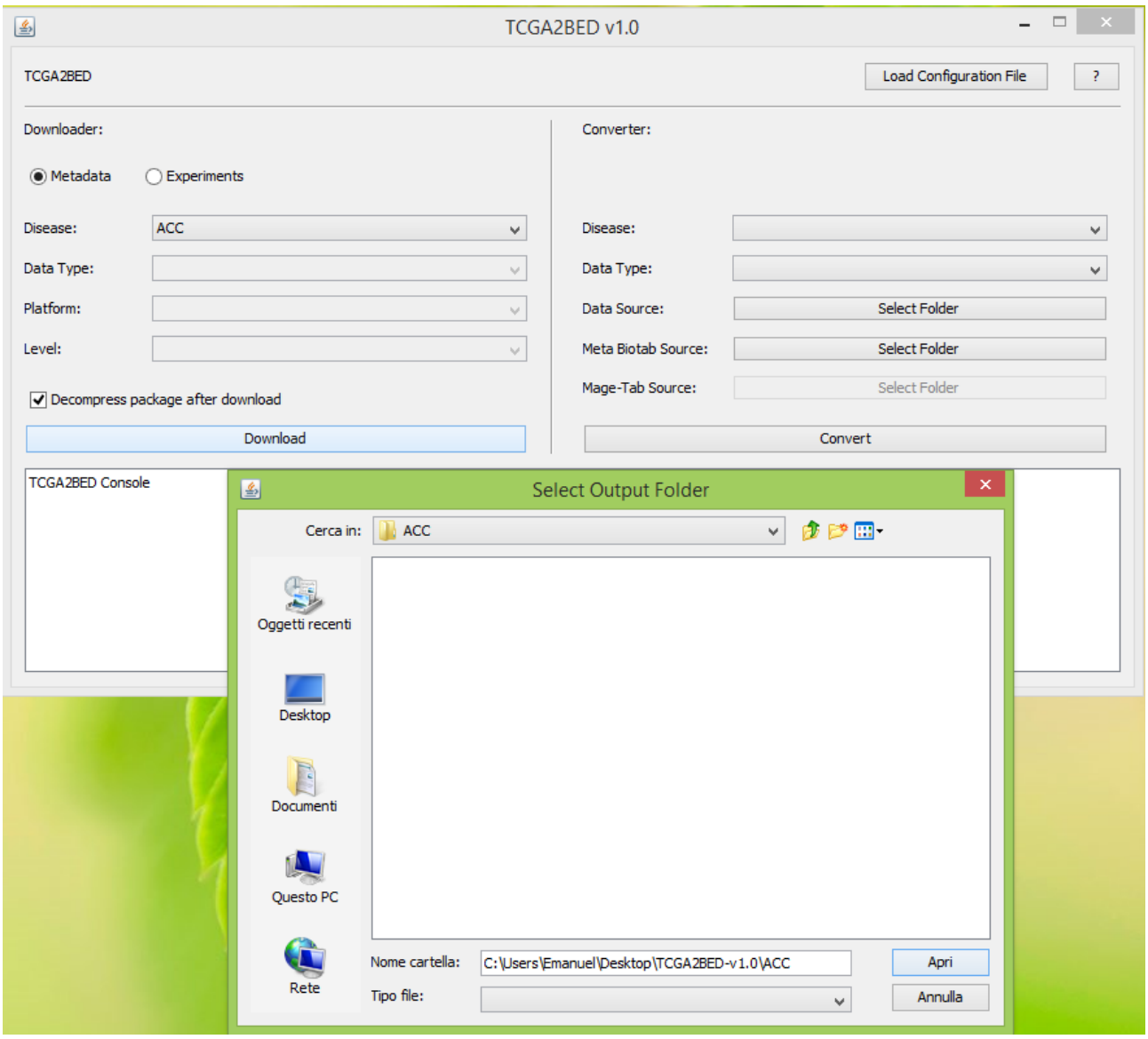
The following main screen of the TCGA2BED software will appear.



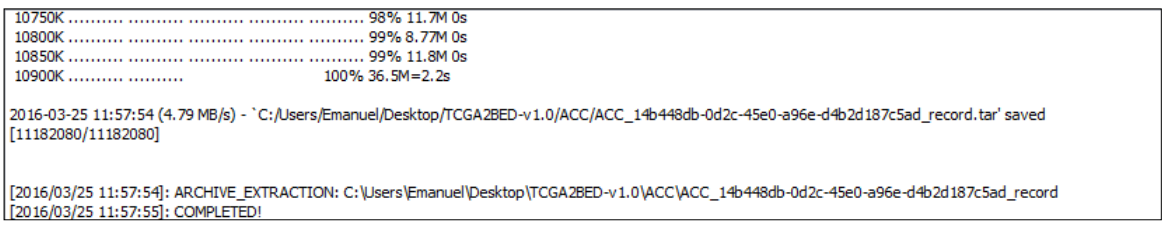

It is composed of two main parts. On the left hand side you can find the *Downloader*, which permits the retrieval of TCGA data. On the right hand side you can find the *Converter*, which allows converting the downloaded data into the BED format.

## Metadata download

The first step to perform is downloading the metadata (clinical and biospecimen biotab files) for the cancer type you want to analyze. Please select the tumor tag from the drop down menu (*Disease*); a list with the available tumor tags and names is provided at the end of this tutorial. Then press the *Download* button and choose a folder where to save the metadata files.

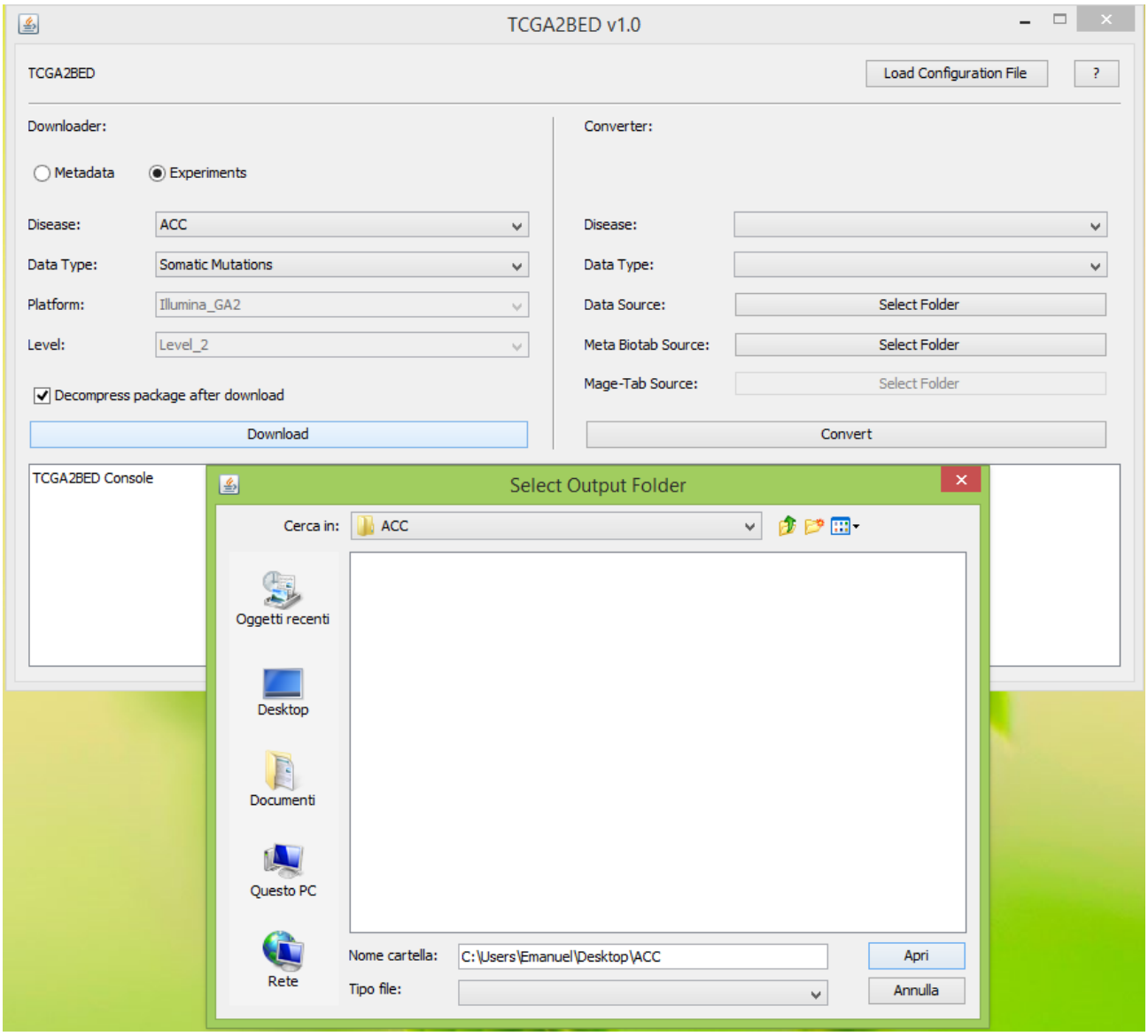



The download will start and you can track the progress from the TCGA2BED console.



## Experimental data download

The second step to perform is downloading the experimental data for the cancer type you want to analyze. Please select the tumor tag from the drop down menu (*Disease*); a list with the available tumor tags and names is provided at the end of this tutorial. Additionally, select the experiment type from the *Data Type* dropdown menu. The available experiment types are: Copy Number Variations (CNV), DNA Methylation, RNA-Seq, RNA-Seq V2, Somatic Mutations (DNA-Seq), miRNASeq. Then press the *Download* button and choose a folder where to save the experimental data files.



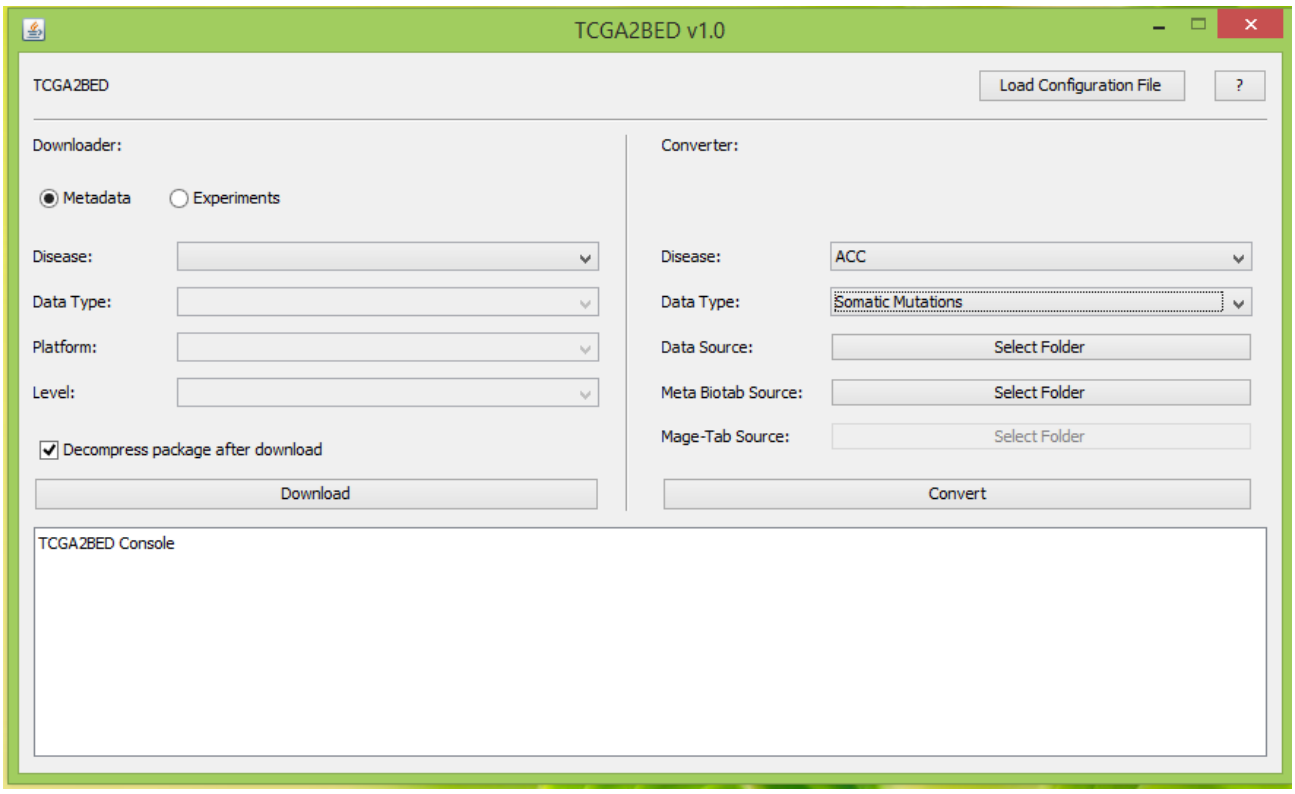

The download will start and you can track the progress from the TCGA2BED console.

```
228100K ..... ..... ..... ..... ..... 99% 2.65M 0s
228150K ..... ..... ..... ..... ..... 99% 1.87M 0s
228200K ..... ..... ..... ..... ..... 99% 2.90M 0s
228250K ..... ..... .....             100% 2.01M=47s

2016-03-25 12:18:08 (4.76 MB/s) - `C:/Users/Emanuel/Desktop/ACC/broad.mit.edu_ACC.IlluminaGA_DNASeq_curated.Level_2.1.0.0.tar.gz' saved [233755806/23375580

[2016/03/25 12:18:09]: extracting package: broad.mit.edu_ACC.IlluminaGA_DNASeq_curated.Level_2.1.0.0.tar.gz ...
[2016/03/25 12:18:12]: ... extraction completed!
```

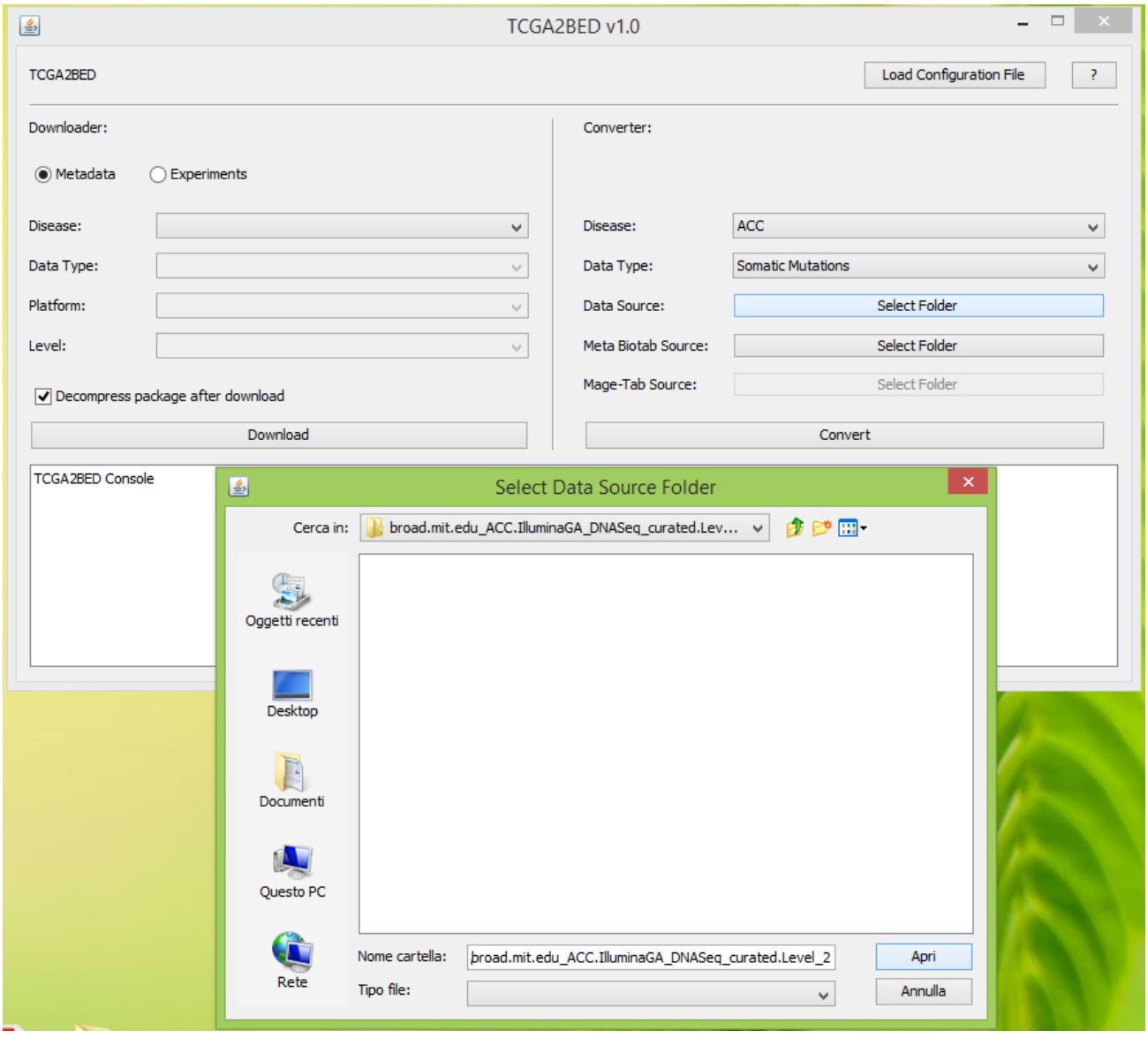
## Conversion into the BED format

After the download of the metadata and experimental data, you can start the conversion into the BED format (see the "`TCGA2BED_format_definition.pdf`" format definition file that is available as Supplemental material and at http://bioinf.iasi.cnr.it/tcga2bed for further details).

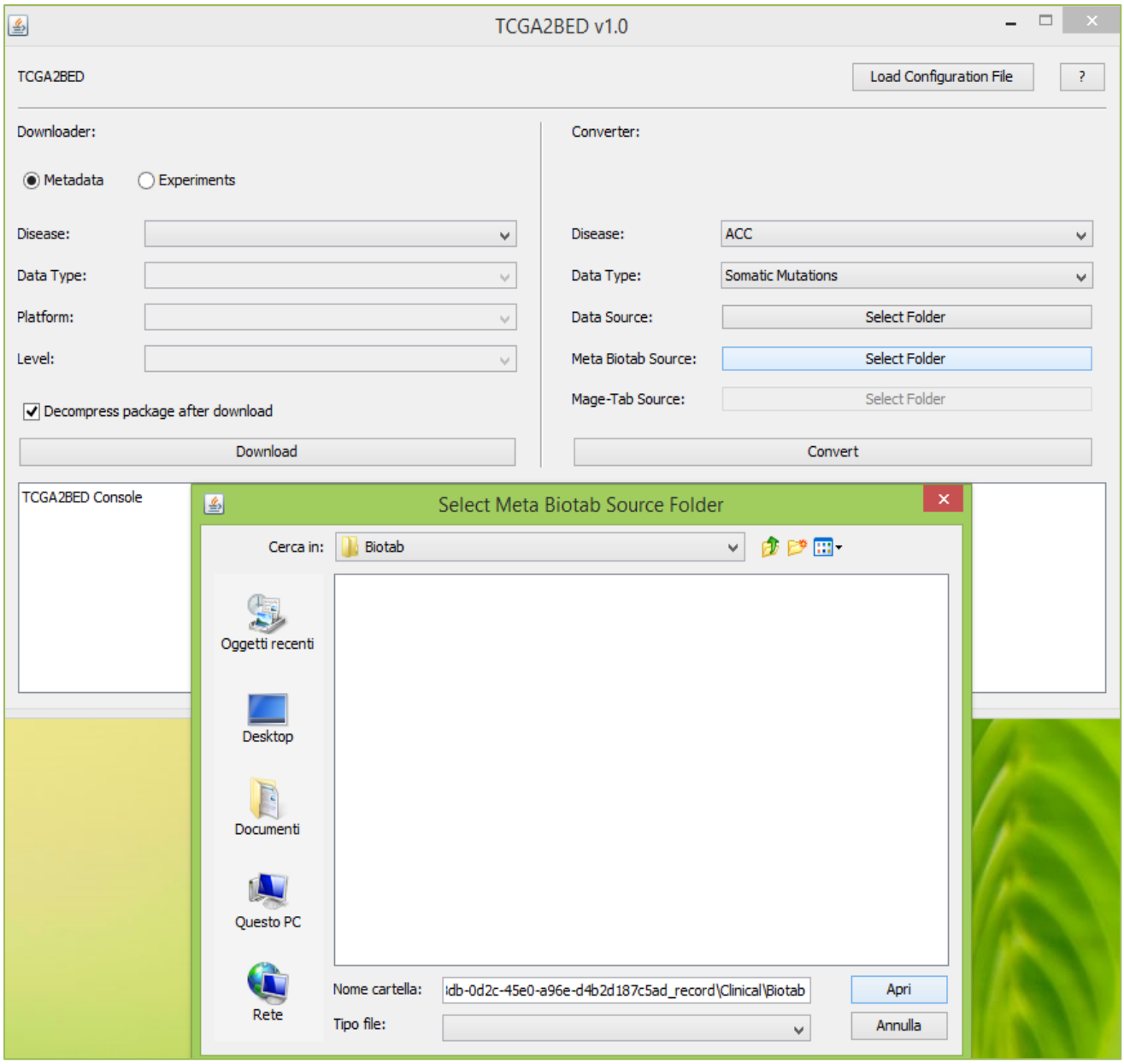
Please select from the drop down menus the *Disease* (through the tumor tag) and the *Data Type* (Copy Number Variations, DNA Methylation, RNA-Seq, RNA-Seq V2, Somatic Mutations, miRNASeq) you want to convert.




Additionally, specify the folder where you downloaded the experimental data.

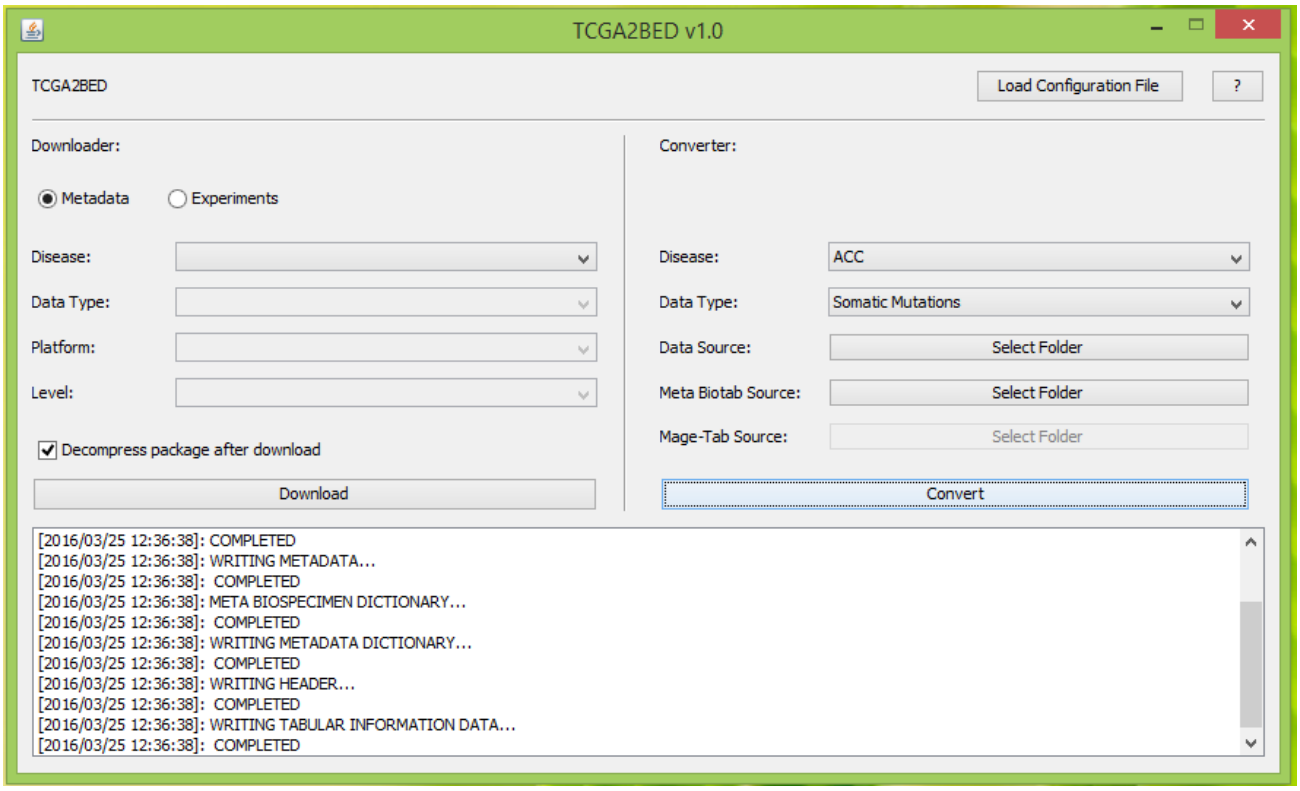



Then, select the folder where you downloaded the metadata biotab files (*Meta Biotab Source*). You have to browse through *Clinical* and *Biotab* in the metadata directory of the extracted archive.




Optionally, if you are converting CNV experiments select the *Mage-Tab Source* directory, which you can find in the root download folder.

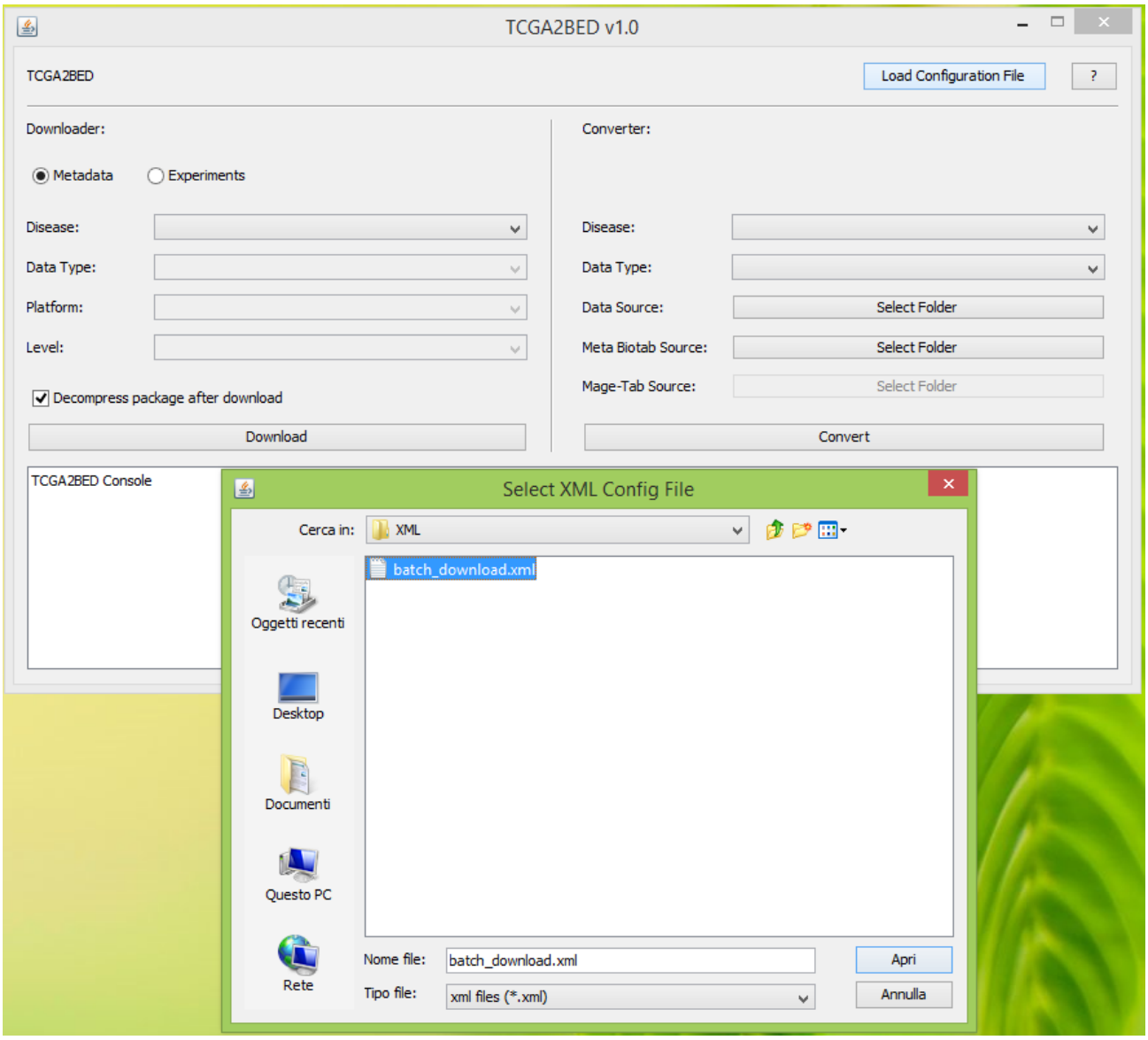
Finally start the conversion by clicking the *Convert* button and by choosing the output folder.
You will find the BED files and tab-delimited attribute-value pair metadata files for each experiment in the selected folder.




You can start the whole process again with new tumor or experiment types.

## Batch download and conversion into the BED format

Through the *Load Configuration File* button you can specify a XML file to download and convert in batch metadata and experimental data of several data types and diseases..




You can find two examples of XML files in the software package. The first one "`config-download-example.xml`" contains the commands to download metadata and experimental data files from TCGA:

```
<tcga2bed>
      <operation id="0">
            <cmd name="downloadmeta" />
```

```
            <attribute name="disease" value="KIRP" />
            <attribute name="output_folder" value="C:/downloads/" />
            <attribute name="autoextract" value="1" />
      </operation>

      <operation id="1">
            <cmd name="downloaddata">
            <attribute name="disease" value="KIRP" />
            <attribute name="data_type" value="DNAMethylation" />
            <attribute name="output_folder" value="C:/downloads/" />
            <attribute name="autoextract" value="1" />
      </operation>
</tcga2bed>
```

The second one "`config-convert-example.xml`" includes the commands for converting the files into the BED format:

```
<tcga2bed>
      <operation id="0">
            <cmd name="convert">
            <attribute name="disease" value="KIRP" />
            <attribute name="metadata" value="C:/downloads/KIRP_1dae287c-cc09-
                  461e-9488-8d31be3a7325_record/Clinical/Biotab/" />
            <attribute name="additional_metadata" value="null" />
            <attribute name="input_folder" value="C:/downloads/jhu-
                  usc.edu_KIRP.HumanMethylation450.Level_3/" />
            <attribute name="output_folder"
                  value="C:/downloads/KIRP_DNAMethylation_BED/" />
            <attribute name="data_type" value="DNAMethylation" />
            <attribute name="data_subtype" value="null" />
            <attribute name="magetab_folder" value="null" />
      </operation>
</tcga2bed>
```

For creating your own XML file, please follow following directions.

Each operation is defined as a XML block denoted by the *operation* tag followed by an incremental numeric identifier needed to preserve the execution sequence.

Two types of XML tags are required to define an operation:

1. *cmd* tag followed by the name of the current operation that can be one of the following commands:
    a. *downloadmeta* to download clinical data about a specific tumor;
    b. *downloaddata* to download a particular type of experiments about a tumor;
    c. *convert* to convert experiments from the TCGA format into the BED format.

2. The following attribute tags are required to configure an operation depending on the previously selected command. Please follow the example files to use them properly.
    a. *disease* denotes a specific tumor tag (all tags are listed at the end of this document);
    b. *metadata* contains the full path to the clinical data in biotab format;
    c. *additional_metadata* is a field and contains the full path to a file with user defined clinical data, if not present please set it to *null*;
    d. *input_folder* is the full path to the folder that contains experiments in TCGA format;

e. *output_folder* is the output directory where the converted BED files will be generated;
f. *data_type* denotes the type of the experiments contained in the folder specified in the *input_folder* field, and could be *DNAMethylation*, *DNASeq*, *RNASeq*, *RNASeqV2*, *miRNASeq*, and *CNV*;
g. *data_subtype* is required for *RNASeq*, *RNASeqV2*, and *miRNASeq* only. The allowed values for this field are *gene*, *exon*, and *spljxn* for *RNASeq*, *gene*, *exon*, *spljxn*, and *isoform* for *RNASeqV2*, and *mirna*, and *isoform* for *miRNASeq*; if you are not converting these experiments please set it to *null*;
h. *magetab_folder* is required for the conversion of *CNV* experiments only and contains the full path to the folder with magetab data; if you are not converting *CNV* please set it to *null*;
i. *autoextract* is a binary parameter (*0* or *1*), if set to *1* the data will be automatically decompressed after the download process.

## Data repository

The ftp site ftp://bioinf.iasi.cnr.it contains an up-to-date archive with the experimental and meta data from TCGA converted into the BED format.

## Contacts

Please contact Fabio Cumbo (fabio.cumbo@iasi.cnr.it) or Emanuel Weitschek (emanuel.weitschek@iasi.cnr.it) for comments and questions.

# Appendix: tumor tags and tumor names

| | |
|---|---|
| ACC | Adrenocortical carcinoma |
| BLCA | Bladder Utothelial Carcinoma |
| BRCA | Breast Invasive Carcinoma |
| CESC | Cervical squamous cell carcinoma and endocervical adenocarcinoma |
| CHOL | Cholangiocarcinoma |
| COAD | Colon adenocarcinoma |
| DLBC | Lymphoid Neoplasm Diffuse Large B-cell Lymphoma |
| ESCA | Esophageal carcinoma |
| GBM | Glioblastoma multiforme |
| HNSC | Head and Neck squamous cell carcinoma |
| KICH | Kidney Chromophobe |
| KIRC | Kidney renal clear cell carcinoma |
| KIRP | Kidney renal papillary cell carcinoma |
| LAML | Acute Myeloid Leukemia |
| LGG | Brain Lower Grade Glioma |
| LIHC | Liver hepatocellular carcinoma |
| LUAD | Lung adenocarcinoma |
| LUSC | Lung squamous cell carcinoma |
| MESO | Mesothelioma |
| OV | Ovarian serous cystadenocarcinoma |
| PAAD | Pancreatic adenocarcinoma |
| PCPG | Pheochromocytoma and Paraganglioma |
| PRAD | Prostate adenocarcinoma |
| READ | Rectum adenocarcinoma |
| SARC | Sarcoma |
| SKCM | Skin Cutaneous Melanoma |
| STAD | Stomach adenocarcinoma |
| TGCT | Testicular Germ Cell Tumors |
| THCA | Thyroid carcinoma |
| THYM | Thymoma |
| UCEC | Uterine Corpus Endometrial Carcinoma |
| UCS | Uterine Carcinosarcoma |
| UVM | Uveal Melanoma |