#### DataAPI 01A Docker SDB on Linux Tod Casasent 2020-06-23-1200

### 1 Introduction

These instructions are aimed at people familiar with Linux administration and GitHub, Docker and Docker-Compose, with root access to their Linux environment. Installation is for external users.

The Docker SDB is an image for viewing, searching, and downloading Standardized Data archives. Standardized Data archives are ZIP files containing batches.tsv and clinical.tsv files, a matrix\_data.tsv file, and an index.json file used by the Standardized Data Browser (SDB).

# 2 Target Operating System and Installation

These instructions were tested on RHEL 7. These instructions with appropriate modifications should work as a basis for installing on other distributions. Perform the installs in the order given in this document. Some steps are dependent on previous steps. All elements of this document expect a Linux host. It may be possible to convert these instructions to Windows or OSX, but no such ability is supported.

### 3 Operating System Prerequisites

Docker and Docker-Compose are required installs.

\$ docker --version Docker version 19.03.11, build 42e35e61f3 \$ docker-compose --version docker-compose version 1.25.4, build 8d51620a

## 4 Clone the GitHub Repository

Clone the GitHub repository with a shallow clone, since you will not be checking anything back in. This clone call grabs the newest version from master.

git clone --depth 1 https://github.com/MD-Anderson-Bioinformatics/DataAPI.git

This places the cloned code into a new DataAPI directory.

# 5 File Preparation from Clone

### 5.1 Optional: Compile

Compiling will be documented in a future release. The apps/DAPI Netbeans 11 project is used for this application.

#### 5.2 Required: Copy to Base Directory

Since Docker Containers do not save internal modifications between runs, SDB expects the following directories:

/DAPI/DATA /DAPI/CONFIG /DAPI/INDEXES /DAPI/LOGS

The contents of DATA will be explained in the future, but contain the ZIP archives referred to in the INDEXES. LOGS stores the log files from Tomcat.

CONFIG contains two files. Both are optional, but when used with the Batch Effects Viewer, the lack of dapi.properties will significantly affect usability.

The dapi.properties file contains XML with URLs for the three possible applications used together with the DAPI application.

```
<?xml version="1.0" encoding="UTF-8" standalone="no"?>
<!DOCTYPE properties SYSTEM "http://java.sun.com/dtd/properties.dtd">
centry key="BEV_URL">http://java.sun.com/dtd/properties.dtd">
centry key="BEV_URL">http://java.sun.com/dtd/properties.dtd">
centry key="BEV_URL">http://java.sun.com/dtd/properties.dtd">

centry key="BEV_URL">http://jocalhost/BatchEffectsViewer
centry key="BQF_URL">http://jocalhost/BEVQF
centry key="STD_URL">http://jocalhost/StandardizedDataBrowser
```

The dapi-filter.tsv contains tab-delimited data that allows remapping of GDC names into more use-friendly, coordinated terminology.

Derivations	Category Platform	Details	Category-New P				Details-New				
current	Copy Number Segment	DNAcopy	•	Copy Number	er	DNAcopy	With CNV				
current	Masked Copy Number Se	gment	DNAcopy		Copy Number	er	DNAcopy	No CNV			
legacy	Copy number variation Affymetrix SNP Array 6.0-hg19-nocnv				Copy Number	Number SNP6					
current	Methylation Beta Value	Liftover	noXY	DNA Methyl	lation	Combined M	Iethylation	No Sex Chror	nosomes		
current	Methylation Beta Value	Liftover	wXY	DNA Methyl	lation	Combined M	Iethylation	With Sex Chr	romosomes		
legacy	DNA methylation	Illumina Hu	ıman Methylat	tion 27	noXY	DNA Methy	lation	Methylation 2	27	No Sex Chromosomes	
legacy	DNA methylation	Illumina Hu	ıman Methylat	tion 27	wXY	DNA Methy	lation	Methylation 2	27	With Sex Chromosomes	
legacy	DNA methylation	Illumina Hu	ıman Methylat	tion 450	noXY	DNA Methy	lation	Methylation 4	150	No Sex Chromosomes	
legacy	DNA methylation	Illumina Hu	ıman Methylat	tion 450	wXY	DNA Methy	lation	Methylation 4	150	With Sex Chromosomes	
current	Gene Expression Quantification HTSeq - Counts					Gene Expre	ssion	HTSeq - Cour	ITSeq - Counts		
current	Gene Expression Quantification HTSeq - FPKM				Gene Expre	ssion	HTSeq - FPKM				
current						Gene Expression HTSeq - FPKM-UG			M-UQ		
legacy	Gene expression RNA-Seq-gene-unnormalized-v2					Gene Expression RNA-Seq-gene-unnormalized-v2			ized-v2		
legacy						Gene Expression RNA-Seq-isoform-unnormalized-v2					
legacy	Gene expression RNA-Seq-v1 Gene Expression					RNA-Seq-v1					
current	Isoform Expression Quantification BCGSC miRNA Profiling				miRNA	miRNA-Seq Isoform Quantification					
current	miRNA Expression Quantification BCGSC miRNA Profiling				miRNA	miRNA-Seq	q Gene Quantification				
legacy	miRNA-Seq miRNA gene quantification-gene-hg19-miRNA				miRNA	miRNA-Seq	Gene Quantification				
legacy	miRNA-Seq miRNA isoform quantification-hg19-isoform-miRNA					miRNA	miRNA-Seq Isoform Quantification				
legacy	Simple somatic mutation DNA-Seq-Illumina MiSeq Mutations					DNA-Seq-Illumina MiSeq					
current	Gene Level Copy Number	r Scores	GISTIC - Cop	py Number S	Score		Mutations	GISTIC Copy	Number		
current	Masked Somatic Mutation MuSE Variant Aggregation and Maski				ng		Mutations	MuSE Soma	tic		
current	Mutations Call Analysis Mutations MutBatch Ana										
legacy	Mutations Call Analysis Mutations MutBatch A				nalysis						
current			MuTect2 Variant Aggregation and Mas					Mutations	MuTect2 Son	matic	
current				er Variant Aggregation and Masking					SomaticSnip		
current	Masked Somatic Mutation Var		VarScan2 Var	arScan2 Variant Aggregation and Mas				Mutations '	VarScan2 So	omatic	
legacy	Protein expression	MDA_RPPA	_Core		Protein Exp	ression	RPPA				

# 1 Setup Local Information from Base Directory

#### 1.1 Template Dockerfile Settings

The Dockerfile template file should be updated and renamed.

Replace <IMAGE\_NAME> with the IMAGE\_NAME used below. This is informational on the image only.

Replace <RELEASE\_VERSION> with "latest" or some other version number. This is informational on the image only.

Replace <USERID> with a Linux UID that has access to the /DAPI directories described elsewhere.

#### 1.2 Template docker-compose.yml Settings

The docker-compose template file looks like this. Is should be updated and renamed.

```
# this is the docker-compose version
version: '3'
# file version 2020-06-23-1200
services:
  <IMAGE_NAME>_service:
    # use existing default network
    network mode: bridge
    # restart this container if it crashes
    restart: always
    build:
       # build from directory in context and Dockerfile
      context:.
       dockerfile: Dockerfile
    container_name: <IMAGE_NAME>_cont_<ENVIRON>
    # update :latest to desired version
    image: <IMAGETXT>:<DESIREDTAG>
    volumes:
       # outside access for data files outside:inside
       - <INDEXPATH>:/DAPI/INDEXES:ro
       - < CONFIGPATH>:/DAPI/CONFIG:ro
      - <OUTSIDE_GDC_DATA_PATH>:/DAPI/DATA/GDC:ro
       - <LOGPATH>:/opt/tomcat/logs
      # read-only file to set time and timezone to same in image as on server

    - /etc/localtime:ro

       - /etc/localtime:/etc/timezone:ro
    ports:
       # (outside)host port:container port(inside) for Tomcat
       # outside/host port is only set here (other docker compose have ports in more than one place)
       - "<OUTSIDE PORT>:8080"
    tty: true
```

Below, find the all capital text (surrounded by pointy-brackets < and >) in the Docker Compose Template and replace with the information described below.

TAMACITA NIA NATA	m1
IMAGE_NAME	The container name is described in the file as
	" <image_name>_cont_<environ>".</environ></image_name>
	IMAGE_NAME is part of that name. Use something
	appropriate for your environment.
ENVIRON	The container name is described in the file as
	" <image_name>_cont_<environ>".</environ></image_name>
	IMAGE_NAME is part of that name. Use something
	appropriate for your environment.
IMAGETXT	The image used by the Docker Compose file is
	" <imagetxt>:<desiredtag>". The image is</desiredtag></imagetxt>
	stored in <a href="https://hub.docker.com/u/mdabcb">https://hub.docker.com/u/mdabcb</a> . Use
	mdabcb/sdb_image to use this image.
DESIREDTAG	The image used by the Docker Compose file is
	" <imagetxt>:<desiredtag>". The image is</desiredtag></imagetxt>
	stored in <a href="https://hub.docker.com/u/mdabcb">https://hub.docker.com/u/mdabcb</a> . Use latest
	to use the newest image.
INDEXPATH	This gives the path to the index file. For these
	directions, use /DAPI/INDEXES.
CONFIGPATH	This gives the path to the config files. For these
	directions, use /DAPI/CONFIG.
OUTSIDE_GDC_DATA_PATH	This gives the path to the data (ZIP archives). For
	these directions, use /DAPI/DATA.
LOGPATH	This gives the path to the log directory. For these
	directions, use /DAPI/LOGS.
OUTSIDE_PORT	Use the outside port you wish to use for connection to
	the application. (This should be reflected in the
	dapi.properties file.)
	, <u>*</u> * * ·

### 1.3 Dockerfile Settings

The Dockerfile uses the installations directory at docker-build/SDB/installations. The apps/DAPI Netbeans 11 should be compiled, and the resulting WAR renamed to StandardizedDataBrowser.war and placed in the installations directory.

Additional build docs will be released in the future.

# 2 Images

### 2.1 Recommended: Pull Images from Docker Hub

In the directory with the update docker-compose.yml file using the name given it when editing, pull the image with:

docker-compose -f docker-compose.yml pull

# 3 Starting and Stopping the Docker Compose Stack

In the directory with the docker-compose.yml file, the container is started using: docker-compose -p EXT -f docker-compose.yml up -d

The EXT may be varied if needed on your system to ensure unique ids for the container.

The Docker Compose container can be stopped using:

docker-compose -p EXT -f docker-compose.yml down