

USER MANUAL

Latest version available at https://github.com/WebDataScience/GUIdock

GUIdock is a Docker Package containing the entire computational environment to run applications with a graphical user interface. As a proof of concept, we focus on supporting Cytoscape, a Java-based standalone program with a graphical user interface for the visualization and analyses of gene networks in biology. In addition to Cytoscape, our container includes R, Rserve, Bioconductor packages igraph, networkBMA and a Cytoscape app called CyNetworkBMA. GUIdock contains the entire pipeline and all the tools (including Cytoscape that connects to preloaded RServe, a Bioconductor package called "networkBMA" and all its dependencies) to generate gene regulatory networks.

This manual demonstrates the installation and instructions to run GUIdock.

Docker Image : <u>https://hub.docker.com/r/kristiyanto/guidock/</u> Dockerfile : <u>https://github.com/WebDataScience/GUIdock</u>

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Quick Start

Linux

Running GUIdock (SCRIPT)

A bash script to run and install GUIdock is available in: <u>https://github.com/kristiyanto/GUIdock/tree/master/Install%20and%20Run%20/LINUX</u>

Download a file from the link above and run the script with following command to start GUIdock.

```
#Locate to script file
#Use following command to start GUIdock
sh runGUIdockLinux.sh
```

Alternatively, a tarball file is also available.

The script and tarball will attempt to start Docker Engine or install it if it is not installed. Once started, it pulls the Docker Image and run it.

During the run, a folder .guidock/GUIdock-SHARED is created under user home directory. ~/.guidock/GUIdock-Shared in the Linux system is linked with /root/GUIdock-SHARED within the container.

GUIdoci

OS X

Installation (SCRIPT)

As shortcut, a bash script to run installation commands below is available in: <u>https://github.com/WebDataScience/GUIdock/tree/master/Install%20and%20Run%20/MAC</u>

Once downloaded, unzip a file and run the script with following command to install all the required softwares.

```
# Install from script
sh install-mac.sh
```

The script, however does not install Docker Toolbox. Docker Toolbox will have to be downloaded from their website and installed separately. Docker Toolbox can be downloaded from: <u>https://www.docker.com/toolbox</u>.

Running GUIdock (SCRIPT)

A script to run GUIdock is available in: <u>https://github.com/WebDataScience/GUIdock/tree/master/Install%20and%20Run%20/MAC</u>

Download a file from the link above and unzip a file.

To run GUIdock, run the script using the following command:

Download and locate to installation file. # Use following command to start GUIdock sh mac-start.sh

WINDOWS

Installation (SCRIPT and MANUAL)

1) Docker ToolBox

Install Docker ToolBox. Docker ToolBox can be downloaded from: <u>https://www.docker.com/toolbox</u>

Click the link above and choose "Download (Windows)".



Go to folder where the installation file is saved and run the installation file.



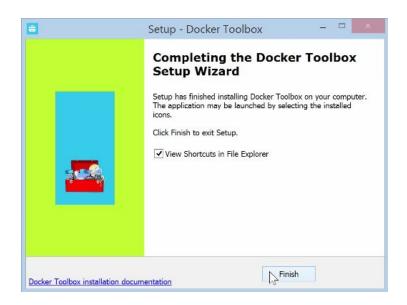
Click "Next" until you see "Selection Components" window. This will install Docker client, Docker machine, VirtualBox, Kitematic and Git for Windows.

elect Components	
Which components should be installed?	
Select the components you want to instal install. Click Next when you are ready to	ll; clear the components you do not want to continue.
Full installation	Ŷ
Docker Client for Windows	9.2 MB
Cocker Machine for Windows	41.1 MB
✓ VirtualBox	81.2 MB
✓ Kitematic for Windows (Alpha)	155.7 MB
Git for Windows	29.5 MB
Current selection requires at least 317.8 I	MB of disk space.

Click "Next" until you see "Ready to Install" window and click "Install".

Ready to Install Setup is now ready to begin installing Do	ocker Toolbox on your co	mputer.
Click Install to continue with the installat change any settings.	ion, or click Back if you	want to review or
Destination location: C:\Program Files\Docker Toolbox		^
Setup type: Full installation		
Selected components: Docker Client for Windows Docker Machine for Windows VirtualBox Kitematic for Windows (Alpha)		
Git for Windows		`
	< Back	Install Cance

Click "Finish" to complete the installation.



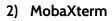
To run the Docker Engine, double click on "Kitematic (Alpha)" shortcut.

🔁 Kitematic (Alpha)	🛛 Kite	ematic	(Alp	ha)	
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On the first run, it will create the Docker VM and all the required environments. If you have a Docker account, enter your username and password. If you don't have an account, click "Skip for now".

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		Containers		Recomm	rch for Docker images from Dock	FILI	TER BY All Rec	ommended My Repos
())) (53)				Recomm	kitematic hello-world-nginx	≓ghost	official ghost	2
					A light-weight nginx container that demonstrates the features of Kitematic		Ghost is a free ar blogging platfor JavaScript	
Username					♥ 9 000 CREATE		♥ 117	000 CREATE
Password	Connect to Docker Hub Pull and run private Docker Hub images by			(official 🕅	4	official redis Redis Is an open store that function structure server.	source key-value ons as a data
Forgot your password?	connecting your Docker Hub account to Kitematic.				♥ 609 000 CREATE		♡ 1096	000 CREATE
LOG IN				RetionLDB	official R rethinkdb RethinkDB is an open-source, document database that makes it easy to build and scale realtime		kitematic minecraft The Minecraft min allows two or mo Minecraft togeth	ore players to play
son chart an account jet, sign op					♥ 91 000 CREATE		© 20	000 CREATE
	SKIP FOR NOW	Contraction CLI	<u>چ</u>	*	official 👷	G	official postgres	8

GUIdock



To have GUI delivered in Windows, install MobaXterm to set up X11 forwarding. MobaXterm is an open source X11 emulator for Windows which allows remote GUI access to the application. MobaXterm can be downloaded from:

http://mobaxterm.mobatek.net/download-home-edition.html

Click the link above and choose version you want to download. We chose "MobaXterm Home Edition (Installer edition)" in this tutorial.



Go to folder where the installation file is saved and run the installation file.

P	MobaXterm	Setup	8.2	
-				

Click "Next" until you see "Ready to install MobaXterm" and click "Install" to install MobaXterm.







Running GUIdock (SCRIPT)

A shell script to run GUIdock is avilable in: https://github.com/WebDataScience/GUIdock/tree/master/Install%20and%20Run%20/WINDOWS

Download a file from the link above and unzip a file. Double click on "RunGUIdock.sh" shell script file to run GUIdock. The script, however does not install Docker Toolbox and MobaXterm. Docker Toolbox and MobaXterm will have to be downloaded from their websites and installed separately.



Manual

OS X

Installation (MANUAL)

Alternatively, required packages can also be installed independently by running following instructions:

1) Docker Toolbox

Docker Toolbox contains Docker Virtual Machine and Kitematic as a Docker Client for Macintosh and Windows User. Docker Toolbox can be downloaded from: https://www.docker.com/toolbox

2) Home Brew

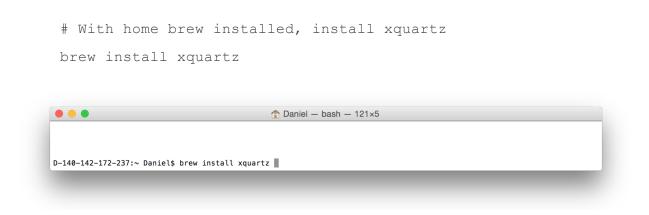
Using only Docker Toolbox gives all that Docker Engine promises. However, to have GUI delivered in Mac from Docker containers, more software are needed. To make installation easier, software can be installed using home brew (<u>http://brew.sh/</u>).

To install Home Brew, enter this command in OS X terminal window:

```
# Install Home Brew
ruby -e "$(curl -fsSL
https://raw.githubusercontent.com/Homebrew/install/master/insta
ll)"
D-140-142-172-237:~ Daniel$ ruby -e "$(curl -fsSL https://raw.githubusercontent.com/Homebrew/install/master/install)"
```

3) XQuartz

XQuartz is an open source program to enable X Windows on OS X. With Home Brew installed, XQuartz can be installed entering this command in OS X terminal window:



4) Socat

XQuartz is an open source program to enable X Windows on OS X. With Home Brew installed, enter the following command in terminal window:

	prew installed, install socat
brew install	socat
• • •	👚 Daniel — bash — 121×5
	\$ brew install socat

Running GUIdock (MANUAL)

Alternatively, GUIdock can also be launched manually by following instructions below:

1) Preparation

Docker engine runs in a virtual machine in OS X. To enable Display to be delivered to Mac OS, use socat to open incoming X11 Graphic interaction from Docker Machine and Xquartz to display the graphics.

GUIdoc



It may also a good idea to check if the firewall is blocking the incoming connection from docker container.

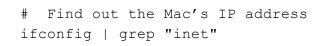
2) Running GUIdock

Once Mac OS is ready to receive graphic streams from Docker container, ensure that Docker Engine (Kitematic) is up and running. Click on the Docker CLI in Kitematic to launch a new terminal



Within Docker CLI terminal windows, run GUIdock by running following commands:

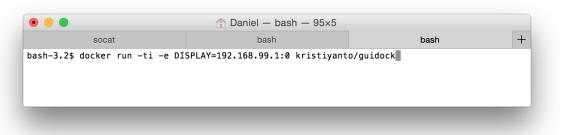
```
# Pull latest image of GUIdock from repository.
docker pull kristiyanto/guidock
```



The MAC-IP-ADDRESS number you want to identify is immediately after the "inet" field.

Run the GUIdock. Once loaded, a Cytoscape GUI Window pops up. # Replace MAC-IP-ADDRESS with the IP number you identified from ifconfig

docker run -ti -e DISPLAY=MAC-IP-ADDRESS:0 kristiyanto/guidock



-ti : To enable docker container in interactive mode.

-e : To set up the DISPLAY environment variable into the docker container so that the GUI can be sent to Mac OS machine.

IP address : MAC OS private address (VirtualBox's interface), this address should be reachable by Docker Machine.

Port Number : Port number of X11 is O (zero).

Next: Cytoscape Demo

GUIdoc



Installation (MANUAL)

Please refer to the Quick Start installation page on how to install Docker ToolBox and MobaXterm. Installation (SCRIPT and MANUAL)

Running GUIdock (MANUAL)

1) Preparation

Firewall

Make sure Firewall allows Docker Machine to access MobaXterm X11 service. This can be done either by disabling the firewall for Private Networks, or by manually list MobaXterm in Firewall as follow:

Control Panel -> System and Security -> Windows Firewall -> Allow an app or feature through Windows Firewall; check boxes for MobaXterm

Name	Private	Public	^
☑ xwin.exe			
☑ xwin_1.16.3.exe			
☑ xwin_mobax.exe			
☑ xwin_mobax.exe			
☑ Zinio			
			~

IP Addresses

Open "Docker QuickStart Terminal".

Docker Quickstart Terminal

To obtain IP Addresses, type the following command in "Docker QuickStart Terminal":

docker-machine inspect default

docker-machine inspect default

Locate to the IP Address of Docker Machine.

"IPAddress": "192.168.99.100",

Locate to IP Address of Docker Client.

```
"HostOnlyCIDR": "192.168.99.1/24"
```

2) Running GUIdock

Open MobaXterm, click "Start local terminal".



Type the following command to use SSH to connect Docker host in terminal.

```
# 1. SSH with X11 forwarding to Docker host.
ssh -X docker@DockerMachineIPAdress
```

ssh -X docker@192.168.99.100

Docker default username is "docker" and password is "tcuser". Enter "tcuser" when a password is asked. Password can be saved after the first login.

```
#2. Login with password "tcuser"
tcuser
```

docker@192.168.99.100's password:

Pull the latest GUIdock image from the repository by typing the following command in terminal:

3. Pull latest image of GUIdock from repository. docker pull kristiyanto/guidock

docker@default:~\$ docker pull kristiyanto/guidock



Run GUIdock image by typing the following command in terminal

```
#4. Run the GUIdock. Once loaded, a Cytoscape GUI Window pops
up.
docker run -ti -e DISPLAY=WindowsIPAddress:0
kristiyanto/guidock
```

docker@default:~\$ docker run -ti -e DISPLAY=192.168.99.1:0 kristiyanto/guidock

-ti : To enable docker container in interactive mode.

-e : To set up the DISPLAY environment variable into the docker container so that the GUI can be sent to Windows machine.

IP address : Windows private address (VirtualBox's interface), see Preparation Section to check IP Address. This address should be reachable by Docker Machine.

Port Number : Port number of X11 is O (zero).

Next: Cytoscape Demo

Cytoscape Demo

Demo files and saved-sessions are included in the GUIdock container, located in /root/DEMO folder.

The files and the demo including:

- Dream4.cys : A 210 by 101 table in which the first column identifies time and the remaining columns are the expression levels for 100 genes in a simulated network after an application (at t=0) and removal (at t=500) of a perturbation (21 time points in each time series). Based on the time series file for the first network in the 100-gene in silico network sub-challenge from DREAM 4, Challenge 2 (Marbach *et al.* 2009, Marbach *et al.* 2010, Prill *et al.* 2010). A key column was added to the original file to facilitate import into Cytoscape.
- 2. RNAseq.cys : 84-gene subset of the RNAseq Cancer cell line data. Klijn *et al.* generated an extensive RNAseq gene expression data across 675 frequently used human cancer cell lines. We downloaded the the variance stabilized version of the normalized RNAseq data produced by the DESeq Bioconductor package from http://research-pub.gene.com/KlijnEtAl2O14/. We then extracted a subset of 84 genes that belong to 21 cancer-related pathways that are known to be functionally altered in cancer (see Supplementary Table 12 in Klijn *et al.* Note that this is a steady-state (non-time series) dataset.
- 3. Yeast.cys : A 582 by 102 table in which the first two columns identify the replicate and time (in minutes) after drug perturbation, and the remaining 100 columns are the expression measurements for a subset of 100 genes from the yeast-rapamycin experiment described in Yeung et al. (2011). There are 582/6 = 97 replicates (the 95 segregants plus two parental strains of the segregants), each with measurements at 6 time points. The complete time series data is available from Array Express (Parkinson et al. 2007) with accession number <u>E-MTAB-412</u>. When using this file, please remember to adjust source format in the inference dialog. Also, exclude replicate and time columns from input to the algorithm.

Open Demo Session

Once Cytoscape application is started, click "File" and "Open" to open one of the session files from "/root/DEMO" folder.



Recent Session New		Look In: DEMO
Open	Ctrl+0	DREAM4.txt RNAseq.cys
Save Save As Open Sessio Import Export	Ctrl+S n Ctrl+Shift+S	RNAseq.txt
Run		Files of Type: All Files
Print Current Network	Ctrl+P	Open Cance
0	atul i a	

Select any of the .cys file to open saved cytoscape session. The following image is gene networks of RNAseq.cys file.

File Edit View Select Layout Apps Tools Help		
📁 🗂 💸 🚯 🚚 🚱 🦘 📁	🐄 🔍 🔍 🔃 🌾 🐂 🐂 🖓 Coter search term	
Control Panel	CyNetworkBMA	
Network * Style Select		
CyNetworkBMA	VOTCH2 IDH2 KDH3C MAP2K1 TSC2 CDX2 KSH6 NF1 TP53	
CyNetworkBMA 84(0) 18	4(0) JAK2 APC ROSI RET ALK SOX2 NKX2.1 NSD1 BCL2L1	
	EGFR CDKN2B SMAD2 SMAD4 KDM6A PTEN CDKN1B ERG AKT1	
	PBRM1 WHSCILL PIK3R1 MET BRAF IDH1 FBXW7 CCNE1 STK11	
	MSH2 MLH1 TGFBR2 PRPF408 TSC1 MSH3 ZRSR2 AXIN1 NOTCH:	
	MARCA1 WVP1 KDM5A KRAS XBP1 ATM ARID2 MITF EZH2	
	PIK3CA ARID18 MYC SPOP UZAF2 SMARCA4 FGFR2 NOTCH1 NRAS	
	ERBBZ SF3A1 EP300 FGFR1 UZAF1 CCND1 MCL1 CTNNB1 MDM2	
	ARIDIA FGFR3 FAMAGC CREBBP CRKL AXINZ AKT3 ETV1 BCL2A1	
	857 (93) (000)A	
	Table Panel	0
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	share name Indegr Outde	
TOPHI MISCILL PRIMI HET BAN BILM FORMUT CONCL	KDM5C KDM5C 1 1 U2AF1 U2AF1 1 0	
MINE - FEINE TEXANE PRIMACINE TSCT - FEINE - 20082 - AUNIE	ARID18 ARID18 1 0	
ARACAL WARY CONSE 1986 EEFL ATM AND MADE AND	WHSCILI WHSCILI 1 0 FGFR1 FGFR1 1 2	
PRICK WEEKE HIC STOP UDV2 SHALCH FORE VOTEL HERE STATE FORE FORE UDV2 COND HICLE CONST	BRAF BRAF 1 1	
ARTIA TOPAL AND ARTICLES	CRKL CRKL 1 0	
54572 57382 CENIDA	Node Table Edge Table Network Table Unassigned Tables	
	(node name), coge name (network name (offassigned hables)	
		Memory: OK

Inferring Gene Networks

Demo files can also be imported into Cytoscape by using the Import menu. On Cytoscape, open test data by going to File -> Import -> Table -> File



Recent Session	•			
New	•			
Open	Ctrl+0			
Save	Ctrl+S			
Save As	Ctrl+Shift+S			
Import	•	Network	•	
Export	•	Table	•	File
Run		Style		URL
Print Current Network	Ctrl+P	Ontology and Annotation	-	Public Databases Alt+T
Quit	Ctrl+Q			

And select any of the .txt files to load demo files into Cytoscape. The files are located in "/root/DEMO"

Look In:	DEMO	 T		
DREAM4.c DREAM4.t RNAseq.c RNAseq.b Yeast.cys Yeast.txt	xt ys kt			
File <u>N</u> ame:	Yeast.txt		 	
Files of Type:	All Files			•
			<u>O</u> pe	n Cancel

In the following dialog window, choose the option to import data into an unassigned table and enter new table name.

Wh Set New Table	and the second	ole Data To	an unassigned table	•
New Table Na	ime		demo	
dvanced				
Show Mappir	a Options 🗔 Show	w Text File Imp	ort Options 📝 Case S	Sensitive
Preview				
	off Click: Enabl	le/Disable (Column Pight Click	k: Edit Colum
	.eft Click: Enab	le/Disable (Column, Right Clicl	k: Edit Colun
Text File L	.eft Click: Enab	le/Disable (Column, Right Clicl	k: Edit Colun
Text File L				
Text File L ∫newTable ∕∕ name	✓ replicate	v time	✓ YBL103C	✓ YKL112
Text File L newTable newTable Prame BY4716.0	replicate 1	v time 0	✓ YBL103C 9.531639971	✓ YKL112 11.32400
Text File L newTable rame BY4716.0 BY4716.10		✓ time 0 10	✓ YBL103C 9,531639971 9,58783932	✓ YKL112 11.32400 11.1152€
Text File L newTable ✓ name BY4716.0 BY4716.10 BY4716.20	l √ replicate 1 1 1 1 1 1 1 1 1		✓ YBL103C 9.531639971 9.58783932 9.948749983	✓ YKL112 11.32400 11.11526 10.69329
Text File L newTable ✓ name BY4716.00 BY4716.20 BY4716.30	✓ replicate 1 1 1 1		✓ YBL103C 9.531639971 9.58783932 9.948749983 10.10961617	✓ YKL112 11.32400 11.11526 10.69329 10.4415
Text File L newTable	✓ replicate 1 1 1 1 1 1 1 1 1 1		✓ YBL103C 9.531639971 9.58783932 9.948749983 10.10961617 10.31740555	✓ YKL112 11.32400 11.11526 10.69325 10.4415 10.21360
Text File L newTable ✓ name BY4716.00 BY4716.20 BY4716.30	✓ replicate 1 1 1 1		✓ YBL103C 9.531639971 9.58783932 9.948749983 10.10961617	✓ YKL112 11.32400 11.11526 10.69329 10.4415
► Text File L ■ Text File L ■ NewTable ■ Y4716.0 BY4716.10 BY4716.20 BY4716.40 BY4716.40 BY4716.50		<pre></pre>	✓ YBL103C 9.531639971 9.58783932 9.948749983 10.10961617 10.31740555 10.51886838	✓ YKL112 11.32400 11.11526 10.69320 10.4415 10.21360 10.07046
Text File L newTable ✓ name BY4716.0 BY4716.10 BY4716.20 BY4716.30 BY4716.30 BY4716.40 BY4716.40 BY4716.30 BY4716.41 BY4716.40 BY4716.40 BY4716.40 BY4716.40 BY4716.40 BY4716.40 BY4716.40 BY4716.40 BY4716.40	✓ replicate 1 1 1 1 1 1 1 1 2	✓ time 0 10 20 30 40 50 0	✓ YBL103C 9.531639971 9.58783932 9.948749883 10.10961617 10.31740555 10.51886838 9.692225555	✓ YKL112 11.32400 11.1152€ 10.69329 10.4415 10.21360 10.07046 11.00776

Run the network inference algorithm by going to Apps -> CyNetworkBMA -> Inter Network

Apps Tools Help	
App Manager	
CyNetworkBMA 🕨 🕨	Infer Network
	Assess Network Show Jobs

In the following dialog window, specify the columns to include and source format.

<u>Data file</u>	Columns to include	Source format
Dream4.txt	Select all columns except "Time"	 Genes as columns Data Type: Time series Number of time points: 21
RNAseq.txt	Select all	Genes as rowsData Type: Steady state
Yeast.txt	Select all columns except "replicate" and "time"	 Genes as columns Data Type: Time series Number of time points: 6

Address: loca	lhost		Port	6311
_			, orei	BOIL
Username:		Password:		
ata source				
Select table:	demo			•
Table key: n	ame			
Columns to incl	ude:			
replicate				-
time YBL103C				
YKL112W				
YDR216W				
YMR280C				<u>v</u>
ource format				
	ws, experiment			
🥑 Genes as co	lumns, experim	ents as rows		
Data type: 🛛 Ti	me series			•
Number of time	points: 6	÷		
letwork name	•			
				_
yeast-rapamyo	in			

Control Panel	0 × 0	yeast-rapamycin 📃 🖬 🔀	
Network 2 Style Select			
	as Edges		
Y di yeast-rapamycin 100	0) 508(0)		
	1		
		Start	c
1111111		ade trans ■ ① ## co ① ③ ■ ∞ f(r)	c
			c
		Image: star co Image:	c
		Image Image <th< td=""><td>C</td></th<>	C
		Image: Second Control Image: Second Contro Image: Second Contro <	c
		Image: system mass f(x) share name f(x) share 0.436 0.436 share	

Transferring files between a container and the local filesystem

Transferring files (Linux)

To transfer files in Linux, run the script using the following command to start GUIdock.

```
#Locate to script file
#Use following command to start GUIdock
sh runGUIdockLinux.sh
```

The script creates a shared folder ".guidock/GUIdock-SHARED" under user home directory. ~/.guidock/GUIdock-Shared in the Linux system is linked with /root/GUIdock-SHARED within the container.



-	able file	V		
	e-unix-3.2.1 eConfiguration SHARED			
File <u>N</u> ame: Files of <u>T</u> ype:	All Files			•
			<u>O</u> pen	Cancel

To open shared folder in Linux system, type the following commands in terminal:

#Locate to	.guidock	directory
cd .guidocł	٢/	
cd .guida	ock/	
#Open share	ed folder	
xdg-open . xdg-open		

Double click on the shared folder "GUIdock-SHARED".



In shared folder, copy and paste a file or folder you want to share. The folder is added to the "/root/GUIdock-SHARED" directory in the container.



8	0.0	GUIdock-SH	ARED	
<		ŵ Home	.guidock	GUIdock-SHARED
0	Recen	nt		
â	Home			
in i	Deski	op	CA	NCER-CELL-LINES

To share files or folders between a container and Linux system, add them in "GUIdock-SHARED" folder.

Transferring files (OS X)

To transfer files between a container and the local filesystem in OS X, run the script using the following command to start GUIdock.

```
# Download and locate to installation file.
# Use following command to start GUIdock
sh mac-start.sh
```

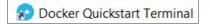
Open terminal and follow the steps for "**Transferring a file from the local machine to running container**" and "**Transferring a file from running container to the local filesystem** "below.

Transferring files (Windows)

To transfer files between a container and the local filesystem in Windows, double click on the shell script file to start GUIdock.



Open "Docker QuickStart Terminal" and follow the steps for "**Transferring a file from the local machine to running container**" and "**Transferring a file from running container to the local filesystem**" below.



Transferring a file from the local filesystem to running container

Check running container by typing the following command in terminal :

#List running containers docker ps

<pre>\$ docker ps CONTAINER ID</pre>	IMAGE	COMMAND	CREATED
STATUS	PORTS	NAMES	35 minutes ag
da229e046dc8	kristiyanto/guidock	"/bin/sh -c 'sh /root"	
o Up 35 minut	es 8787/tcp	gloomy_bardeen	

Transfer a file from the local filesystem to running container by typing the following command in terminal:

#Transfer file from the local filesystem to a container.

docker cp localPath containerID:path

\$ docker cp Desktop/CANCER-CELL-LINES/CancerCellLine.txt da229e046dc8:/root/DEMO

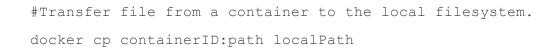
Data file is added to "/root/DEMO" directory.

▶ This PC → Desktop → CANCER-CELL-LINES	Session file to load@da229e046dc8
Anme CancerCellLine.txt directed2.xml	Look In: DEMO

Transferring a file from running container to the local filesystem

To transfer a file from running container to the local filesystem, type the following command in terminal:

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\$ docker cp da229e046dc8:/root/DEM0/Test.cys Desktop/CANCER-CELL-LINES/

Data file is saved in "Desktop/CANCER-CELL-LINES" directory from running container.

Session file to load@da229e046dc8	▶ This PC ▶ Desktop ▶ CANCER-CELL-LINES
Look In: DEMO CancerCellLine.txt Yeast.cys DREAM4.cys Yeast.txt DREAM4.txt RNAseq.cys RNAseq.txt Test.cys	Name CancerCellLine.txt directed2.xml Test.cys
File Name: Files of Type: All Files	

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