# **TED Documentation**

Release 0.0.1

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Apr 08, 2018

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#### A comprehensive approach for convenient transcriptomic profiling as a clinically-oriented application.

#### TED toolkit Manual-

Our Galaxy Page: http://galaxy.hunter.cuny.edu/u/bioitcore/p/transcriptomics-profiler-for-easy-discovery-ted-toolkit includes all instructions and sources in accessing and using the TED toolkit in full details, as well as the following content below.

Where to find TED

## 1.1 Pre-requisites

How to run TED

## 2.1 Setting up Data Inputs

## Chapter $\mathbf{3}$

## TED Virtual Machine (VM)

How to run the TED toolkit Virtual Machine (VM) Application

## 3.1 Pre-requisites

Download VirtualBox: http://www.virtualbox

### 3.2 Setting up TED VM Application

#### 3.2.1 Downdload TED VM files from Galaxy Data Libraries

Galaxy Data Libraries link: http://galaxy.hunter.cuny.edu/library/list#folders/Fb56e686e7a485784

Galaxy And			Shared Data - Visi			
DATA LIBRARIES (0 1 2 > showing 2 of 2 items inc Libraries / TED Virtual Machine (VM6 Application	lude deleted	••	Data Libraries Histories Workflows Visualizations	A Download +	* Delete	Ortails
same II		desci	Pages		data type	size
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C D RSA-Sea.coa					data	6.9 CB

## 3.2.2 Select Appliance on VM

9	Oracle VM VirtualBox Manager		×
File	Machine Help		
0	Preferences	Ctrl+G	Pasale Stranshots
Q	Import Appliance	Ctrl+I	
0	Export Appliance	Ctrl+E	elcome to VirtualBox!
	Virtual Media Manager Network Operations Manager Check for Updates Reset All Warnings	Ctrl+D	e left part of this window is a list of all virtual machines on your computer. The list is empty now cause you haven't created any virtual machines yet. order to create a new virtual machine, press the <b>New</b> button in the in tool bar located at the top of the window.
$\checkmark$	Exit	Ctrl+Q	w.virtualbox.org for the latest information and news.
Imp	ort an appliance into VirtualBox		a la construcción de la construcción

#### 3.2.3 Import OVA Appliance on VM



#### 3.2.4 TED Appliance settings for import on VM



#### 3.2.5 TED Appliance Importing on VM



## 3.3 TED Appliance Settings on VM

#### 3.3.1 Go to Settings



#### 3.3.2 System Requirements

Open virtual disk file for TED Appliance on VM

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	System	Storage Tree	i	Attributes					
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	File name:	boot2docker			~	All virtual op	tical disk fi	les (*.c	fr ~
						Open		Cancel	
						1			

#### 3.3.3 Network

Setup Adapter 1



Setup Adapter 2



#### 3.3.4 Shared Folders

Setup Adapter 1

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RNA-Seq - Settings		?	×
E General	Shared Folders		
🗾 System	Folders List		
Display	Name Path	Auto-mount Access	
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Audio			
Network			
Serial Ports			
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Shared Folders			
User Interface			
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		UN Carte	
	I INP RECIVORK		
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	Adapter 1: Intel PRO/1000 MT ( Adapter 2: Intel PRO/1000 MT ( Adapter)	Desktop (NAT) Desktop (Host-only Adapter, 'VirtualBox Host-Only	Ethen

## 3.4 Connecting TED Appliance on VM

#### 3.4.1 Go to Settings



#### 3.4.2 Broad casted Galaxy instance IP address

R R	NA-Seg [R	unning)	- Oracle	VM Virtual	lex				_		×
File	Machine	View	Input	Devices	Help						
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****	*****	*****	****	*****	*****	****	******	****	****	****	***
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							8	0 7 🗆 🗏 🕯	100	) 💽 Rig	ht Ctrl

#### 3.4.3 Web Browser connection of Galaxy instance on VM

/ ₹ Galaxy × ← → C © 192.168.56.10	05.8080			- □ ×
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Tools	1		History	00
search tools	0	Your Galaxy is running!	search datasets	0
Rev_Trans Get.Data Lift-Over		To learn how to use Galaxy please see the <u>wiki</u> To install new tools to your Galaxy follow the <u>tutorial</u> To set up your Galaxy for others to use please read <u>this</u> Thank you for trying Galaxy.	Unnamed history 0 bytes O This history is er	npty. You can
Filter and Sort Join, Subtract and Group Convert Formats Extract Features		To customize this page edit static/welcome.html	load your own d from an externa	ata or <u>oet data</u> Lisource
Fetch Sequences Fetch Alianments Get Genomic Scores Statistics Graph/Display. Data Phenotype Association		<u>Galaxy</u> is an open, web-based platform for data intensive biomedical research. The <u>Galaxy</u> team is a part of <u>BX</u> at <u>Penn Stats</u> , and the <u>Biology</u> department at <u>Johns Hopkins</u> <u>University</u> . The <u>Galaxy Project</u> is supported in part by <u>NHGRI. NSF</u> . The <u>Huck Institutes of</u> the Life Sciences. The Institute for CyberScience at Penn State, and Johns Hopkins.		
NGS TOOLBOX BETA NGS: OC and manipulation NGS: Mapping				

## 3.5 How to access TED toolkit on VM

### 3.6 TED VM Troubleshoot

#### 3.6.1 Galaxy instance IP address unreachable

192.168	56.105 ×	▲ - ¤ ×
< → C	192.168.56.105.8080	ŵ i
	This site can't be reached	
	192.168.56.105 refused to connect.	
	Search Google for 192 168 105 8080	
	ERR_CONVECTION_REPUSED	

#### 3.6.2 Reinitialize TED appliance



#### 3.6.3 Reconnect Galaxy instance IP address on web browser

/ ₹ Galaxy 3 ← → C (© 192.168.56	× \		4	- D	×
\Xi Galaxy		Analyze Data Workflow Shared Data + Visualization Help+ User+		Using 0 byt	tes
Tools	1		History	0	0
search tools	0	Your Galaxy is running!	search datasets		0
Rev_Trans Get.Data Lift-Over Text Manipulation Citize and Cost		To learn how to use Galaxy please see the <u>wiki</u> To install new tools to your Galaxy follow the <u>batorial</u> To set up your Galaxy for others to use please read <u>this</u> <b>Thank you for trying Galaxy.</b>	Unnamed history © bytes O This history is en load your own do	npty. You can ata or get data	8
Eilter and Sort Join, Subtract and Group Convert Formats Extract Features		To customize this page edit static/welcome.html			
Fetch Sequences Fetch Alianments Get.Genomic Scores Statistics Graph/Display.Data Phenotype Association		<u>Galaxy</u> is an open, web-based platform for data intensive biomedical research. The <u>Galaxy</u> team is a part of BX at <u>Penn State</u> , and the <u>Biology</u> department at <u>Johns Hopkins</u> <u>University</u> . The <u>Galaxy Project</u> is supported in part by <u>NHGRI. NSF</u> . The <u>Huck Institutes of</u> the Life Sciences. The Institute for CyberScience at Penn State, and <u>Johns Hopkins</u> .			
NGS TOOLBOX BETA NGS: OC and manipulation NGS: Mapping					

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