Set up and run a R project in MLflow

In this story I have described how to use *MLflow* to track machine learning model training. *MLflow* also comes with a `Projects` component that packs data, source code with commands, parameters and execution environment setup together as a self-contained specification. Once a *MLproject* is defined, users can run it everywhere. Currently *MLproject* can run Python code or shell command. It can also set up the Python environment for the project specified in the `conda.yaml` file defined by users.

For R users, it is common to load some packages in the R source codes. These packages need to installed for the R code to run. In the future, it could be a good enhancement for *MLflow* to add something similar to `conda.yaml` to set up R package dependencies. But we do not have to wait for it. I will show how to create a *MLproject* containing R source code and run it with `mlflow run` command.

First, create a directory and copy the data and R source codes to that directory. For example,

```
.
└── R
    ├── MLproject
    ├── prep.R
    ├── rpart-example.R
    └── wine-quality.csv
```

In this example, the data to be learned is `wine-quality.csv`. The example is to run the `rpart-example.R` to fit a tree model:

```
# Source prep.R file to install the dependencies
source("prep.R")

# Import mlflow python package for tracking
library(reticulate)
mlflow <- import("mlflow")

# Load rpart to build a tree model
library(rpart)

# Read in data
wine <- read.csv("wine-quality.csv")

# Build the model
fit <- rpart(quality ~ ., wine)

# Save the model that can be loaded later
saveRDS(fit, "fit.rpart")

# Save the model to mlflow tracking server
mlflow$log_artifact("fit.rpart")

# Plot
jpeg("rplot.jpg")
par(xpd=TRUE)
plot(fit)
text(fit, use.n=TRUE)
dev.off()

# Save the plot to mlflow tracking server
mlflow$log_artifact("rplot.jpg")
```

The R code above includes three parts: the model training, the artifacts logging through *MLflow*, and the R package dependencies installation. In this example, these two R packages, `reticulate` and `rpart`, are required for the code to run. To pack these codes into a self-contained project, some sort of script should be run to automatically install these packages if the platform does not have them installed.

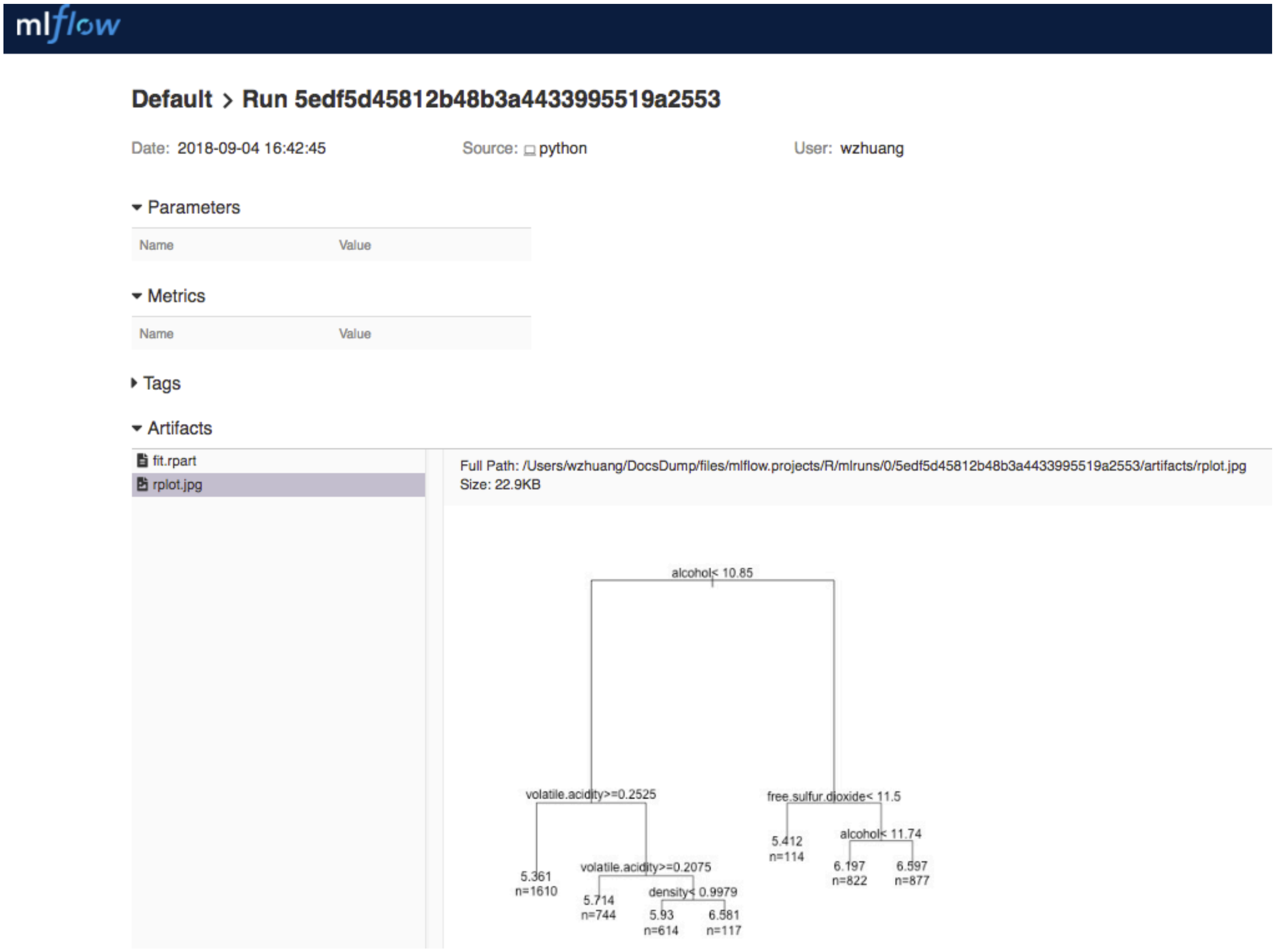
With our approach, any specific R package needed for the project is going to be installed through `prep.R` with these codes:

```
# Accept parameters, args[6] is the R package repo url
args <- commandArgs()

# All installed packages
pkgs <- installed.packages()

# List of required packages for this project
reqs <- c("reticulate", "rpart")

# Try to install the dependencies if not installed
sapply(reqs, function(x){
  if (!x %in% rownames(pkgs)) {
    install.packages(x, repos=c(args[6]))
  }
})
```

Before packaging these into a *MLproject*, try to test by directly invoking `Rscript` command as follow:

```
Rscript rpart-example.R https://cran.r-project.org/
```

From the *MLflow* UI, you should see this run been tracked like this screen snapshot:



Default > Run 5edf5d45812b48b3a4433995519a2553

Date: 2018-09-04 16:42:45 Source: python User: wzhuang

Parameters

Name	Value

Metrics

Name	Value

Tags

Artifacts

fit.rpart
rplot.jpg

Full Path: /Users/wzhuang/DocsDump/files/mlflow.projects/R/mlruns/0/5edf5d45812b48b3a4433995519a2553/artifacts/rplot.jpg
Size: 22.9KB

Now let's write the spec and pack this project into a *MLproject* that *MLflow* knows to run. All needed to be done is creating the `MLproject` file in the same directory.

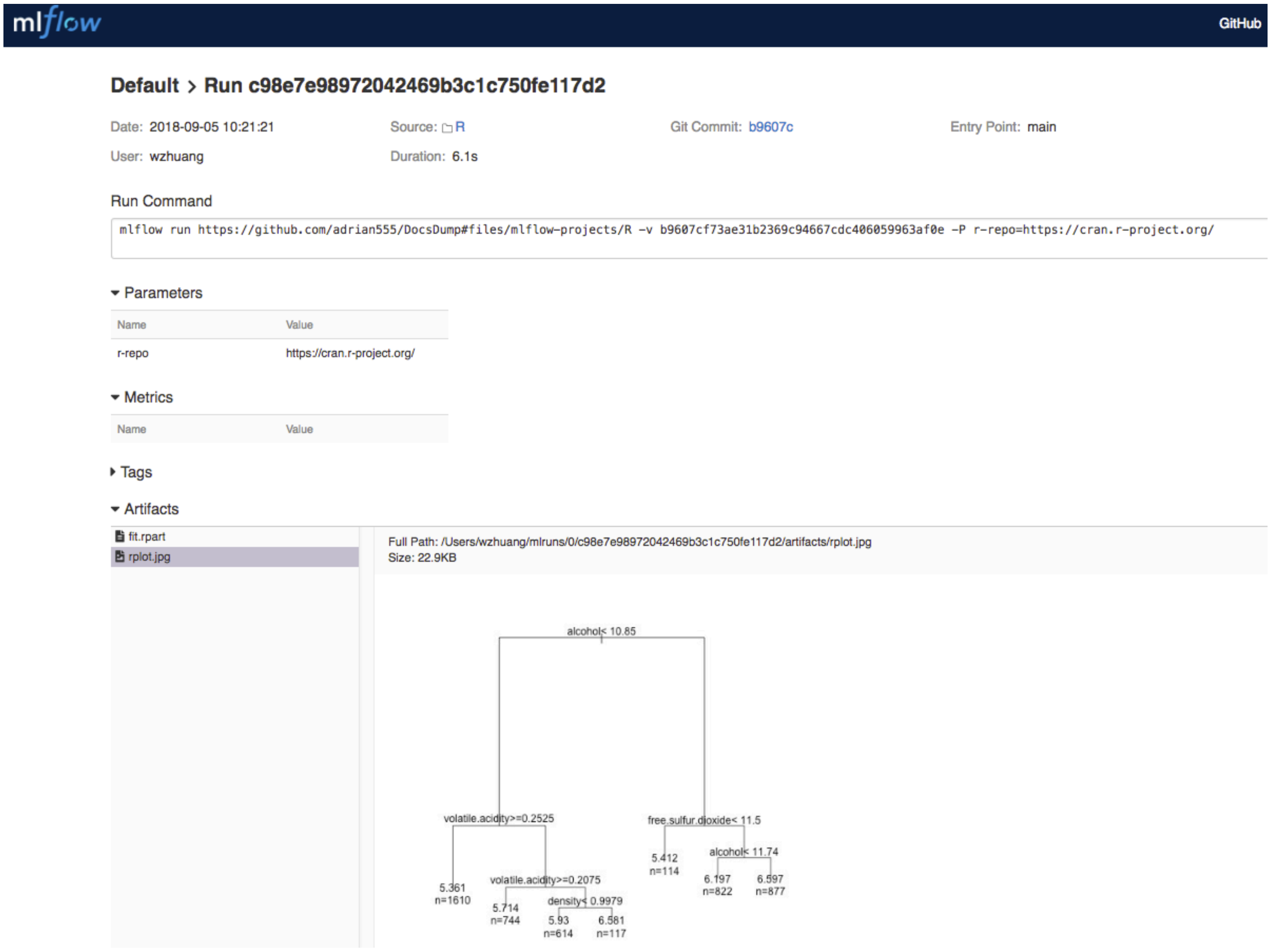
```
name: r_example

entry_points:
    main:
        parameters:
            r-repo: {type: string, default: "https://cran.r-project.org/"}
        command: "Rscript rpart-example.R {r-repo}"
```

In this file, it defines a `r_example` project with a `main` entry point. The entry point specifies the command and parameters to be executed by the `mlflow run`. For this project, `Rscript` is the shell command to invoke the R source code. `r-repo` parameter provides the URL string where the dependent packages can be installed from. A default value is set. This parameter is passed to the command running the R source code.

Now that all are set so the project can be checked in and pushed to github repository. With following command, it can be run on any platform that has R installed.

```
mlflow run https://github.com/adrian555/DocsDump#files/mlflow-projects/R
```

The project can also be viewed from the *MLflow* tracking UI like this screen snapshot:



Default > Run c98e7e98972042469b3c1c750fe117d2

Date: 2018-09-05 10:21:21
Source: R
Git Commit: b9607c
Entry Point: main
User: wzhuang
Duration: 6.1s

Run Command

```
mlflow run https://github.com/adrian555/DocsDump#files/mlflow-projects/R -v b9607cf73ae31b2369c94667cdc406059963af0e -P r-repo=https://cran.r-project.org/
```

Parameters

Name	Value
r-repo	https://cran.r-project.org/

Metrics

Name	Value

Tags

Artifacts

fit.rpart
rplot.jpg

Full Path: /Users/wzhuang/mlruns/0/c98e7e98972042469b3c1c750fe117d2/artifacts/rplot.jpg
Size: 22.9KB

The differences between this view and previous run without `Mlproject` spec are the `Run Command` which captures the exact command to run the project, and the `Parameters` which automatically logs any parameters passed to entry points.

This is exactly what `Projects` component of *MLflow* is designed for, to define the project and make it easily to be rerun. R users can quickly set up their projects and enjoy the easiness of tracking and running projects with *MLflow* once going through this example.