

## Stuart Robinson <stuart.clifford@gmail.com>

# **Chat with Bobby Madamanchi**

January 22, 2014

**Stuart Robinson** - 10:56 AM you there

**Bobby Madamanchi** - 10:57 AM hey

**Stuart Robinson** - 10:57 AM emailed test file, does this format look okay? alphabetized column names

Bobby Madamanchi - 11:01 AM so each row is a new patient thats great i hope that did not take you all night

**Stuart Robinson** - 11:03 AM 20 minutes last night, hour this morning it's running now, will take a few minutes

**Bobby Madamanchi** - 11:03 AM oh ok great thanks saved a ton of time on my end

Stuart Robinson - 11:04 AM yeah one line per patient oh i like doing this stuff. good practice, and a nice break from the stocks stuff.

**Bobby Madamanchi** - 11:05 AM so are you backtesting for 3 hours still? i mean 5years?

Stuart Robinson - 11:05 AM
oh no
forward testing now
set up interactivebrokers.com account

**Bobby Madamanchi** - 11:05 AM ok

**Stuart Robinson** - 11:06 AM they let you set up fake money account so they simulate market for me

Bobby Madamanchi - 11:12 AM

hey um

i need to have the ID in the row

i just noticed that

# Stuart Robinson - 11:13 AM

patientID?

## Bobby Madamanchi - 11:13 AM

its the TCGA-###-#####

#### Stuart Robinson - 11:13 AM

oh, in the filename

?

## Bobby Madamanchi - 11:13 AM

yeah

it should also be somewhere within thefile

as well

#### Stuart Robinson - 11:13 AM

hmm

#### Bobby Madamanchi - 11:13 AM

but but just pulling from the filename would befine too

#### Stuart Robinson - 11:14 AM

oh fuck i see what i did

okay

it missed values containing weird characters like "-" and maybe "." hold on

### Bobby Madamanchi - 11:15 AM

yeah these things are so badly curated and this is both the thyroid file and skin file together? they ahve the same headings?

#### Stuart Robinson - 11:16 AM

yeah they're all dumped together do you need separate files?

# Bobby Madamanchi - 11:16 AM

no

### Stuart Robinson - 11:21 AM

did you see email?

any idea why my program would have skipped like 40+ patients?

## Bobby Madamanchi - 11:22 AM

with this stuff its possible they were duplicates or they were empty i cant believe how badly the stuff is done 810 is closer to what i was expecting 497+306 is what i have sequencing data for anyway

so if that is within these 810, thats great

**Stuart Robinson** - 11:26 AM ok it's re-running, have to shower

**Bobby Madamanchi** - 11:29 AM alright, thanks again