Gmail

xmls

6 messages

Bobby Madamanchi <akmadamanchi@gmail.com>   Tue, Jan 21, 2014 at 1:14 PM
To: Stuart Robinson <Stuart.clifford@gmail.com>

hey attached are the 2 batches of xml files

if you can easily parse them great. otherwise, i will find an R utility to grind through these tonight.

i only need fields such as Tumor Grade, alive/dead, progression/remission, survival days, metastasis, and those types of outcome or staging related fields. I haven't really see whats on there yet.

thanks

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2 attachments

📎 **ThyroidCancerXMLs - Copy.zip**
2453K

📎 **TCGA_SKCMxmls.zip**
1342K

Stuart Robinson <stuart.clifford@gmail.com>   Wed, Jan 22, 2014 at 12:15 AM
To: Bobby Madamanchi <akmadamanchi@gmail.com>

looking now
[Quoted text hidden]

Stuart Robinson <stuart.clifford@gmail.com>   Wed, Jan 22, 2014 at 11:10 AM
To: Bobby Madamanchi <akmadamanchi@gmail.com>

ok here is final output, i thought it should be all the patients. but it's only 810 lines.

you sent me 856 files

could some of the files not contain data? i'm running again checking for data contents

[Quoted text hidden]

📄 **bobbyOutput.txt**
230K

Stuart Robinson <stuart.clifford@gmail.com>   Wed, Jan 22, 2014 at 11:30 AM
To: Bobby Madamanchi <akmadamanchi@gmail.com>

how are these? still don't know why its missing files, it could be my fault. i don't want you to lose 5% of patients
[Quoted text hidden]

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2 attachments

bobbyOutput ThyroidCancerXMLs - Copy.txt

📄 310K

📄 **bobbyOutput TCGA_SKCMxmls.txt**
161K

Bobby Madamanchi <akmadamanchi@gmail.com>   Wed, Jan 22, 2014 at 11:33 AM
To: Stuart Robinson <stuart.clifford@gmail.com>

this looks fantastic

[Quoted text hidden]

Stuart Robinson <stuart.clifford@gmail.com>   Wed, Jan 22, 2014 at 5:09 PM
To: Bobby Madamanchi <akmadamanchi@gmail.com>

oh nm. you sent me 808 patient files. i can't add.
[Quoted text hidden]