Chapter 1. First Class of Linux and Lexical analysis (Borrow Alex's case)

Jingbo Xia College of Informatics, HZAU

HZAU, xiajingbo.math@gmail.com

http://www.linuxcommand.org/man_pages/tr1.html

Linux command tr:

tr - translate or delete characters SYNOPSIS

tr [OPTION]... SET1 [SET2]

DESCRIPTION

Translate, squeeze, and/or delete characters from standard input, writing to standard output.

-c, --complement

first complement SET1

-d, --delete

delete characters in SET1, do not translate

-s, --squeeze-repeats

replace each input sequence of a repeated character that is listed in SET1 with a single occurrence of that character

-t, --truncate-set1

first truncate SET1 to length of SET2

HZAU, xiajingbo.math@gmail.com

http://www.tecmint.com/13-basic-cat-command-examples-in-linux/

Linux command cat:

The cat (short for "concatenate") command is one of the most frequently used command in Linux/Unix like operating systems. cat command allows us to create single or multiple files, view contain of file, concatenate files and redirect output in terminal or files. In this article, we are going to find out handy use of cat commands with their examples in Linux.

HZAU, xiajingbo.math@gmail.con

http://www.thegeekstuff.com/2013/04/sort-files

Sort command is helpful to sort/order lines in text files. You can sort the data in text file and display the output on the screen, or redirect it to a file. Based on your requirement, sort provides several command line options for sorting data in a text file.

Sort Command Syntax:

\$ sort [-options]

HZAU, xiajingbo.math@gmail.com

Case study:

Text complexity comparison of plain text and biomedical text

Corpora are borrowed from DSG group. http://dsg.ctl.cityu.edu.hk

HZAU, xiajingbo.math@gmail.com

Linux commands for lexicon

\$cat pubmed-a.txt |tr -cs "[:alnum:]" "\n" |tr [:upper:] [:lower:] |split -1000

\$ wc xaa

1000 999 5935 xaa

\$sort xaa |uniq |wc

458 457 3307

\$cat pubmed-a.txt |tr -cs "[:alnum:]" "\n" |tr [:upper:] [:lower:] |split -2000

\$wc xaa

2000 1999 11759 xaa

\$ sort xaa |uniq |wc

782 781 5614

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Case study: Comparison of BROWN corpus and Pubmed

Linux commands for lexicon

\$cat pubmed-a.txt |tr -cs "[:alnum:]" "\n" |tr [:upper:] [:lower:]

>pubmed.a.pure.txt

\$wc pubmed.a.pure.txt

\$sort pubmed.a.pure.txt |uniq |wc

31638 31638 282238

So the token/word ratio is 31638/1032975 = 3.06%.

\$cat BROWN_A.txt |tr -cs "[:alnum:]" "\n" |tr [:upper:] [:lower:]
>BROWN_A.pure.txt

\$wc BROWN A.pure.txt

91064 91063 515866

\$sort BROWN_A.txt |uniq |wc

11927 11926 95306

So the token/word ratio is 11927/91064 = 13.09%.

But this is an unfair comparison.

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Case study: Comparison of BROWN corpus and Pubmed

Assignment:

Currently, you know how to compute token/word ratio of a text and evaluate its lexical complexity.

Select texts with your interests sizes, analyze their differences, and do a comparison.

Find something novel and prepare a 10 minutes talk in next class. Two members win the points.

Chapter 1.

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