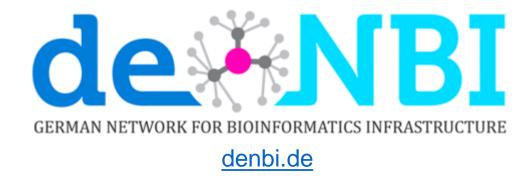
Part of German Network for Bioinformatics Infrastructure







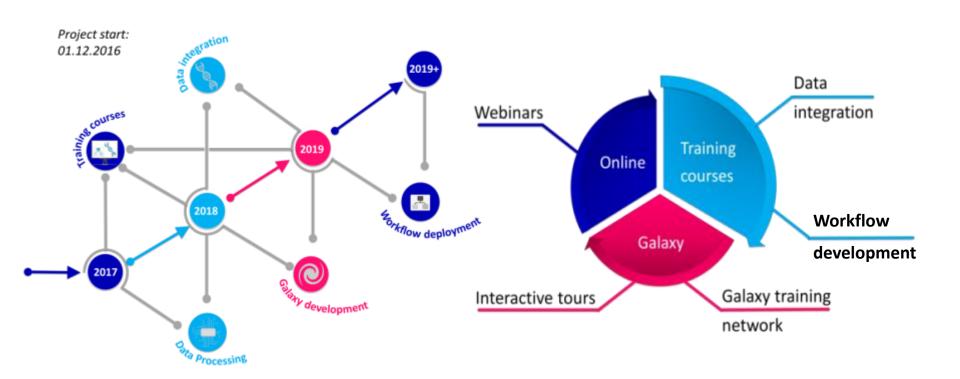
destair.bioinf.uni-leipzig.de

Structured Analysis and Integration of RNA-Seq experiments (de.STAIR)

Our aim is to enable a comprehensive **analysis of RNA-Seq experiments as a service.** To enable maximum usefulness, interconnectivity, and accessibility for the developed approaches and services, we will provide dedicated **workshops**, **training programs and screen casts** for bioinformaticians and other life scientists.

de.STAIR - RNA-Seq analysis and integration







Supporting new data analysis approaches

















Bioinformatics carpentry utilizing Galaxy

Day 2 - Data formatting

David Brauer







Data formatting

- Why is data formatting necessary and important?
- Which data formatting tools does Galaxy offer?
- How can you use them for e.g.:
 - data preprocessing
 - data merging
 - data subsetting
- Regular expressions



Data formatting

- Why is data formatting necessary and important?
 - machine-readable format is mandatory
 - different tools = different formats/standards
 - subsetting for directed analyses



Types of data (1)

- computer-generated data, e.g.:
 - FASTA/FASTQ files
- manually recorded data, e.g.:
 - physiological parameters (weight, blood sugar, ...)
 - cell counts
 - questionnaires



Types of data (2)

- computer-generated data
 - usually standardized
 - machine-readable by nature



Types of data (3)

- manually recorded data
 - usually your metadata
 - the "human" factor
 - data tidiness often only an afterthought



Problems with manually recorded data (1)

- way of recording the data
 - transcribing from a notebook
 - typing into Excel (or LibreOffice Calc etc) sheets
 - optimized for human readability/comfort



Α	В			-	-					12								
А	В	С	D	Е	F	G	Н	I	J	K	L	M	N	0	Р	Q	R	S
		Tabelle 1											Tabelle 2					
		sample_a	sample_b	sample_c	sample_d	sample_e	sample_f					feature_15	feature_16	feature_17	feature_18	feature_19	feature_20	
	feature_1	123	123	123	123	123	123				sample_w	A	4785	4785	5 AB	4785	4785	
	feature_2	456	456	456	456	456	456				sample_y	В	5118	5118	HFG	5118	5118	
	feature_3	789	789	789	789	789	789				sample_z	С	5451	5451	1 WU	5451	5451	
	feature_4	1122	1122	1122	1122	1122	1122				sample_j	D	5784	5784	4 CJH	5784	5784	
	feature_5	1455									sample_q	E	6117			6117		
	feature_6	1788									sample_i	F	6450		CIH	6450		
	feature_7	2121									sample_j	G	6783	6783	3 WI	6783	6783	
	feature_8	2454																
	feature_9	2787																
	feature_10	3120	3120	3120	3120	3120	3120											
							Т	abelle	3									
							1h			5h			12h			24h		
							feature_1	feature_2	feature_3	feature_1	feature_2	feature_3	feature_1	feature_2	feature_3	feature_1	feature_2	feature_3
						sample_a	123											
						sample_b	123											
						sample_c	123											
						sample_d	123											
						sample_e	123											
						sample_f	123											
						sample_g	123											
						sample_h	123	456	789	124	45	790	125	458	3 791	126	459	792



Problems with manually recorded data (2)

- common errors/inconsistencies
 - capitalization
 - varying use of . and , as decimal separators
- common problems
 - small helpers for human readability, e.g.:
 - empty columns to distinguish columns more easily
 - several tables on one sheet



Solving the problems

- takes time (a lot in many cases)
- can be difficult/tedious

easiest solution:

getting it right at the source!



How to (generally) structure data (1)

- actually rather simple:
 - every single sample in its own row
 - every single parameter in its own column
- do not:
 - use subcategories
 - place separate tables on one sheet



How to (generally) structure data (2)

- helpful conventions (esp. for variable names)
 - do not use whitespace characters, rather use:
 - underscores (e.g.: max_velocity)
 - Camel case variations (e.g. maxVelocity or MaxVelocity)
 - do not include special characters, e.g. for units
 - bad: "Serum creatinine level [μmol/l]"
 - better: "serum_creatinine" and an additional plain text file with information about units
 - do not use umlauts etc. (ä, ö, ü, ß, ...)



Other use cases

- merging data
 - by ID to add features
 - to add samples
- subsetting data
 - excluding samples below a certain threshold
 - excluding a certain experimental group



Tools in your toolbox

- many tools available
- context- and problem-dependent uses
- different ways to achieve the same results



What we're going to cover

- transposing rows and columns
- find&replace operations using different tools
- merging two complementary data sets
- excluding samples based on their experimental group



What we're going to use

- existing "GUI" tools
- wrappers for the UNIX utilities sed and awk
- regular expressions



Use Case 1: Wrong orientation (1)

- first, we need to upload the data:
 - click "Choose local files"
 - select "transpose.csv" and "addFeatures.csv" (we'll need it later)
 - click "Start"
- comma-separated, Galaxy mainly works on tabseparated files



Use Case 1: Wrong orientation (2)

- go to "General Text Tools" > "Text Manipulation"
 "Convert delimiters to TAB"
- in the "Convert all" dropdown menu, select "Commas"
- select Multiple Datasets (select both files)
- uncheck "Condense consecutive delimiters in one TAB"
- click "Execute"



Use Case 1: Wrong orientation (3)

- (rename the files)
- go to "General Text Tools" > "Join, Subtract and Group" > "Transpose rows/columns in a tabular file"
- select the correct file
- click "Execute"



Use Case 2.1: Matching IDs (1)

- can be achieved using different tools in Galaxy
- for this we will need regular expressions (Regex)
- "language" to describe string patterns
- can be used to match/find said patterns in text



Digression: Regular Expressions (1)

- character sets:
 - [a-z], [A-Z]
 - [0-9]
 - [a-zA-Z0-9]
- special characters (extended regex syntax):
 - . matches any character once (except newline)
 - ^ signifies beginning of a line
 - \$ signifies end of a line



Digression: Regular Expressions (2)

- special characters (cont.):
 - * previous pattern is matched zero or more times
 - + prev. pattern is matched once or more times
 - ? prev. pattern is matched once at most
 - {...} specifies an expected number of repetitions of the prev. pattern ({n}, {n,}, or {n,m})
 - () group particular pattern for later reference
 - separate alternate possibilities



Use Case 2.1: Matching IDs (2)

- go to "General Text Tools" > "Text Manipulation"
 "Column Regex Find And Replace"
- Select cells from "addFeatures_tabbed"
- using column "Column: 1"
- click "Insert Check"
- Find Regex: "([a-z])"
- Replacement: "sample_\1"



Use Case 2.2: Adding data (1)

- (rename the file)
- go to "General Text Tools" > "Text Manipulation" > "Join two files"
- 1st file: "transposed_tabbed", Column to use: "Column: 1"
- 2nd file: "addFeatures_tabbed_regex", Column to use: "Column: 1"



Use Case 2.2: Adding data (2)

- Output lines appearing in: "Both 1st & 2nd file."
- Check: "First line is a header line"
- we can misuse the "Value to put in unpaired (empty) fields": type in "id" to assign a new column name for column 1
- click "Execute"



Use Case 2.2: Adding data (3)

- (rename the file)
- go to "General Text Tools" > "Text Manipulation" > "Replace Text in entire line"
- select file: "merged_data"
- Find pattern: "Feat"
- Replace with: "feat"
- click "Execute"



Use Case 3: Selecting groups (1)

- upload: "addExpGrp.tsv", then merge
- (rename the file)
- go to "General Text Tools" > "Filter and Sort" > "Filter data on any column using simple expressions"
- select file: "added_Groups"



Use Case 3: Selecting groups (2)

- With following condition: "c22!='expA'"
- Number of header lines to skip: "1"
- click "Execute"



Advanced alternatives: sed and awk

- originally UNIX utilities
- implemented into Galaxy with wrappers
- can be more complex than the "simpler", mostly GUI-based functions we used so far
- have a lot of power and potential
- work row-wise



Text transformation with sed (1)

- <u>s</u>tream <u>ed</u>itor
- usually used for substitutions with the command s
- general structure:
 sed OPTIONS... [SCRIPT] [INPUTFILE...]
- for us here, only the script part is interesting:
 s / [regex to replace] / [replacement] / [flags]



Text transformation with sed (2)

- go to "General Text Tools" > "Text Manipulation" > "Text transformation with sed"
- Select multiple datasets (select both start files)
- SED Program:

```
s/^([a-z]),/sample_\1,/
s/^(,)/id\1/
s/Feat/feat/g
s/,/\t/g
```

|prepends "sample_"
|inserts "id" in first cell
|lower case features
|replaces commas with tabs



click "Execute"

Text transformation with sed (3)

- while theoretically now a tab-separated file, Galaxy doesn't convert it to tabular itself
- on the resulting files, go to "Edit attributes"



- select the tab "Convert"
- Name: "Convert CSV to tabular"
- click "Convert datatype"



Text reformatting with awk (1)

- named after the initials of the authors
- usually used to match a pattern (regex) and perform an action on a match
- general structure:pattern { action 1; action 2; action 3; }
- possible actions include printing only specified fields or arithmetic operations



Text reformatting with awk (2)

- go to "General Text Tools" > "Text Manipulation" > "Text reformatting with awk"
- select file "added_Groups"
- AWK Program:
 \$2>124 && \$22 ~ /exp[A-Z]/ {print \$1, \$2, \$21-\$20, \$22}
- click "Execute"



Text reformatting with awk (3)

• AWK Program:

\$2>124 && \$22 ~ /exp[A-Z]/ {print \$1, \$2, \$21-\$20, \$22}

• pattern:

\$2>124 field 2 needs to be bigger than 124

&& and

 $$22 \sim /\exp[A-Z]/$ field needs to match the regex



Text reformatting with awk (4)

AWK Program:
 \$2>124 && \$22 ~ /exp[A-Z]/ {print \$1, \$2, \$21-\$20, \$22}

• action:

on success, print the values of field 1, field 2, field 21 minus field 20, and field 22

 the commas cause the output to be separated (multiple table cells)



Quick recap

- lots of tools, plenty more available
- lots of use cases, plenty more imaginable
- no need to use anything, but: good to know that you can, should you need to!



Tools in your toolbox...

- learning by doing
- look through the tool list
- play around with the additional files
- play around with your own files



Thank you for listening!

