

analysis of RNA expression on different dietary regimes in obese subjects

Network Based Data Analysis project

12th June 2023

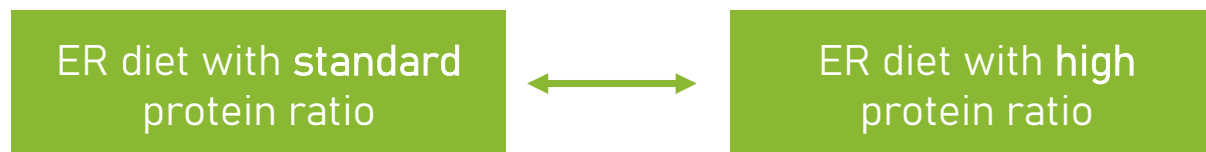
Vittoria Ossanna

introduction

overweight and obesity — growing worldwide problems
current valid strategy — energy restrictive diets (ER)

studies up to 2017 related to animal testing

in this study: assess differences between



main differences in regimes:

- RNA metabolism
- KRAS related pathways

the dataset

22 healthy obese individuals undergo **ER diet**

```
graph TD; A[22 healthy obese individuals undergo ER diet] --> B[12 standard protein level (ER_SP)]; A --> C[10 high protein level (ER_HP)];
```

12 standard protein
level (ER_SP)

10 high protein
level (ER_HP)

samples taken before and after 12 weeks

expression estimates

—● RMA algorithm in the Bioconductor library 'Oligo'

data matrix of **33297 probes x 44 samples**

methods

exploratory analysis

- PCA
- feature reduction
- clustering

ML based classification

- Random Forest
- RIDGE and LASSO
- LDA
- rSCUDO

over representation analysis

network based analysis

- gProfiler
- pathfindR
- STRING

results - PCA

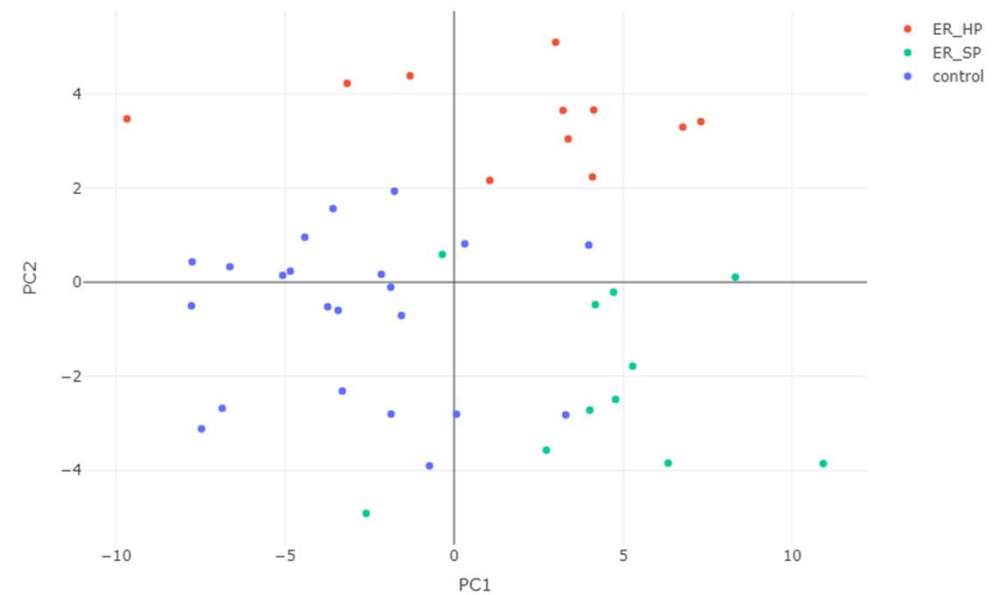
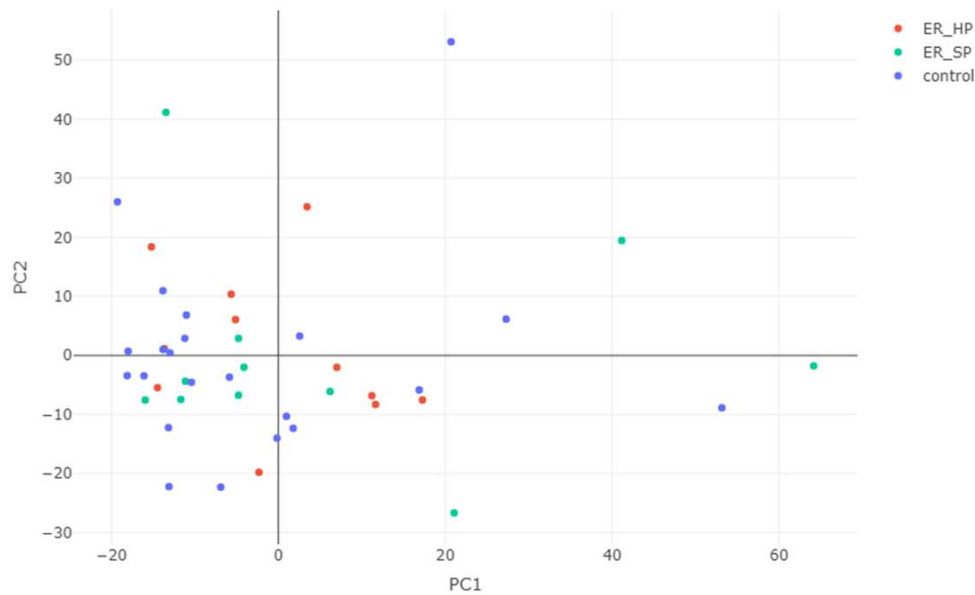
44 samples
33297 probes



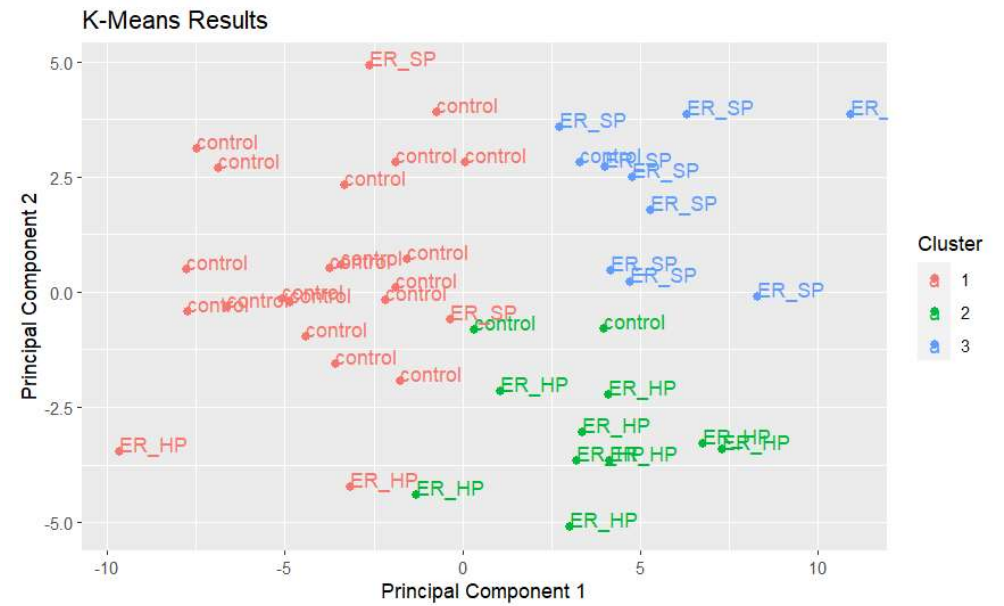
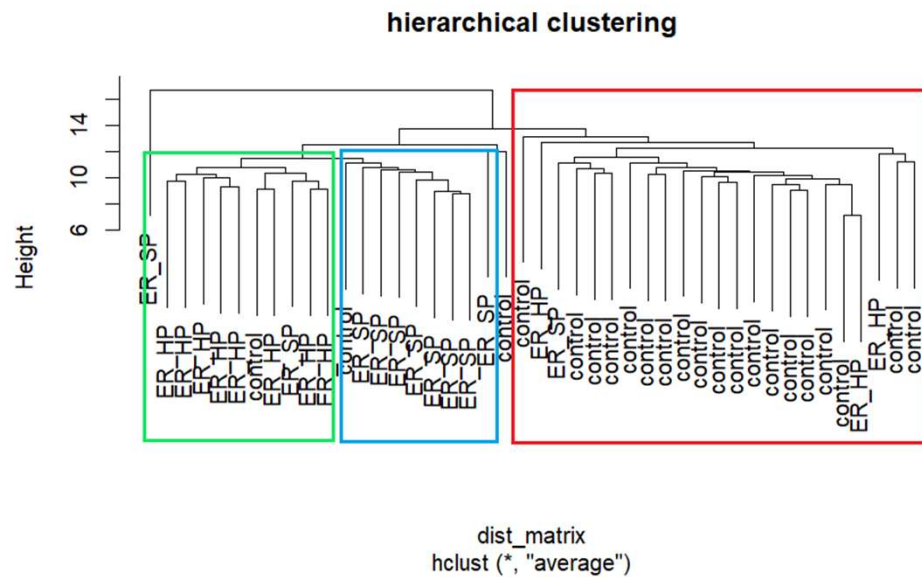
row t-test
 $\alpha = 0.01$



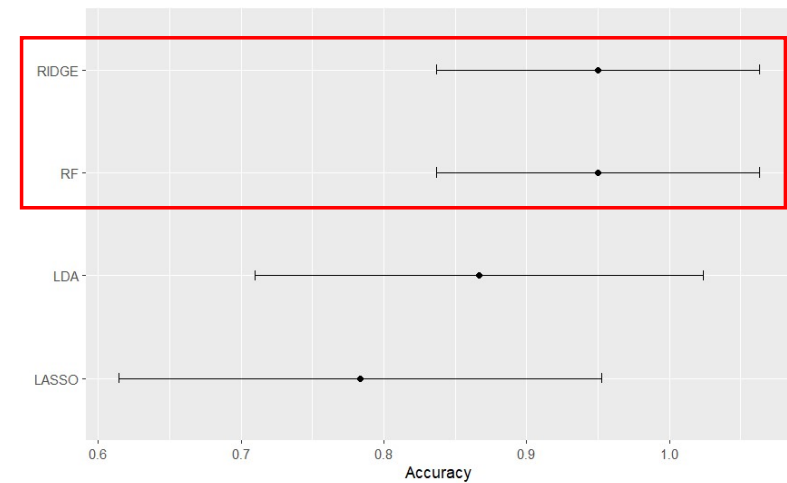
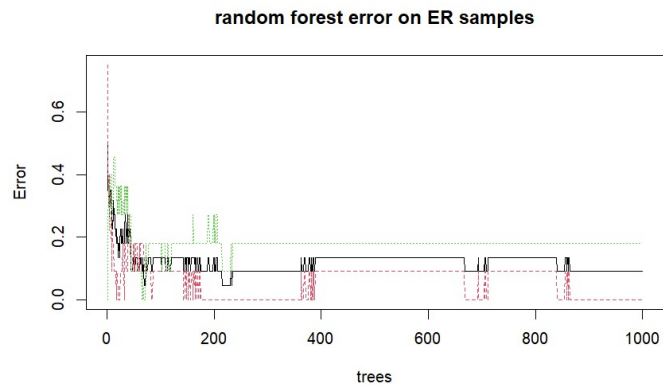
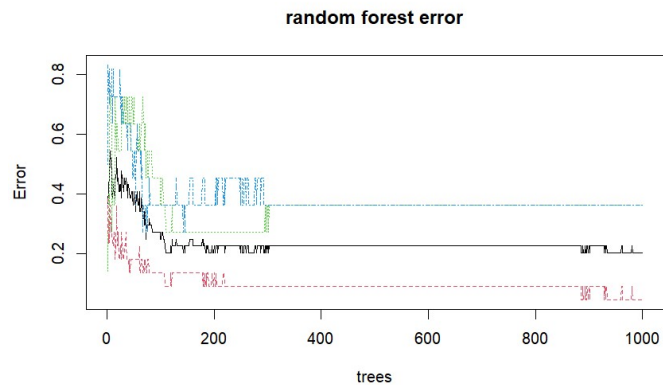
44 samples
1259 probes



results - clustering

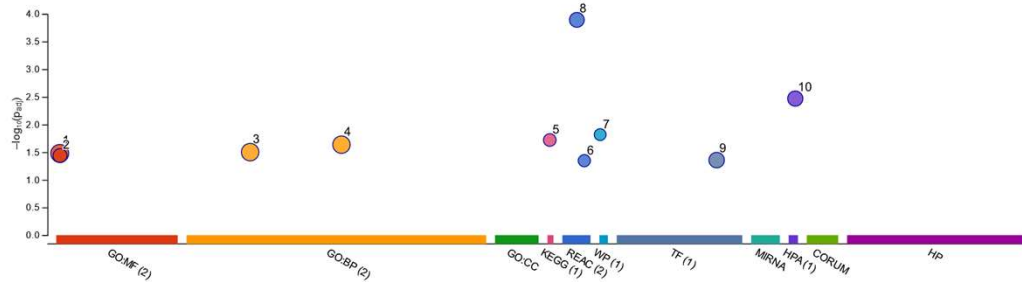


results – classification methods



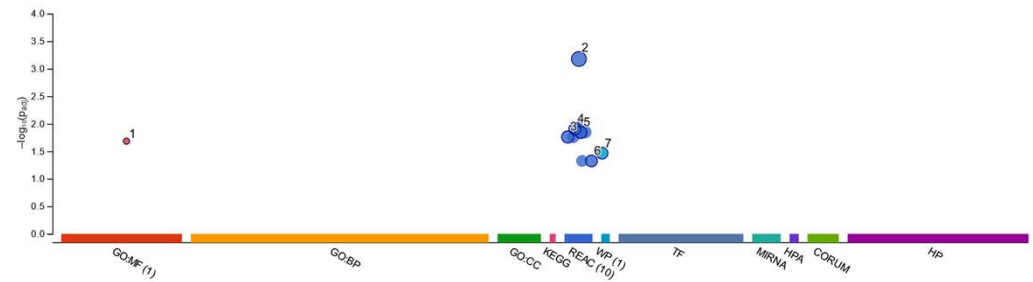
analysis between the two subsets of ER diets

results - ORA



ID	Source	Term ID	Term Name	Padj (query_1)
8	REAC	REAC:R-HSA-89...	Metabolism of RNA	1.283×10^{-4}
10	HPA	HPA:0440343	skeletal muscle myocytes(High)	1.199×10^{-3}
7	WP	WP:WP477	Cytoplasmic ribosomal proteins	3.528×10^{-2}
5	KEGG	KEGG:03040	Spliceosome	3.908×10^{-2}
4	GO:BP	GO:0051252	regulation of RNA metabolic process	2.315×10^{-2}
3	GO:BP	GO:0019219	regulation of nucleobase-containing compound ...	3.159×10^{-2}
1	GO:MF	GO:0003676	nucleic acid binding	3.329×10^{-2}
2	GO:MF	GO:0003729	mRNA binding	3.654×10^{-2}
9	TF	TF:M01597	Factor: Zfp281; motif: TGGGGGAGGGG	4.465×10^{-2}
6	REAC	REAC:R-HSA-17...	SRP-dependent cotranslational protein targeting L...	4.507×10^{-2}

ORA with RIDGE importance list



ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0044716	8-oxo-GDP phosphatase activity	2.006×10^{-1}
2	REAC	REAC:R-HSA-89...	Metabolism of RNA	6.640×10^{-4}
3	REAC	REAC:R-HSA-72...	Cap-dependent Translation Initiation	1.725×10^{-2}
4	REAC	REAC:R-HSA-72...	GTP hydrolysis and joining of the 60S ribosomal su...	3.236×10^{-2}
5	REAC	REAC:R-HSA-92...	Nonsense-Mediated Decay (NMD)	1.432×10^{-2}
6	REAC	REAC:R-HSA-19...	Viral mRNA Translation	4.729×10^{-2}
7	WP	WP:WP477	Cytoplasmic ribosomal proteins	3.416×10^{-2}

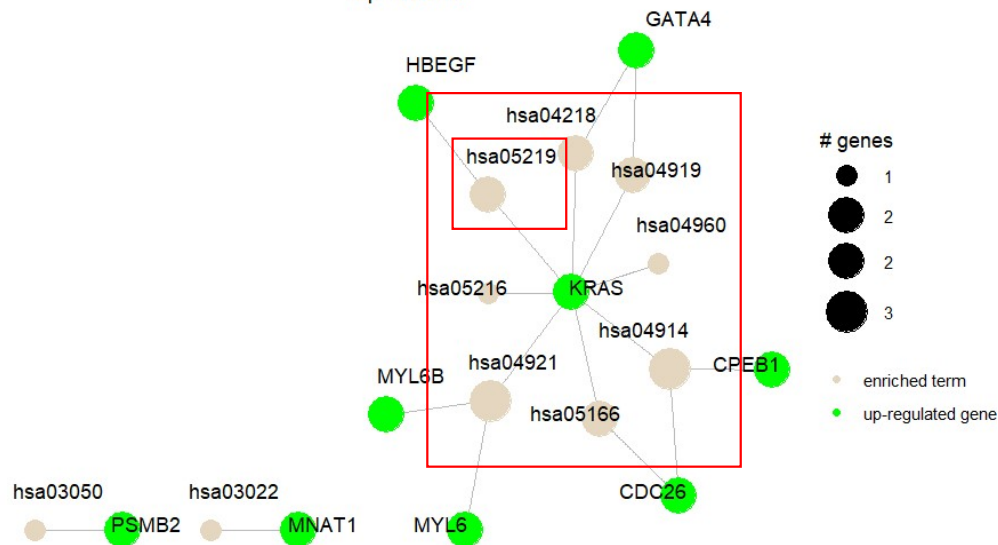
ORA with RF importance list

RNA metabolism
p-value 10^{-4}

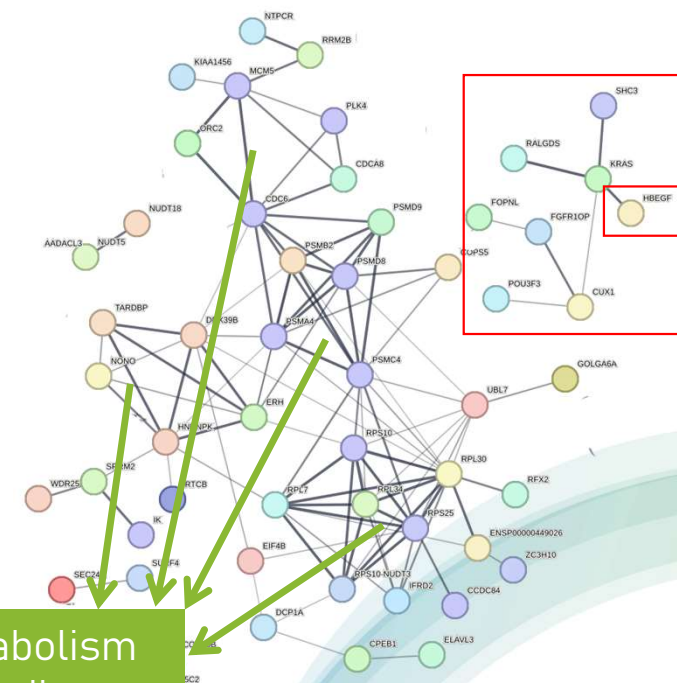
results - NBA

pathfindR

Term-Gene Graph
Top 10 terms



STRING



discussion and conclusion

RIDGE and **Random Forest**: best performing methods for classification
high variance due to low number of samples

gProfiler → increase items belonging to the **RNA metabolism**

STRING → **confirm** of high difference of RNA metabolism
also **confirmed in literature**

pathfindR → **KRAS** associated pathways
item in common with STRING



**thank you for
your attention!**