Sepsis 差异代谢物和热图绘制

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3.1 材料

3.2 方法

Mainly used method:

- R package `Limma` and `edgeR` used for differential expression analysis[1,2].
- R version 4.3.2 (2023-10-31); Other R packages (eg., `dplyr` and `ggplot2`) used for statistic analysis or data visualization.

4 分析结果

5 结论

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6.1 数据来源

Lipid metabolic signatures deviate in sepsis survivors compared to non-survivors (PMID:33304464)[3]

Supplementary Table 7: Rat sepsis model biochemical and metabolomic data.

'LipidMetabolicKhaliq2020 S7' 数据已全部提供。

(对应文件为 `Figure+Table/LipidMetabolicKhaliq2020-S7`)

> 注：文件夹 Figure+Table/LipidMetabolicKhaliq2020-S7 共包含 2 个文件。
>
> 1. 1_Data.csv
> 2. 2_legend.csv

6.2 差异分析

Table 1 (下方表格) 为表格 Sepsis vs Control metabolites 概览。

(对应文件为 `Figure+Table/Sepsis-vs-Control-metabolites.csv`)

> 注：表格共有 86 行 7 列，以下预览的表格可能省略部分数据；表格含有 86 个唯一 'rownames'。

1. logFC: estimate of the log2-fold-change corresponding to the effect or contrast (for ‘topTableF’ there may be several columns of log-fold-changes)
2. AveExpr: average log2-expression for the probe over all arrays and channels, same as ‘Amean’ in the ‘MarrayLM’ object
3. t: moderated t-statistic (omitted for ‘topTableF’)
4. P.Value: raw p-value
5. B: log-odds that the gene is differentially expressed (omitted for ‘topTreat’)

Table 1: Sepsis vs Control metabolites

rownames	logFC	AveExpr	t	P.Value	adj.P.Val	B
interleuki…	4.56047476…	9.12791682…	12.3429495…	1.30461220…	3.28762276…	21.0095510…
Oxytocin	1.20738187…	4.78422477…	10.9425134…	2.89129286…	3.64302900…	17.9003821…
Noradrenaline	2.41244229…	1.15069029…	8.28652664…	2.04135641…	1.71473938…	11.3045654…
Aldosterone	1.70242514…	7.46275850…	7.25768341…	3.29982741…	2.07889127…	8.50900615…
Testosterone	-0.5954417…	6.86184959…	-7.1433392…	4.52972768…	2.28298275…	8.19116098…
interleukin-6	4.56940891…	8.41883936…	6.81407920…	1.13632768…	4.77257629…	7.26902002…
Phosphatid…	-0.6949464…	-1.3426611…	-6.0618145…	9.62990090…	3.46676432…	5.13114219…
Adrenaline	0.58302921…	12.9933938…	5.67339688…	2.94440285…	8.86195594…	4.01670761…
cardiac ou…	-0.4454982…	6.96508434…	-5.6245421…	3.39024672…	8.86195594…	3.87633322…
High-densi…	-0.5885086…	-0.2300975…	-5.4803299…	5.14207569…	0.00011780…	3.46194103…
stroke volume	-0.5317655…	-1.7342613…	-5.4240458…	6.05048026…	0.00012706…	3.30024247…
Proline	-0.8965239…	7.70837944…	-5.2836024…	9.08106627…	0.00017603…	2.89700218…
B-type nat…	2.31639744…	8.34682229…	5.12133438…	1.45166920…	0.00026130…	2.43183728…
lysoPhosph…	-0.4674402…	6.38346176…	-4.8991930…	2.75688431…	0.00043155…	1.79717803…
Aspartate …	1.19509294…	7.43782001…	4.89413846…	2.79736126…	0.00043155…	1.78277497…
…	…	…	…	…	…	…

6.3 热图

注：以下热图去除了包含缺失数据的代谢物。

Figure 1 (下方图) 为图 Defferential metabolites 概览。

(对应文件为 `Figure+Table/Defferential-metabolites.pdf`)

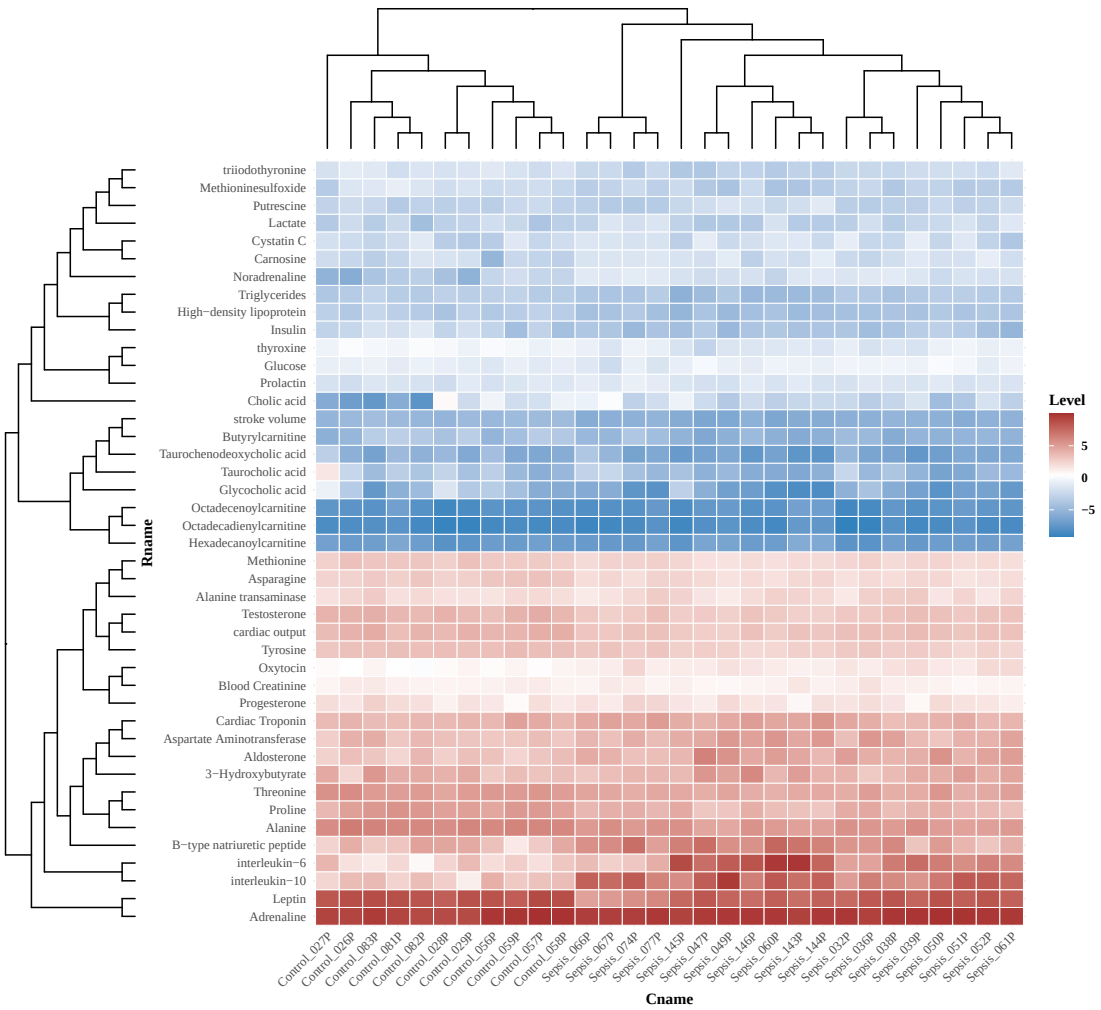

Figure 1: Defferential metabolites

Reference

1. Ritchie, M. E. *et al.* Limma powers differential expression analyses for rna-sequencing and microarray studies. *Nucleic Acids Research* **43**, e47 (2015).

2. Chen, Y., McCarthy, D., Ritchie, M., Robinson, M. & Smyth, G. EdgeR: Differential analysis of sequence read count data user's guide. 119.

3. Khaliq, W. *et al.* Lipid metabolic signatures deviate in sepsis survivors compared to non-survivors. *Computational and structural biotechnology journal* **18**, 3678–3691 (2020).