Identification of heat stress responsive transcripts in Sprague-Dawley rats using mixed linear models

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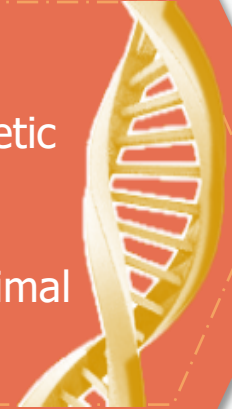
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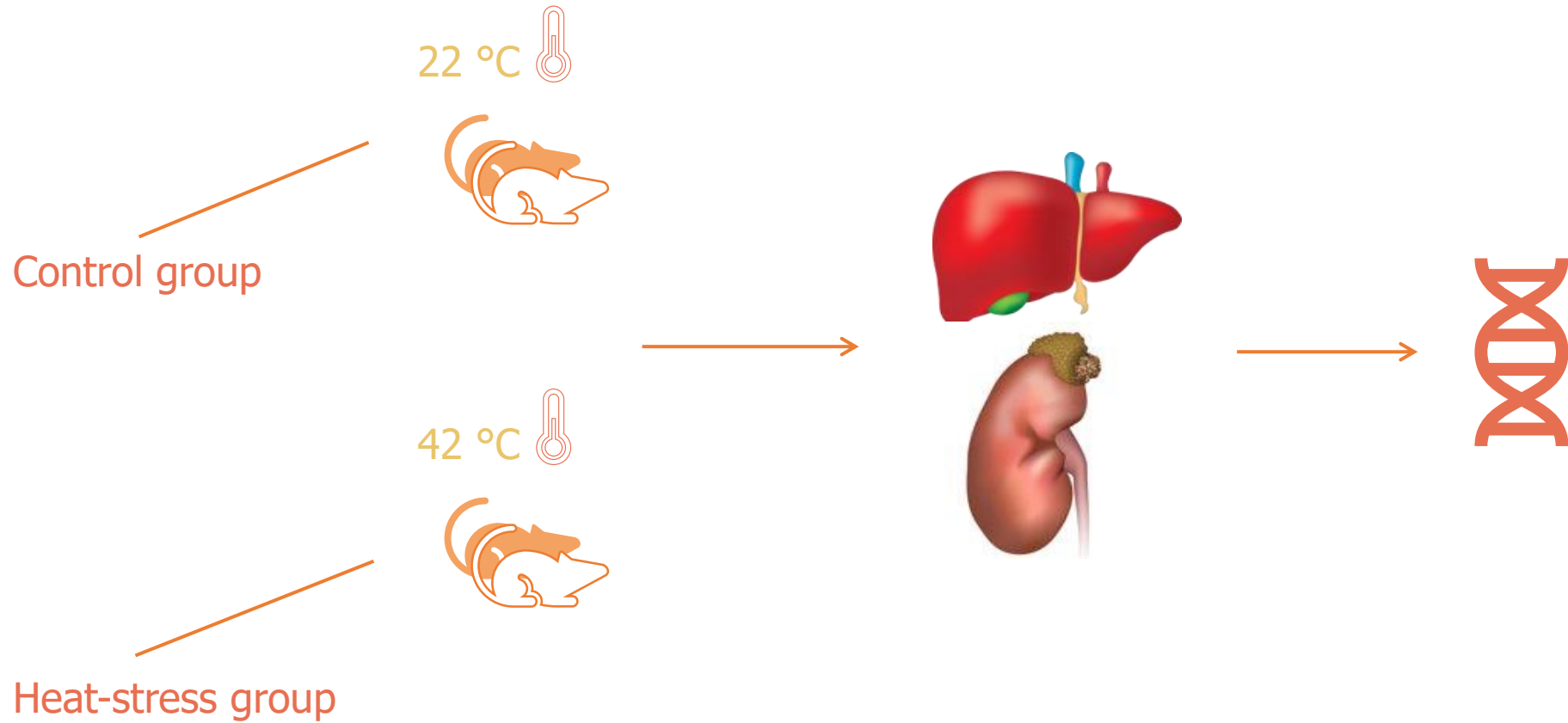
In animal production, heat stress is among the best characterized environmental stressors
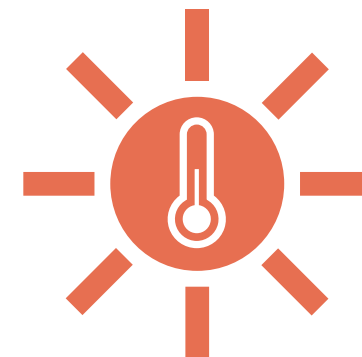
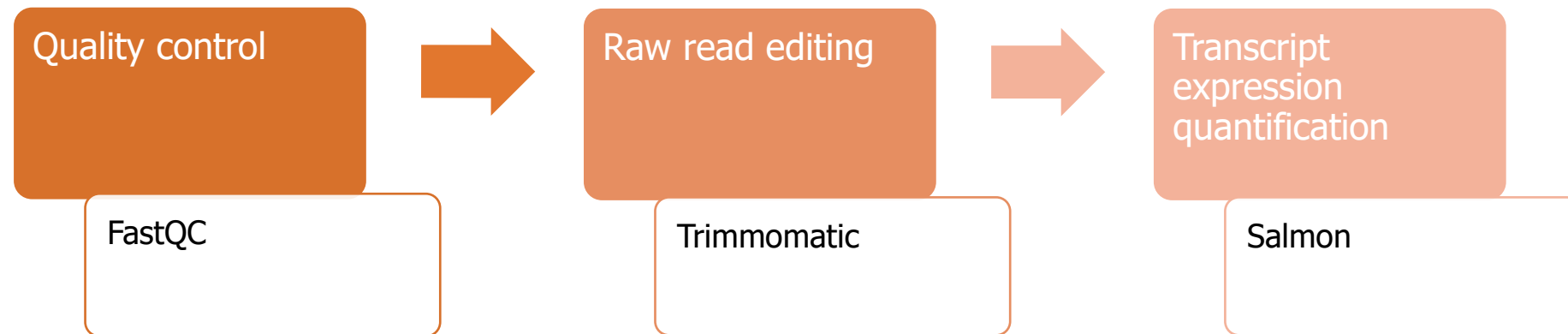Heat stress leads to economic losses and increased health burdens

22 °C

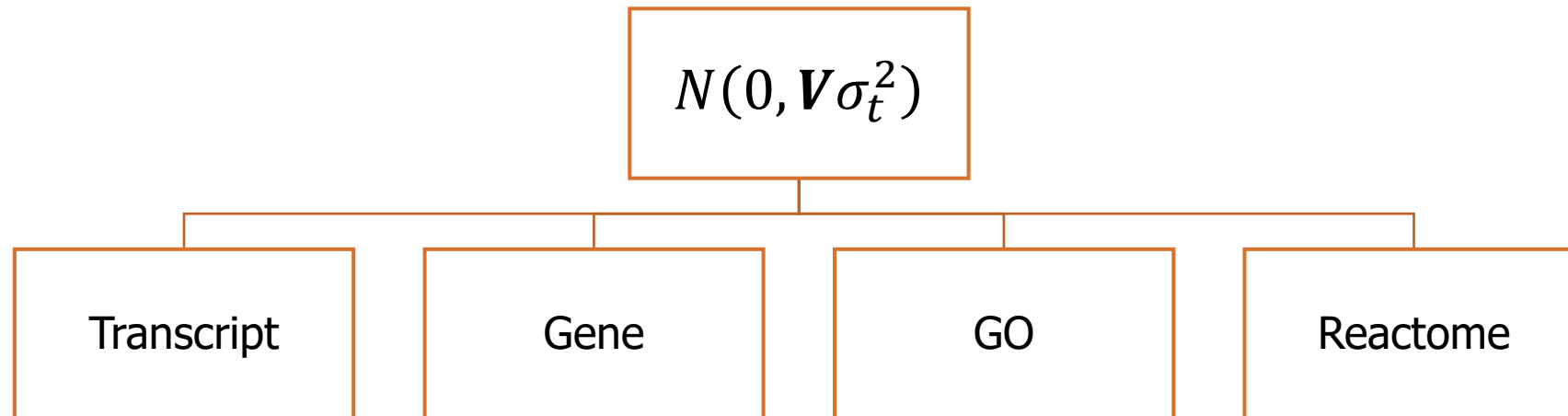Control group

42 °C

Heat-stress group

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┌──────────────────┐      ┌──────────────────┐      ┌──────────────────┐
│ Quality control  │ ──▶  │ Raw read editing │ ──▶  │ Transcript       │
│                  │      │                  │      │ expression       │
│                  │      │                  │      │ quantification   │
└──────────────────┘      └──────────────────┘      └──────────────────┘
  ┌──────────────────┐      ┌──────────────────┐      ┌──────────────────┐
  │ FastQC           │      │ Trimmomatic      │      │ Salmon           │
  │                  │      │                  │      │                  │
  └──────────────────┘      └──────────────────┘      └──────────────────┘
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$$y = \mu + Zt + e$$

- y – transcript $\log_2$(fold change)
- μ – mean
- Z – incidence matrix for t
- t – random effect with a pre-imposed normal distribution defined by N
- e – residuals

$$N(0, \boldsymbol{V}\sigma_t^2)$$
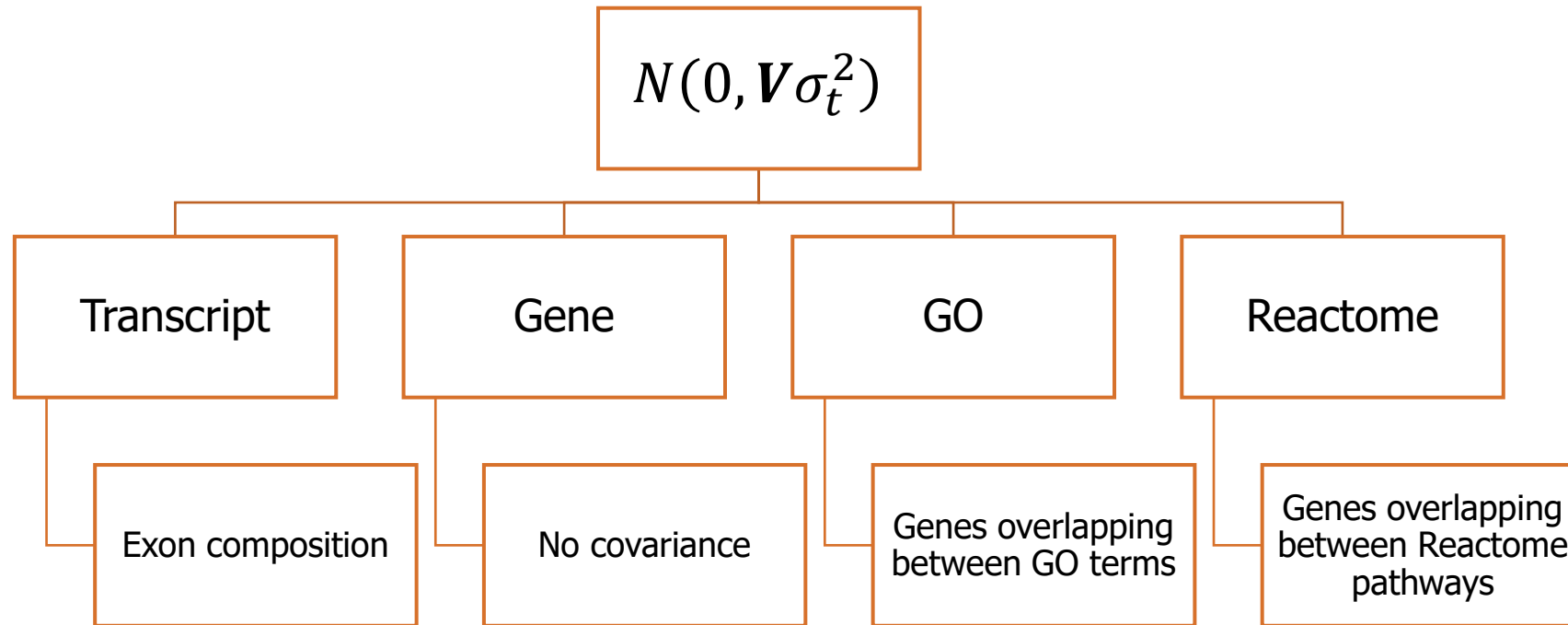
Transcript	Gene	GO	Reactome

- The acovariance expressed by the Jaccard similarity coefficient
- Index measures the similarity between sets

$$J(A,B) =$$

The intersect of A & B

division

The union of A & B

https://medium.com/data-science-bootcamp/understand-jaccard-index-jaccard-similarity

$$N(0, \boldsymbol{V}\sigma_t^2)$$

Transcript	Gene	GO	Reactome

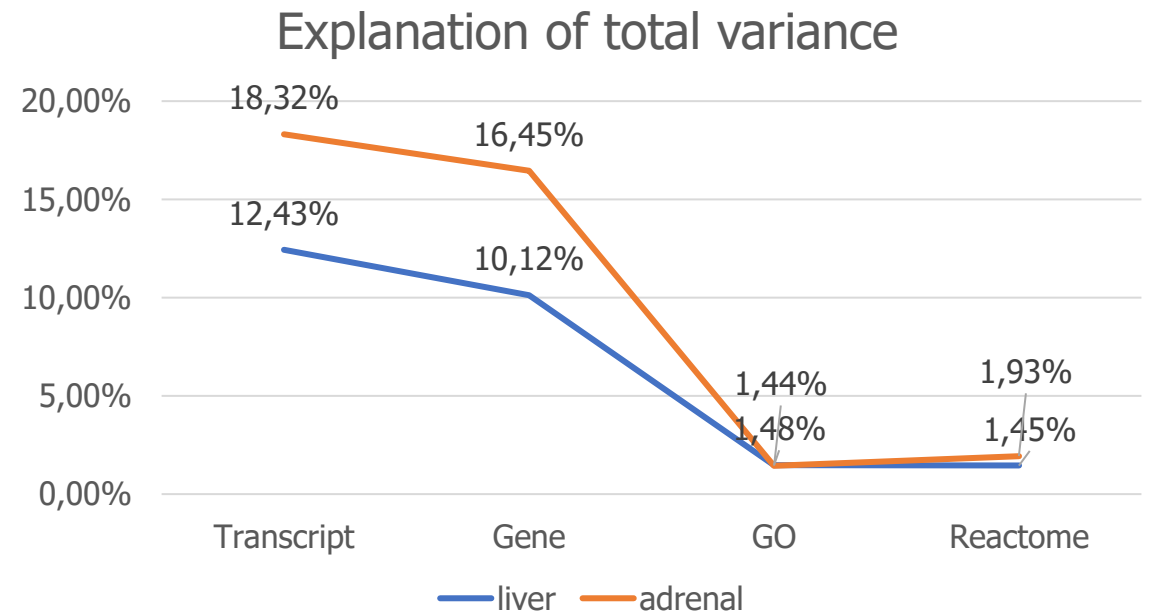| Exon composition	No covariance	Genes overlapping between GO terms	Genes overlapping between Reactome pathways
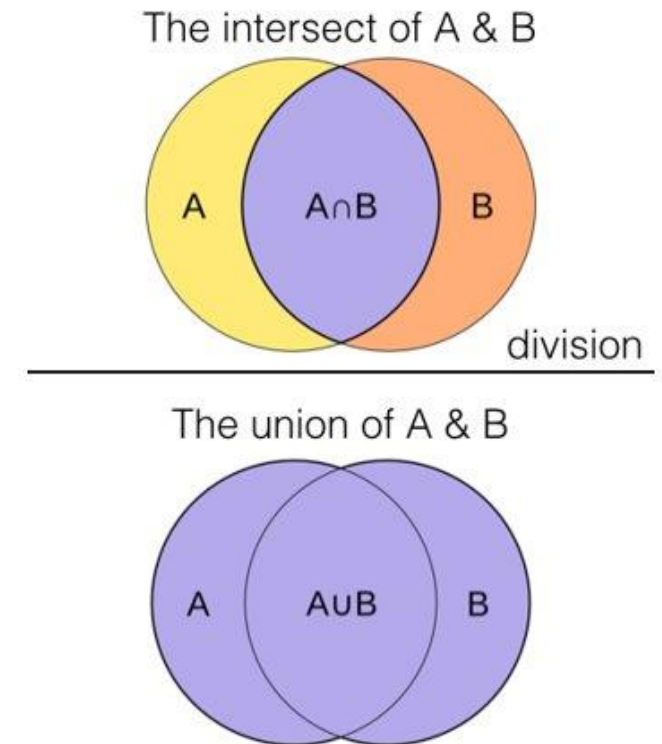
- JIT compiler
- Compiles a Python and NumPy code into the machine code
- Parallelize the code
- Improved the computing time

http://numba.pydata.org/

Explanation of total variance

- Transcripts and genes levels models explained a larger proportion of log2 fold change

	liver	adrenal
Transcript	• PKND • TRIP12	• SUCO • PLEC
Gene	• PKND	• SUCO • PER3
GO	• DNA break repair, • Histone ubiquitination, • Regulation of embryonic development, • Cytoplasmic translation.	-
Reactome	• Cytoplasmic translation	-

Mixed models are a valuable tool for the analysis of high throughput biological data

1#

2#

PER3 and SUCO genes, DNA repair and translation are playing a significant role in heat stress response