

Calopy – an advanced framework for the integration and analysis of indirect calorimetry data



Here we introduce Calopy, an innovative software suite for the intuitive and comprehensive analysis of indirect calorimetry data. Calopy is an open-source, web-based Shiny for Python application that is accessible online or locally; it is platform-independent and available via any web browser at <https://www.calopy.app>.

Indirect calorimetry is a widely used technique for measuring energy metabolism in both humans and animals¹. At its core, indirect calorimetry tracks oxygen consumption ($\dot{V}O_2$) and carbon dioxide production ($\dot{V}CO_2$) to analyse energy metabolism through parameters such as energy expenditure and resting metabolic rate (RMR)² or respiratory exchange ratio (RER), a key indicator of substrate utilization³. In comprehensive indirect calorimetry systems for animals, additional relevant metabolic parameters such as locomotor activity, food and water intake, and body temperature can also be measured at high temporal resolution, along with environmental factors such as cage temperature, lighting and humidity. Continuous or categorical phenotypic variables, such as body weight, genotype and treatments, are also recorded. Noteworthy indirect calorimetry data may further be affected through factors that entail mutual dependencies such as circadian rhythms, food intake, environmental conditions and data noise, which adds further complexity⁴. Together, these data form a complex set of time-resolved, continuous and categorical variables, which require sophisticated statistics and methods for their analysis.

Over the years, the research community has developed several tools to analyse and

interpret indirect calorimetry data, with CalR being the most prominent⁵. However, despite the widespread use of indirect calorimetry and standardized software, flexible and accessible open-source tools for easy use and integration of advanced statistical methods to help harness the full potential of indirect calorimetry data remain lacking^{6–9}.

Calopy addresses this gap by providing an open-source, transparent and reliable platform for indirect calorimetry data analysis with an intuitive, reactive and easy-to-use interface (Fig. 1a). In contrast to other software, Calopy offers advanced preprocessing tools, including outlier detection and removal, and removal of data for individual subjects, ensuring robust and reproducible results. In addition, Calopy provides unique optional filtering for time-resolved variables (Fig. 1b), enabling users to extract meaningful data features that are robust against noise, such as global and daily maxima and minima, amplitude, area under the curve (AUC), and more. Calopy is unique in offering a global and time-resolved estimation method for RMR and basal metabolic rate (BMR) that is based on a linear model incorporating activity and food intake, as introduced by Klinken et al.¹⁰ (Fig. 1c–e). All settings in Calopy are non-destructive and can be reset or changed at any time; all data created and analysed can be downloaded for further use.

Building on these data processing methods, Calopy includes a comprehensive suite of exploratory data analysis tools, enabling statistics to be performed on both raw data and estimated features while incorporating all types of meta-data. This allows in-depth exploration of indirect

calorimetry data through between-group comparison (Fig. 1f–h), temporal-condition analysis (Fig. 1i) and time-window comparison (Fig. 1j). A comprehensive user guide can be found in the Supplementary Information, with the most up-to-date version available through the Calopy Help section.

In summary, Calopy assists the scientific community in easily performing state-of-the-art and extended indirect calorimetry data analysis. Calopy provides a flexible and robust framework to handle and analyse indirect calorimetry data, which can be easily extended with novel features and methods as they are implemented by us or by the community.

Code availability

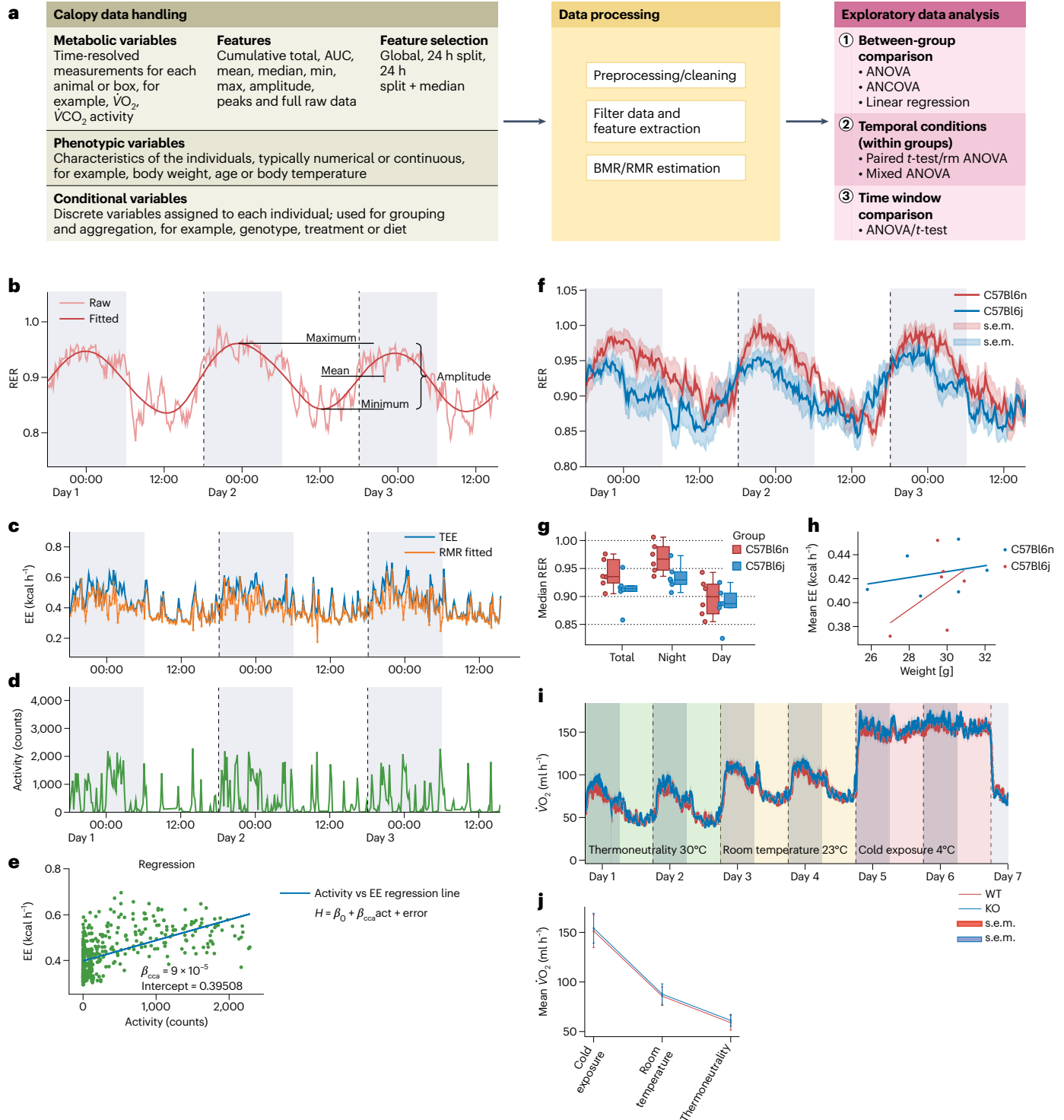
All source code is available from the Gitlab repository: <https://gitlab.com/computational-discovery-research/calopy>

Stefan Loipfinger ^{1,2}, **Matthias Grosholz**^{1,3}, **Santhosh Kumar** ², **Helin Erbilir**², **Kenneth Allen Dyar**^{3,4}, **Timo Dirk Müller** ^{4,5,6}, **Stephan Grein** ^{7,8}, **Jan Rozman** ⁹, **Martin Klingenspor** ^{10,11}, **Carola Meyer** ¹² & **Dominik Lutter** ^{2,4} ✉

¹Department of Medical Oncology, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands. ²Computational Discovery Research Group, Institute for Diabetes and Obesity, Helmholtz Munich, Neuherberg, Germany. ³Metabolic Physiology, Institute for Diabetes and Cancer, Helmholtz Diabetes Center, Helmholtz Munich, Neuherberg, Germany. ⁴German Center for Diabetes Research (DZD), Neuherberg,

Fig. 1 | Indirect calorimetry data analysis with Calopy. **a**, Overview of Calopy's data analysis framework, from data handling to processing and exploratory analysis. **b**, Filter-based feature extraction. Various filters can be applied and fitted to the metabolic variables for extraction of additional data features such as maxima, minima, amplitude and more. **c–e**, Data analysis examples. Estimation of RMR in an individual mouse by removing locomotor activity-related energy expenditure (EE) from total energy expenditure (TEE) (**c**). Locomotor activity counts (**d**) are used to train a regression model to predict EE (**e**). The intercept (β_0) can be used as a basic measure of individual RMR, whereas the regression

coefficient is used to create a time-resolved estimation of the RMR (**c**). See Calopy documentation for details. **f–h**, Between-group comparison of the RER as a metabolic variable. Shown are group-wise mean and s.e.m. for two inbred mouse strains, C57Bl6n and C57Bl6j ($n = 6$ mice per group) (**f**). Global median is compared for day, night and total (**g**). Comparison of 24-h mean EE between two genotypes using an ANCOVA model (**h**). **i, j**, Temporal-condition comparison of oxygen consumption ($\dot{V}O_2$) for three temperature conditions between a wild-type (WT) and a knockout (KO) mouse model ($n = 16$ mice per genotype). A mixed effect model is applied to test for differences in $\dot{V}O_2$ (**j**).



Germany. ⁵Institute for Diabetes and Obesity, Helmholtz Zentrum München, Neuherberg, Germany. ⁶Walther Straub Institute of Pharmacology and Toxicology, Ludwig Maximilian University, Munich, Germany. ⁷Life and Medical Sciences (LIMES) Institute, Rheinische Friedrich-Wilhelms-Universität Bonn, Bonn, Germany. ⁸Bonn Center for Mathematical Life Sciences, Rheinische Friedrich-Wilhelms-Universität Bonn, Bonn, Germany. ⁹Luxembourg Centre for Systems Biomedicine (LCSB), University of Luxembourg, Esch-sur-Alzette, Luxembourg. ¹⁰Chair for Molecular Nutritional Medicine, TUM School of Life Sciences, Research Department of Molecular Life Sciences, Technical University of Munich, Freising, Germany. ¹¹Else Kröner-Fresenius Center for Nutritional Medicine, Technical University of Munich, Freising, Germany. ¹²Institute of Pharmacology, University of Marburg, Marburg, Germany. ¹³Unaffiliated: Matthias Grosholz. ✉e-mail: dominik.lutter@helmholtz-munich.de

Published online: 24 June 2025

References

1. Ferrannini, E. *Metabolism* **37**, 287–301 (1988).
2. Weir, J. B. & de, V. J. *J. Physiol.* **109**, 1–9 (1949).
3. Löffler, M. C. et al. *Mol. Metab.* **51**, 101237 (2021).
4. Tschöp, M. H. et al. *Nat. Methods* **9**, 57–63 (2011).
5. Mina, A. I. et al. *Cell Metab.* **28**, 656–666.e651 (2018).
6. Adamovich, Y. et al. *Cell Metab.* **29**, 1092–1103.e3 (2019).
7. Cortopassi, M. D. et al. in *Brown Adipose Tissue. Methods in Molecular Biology* Vol. **2448** (eds. Guertin, D. A. & Wolfrum, C.) 43–72 (Humana Press, 2022).
8. Müller, T. D., Klingenspor, M. & Tschöp, M. H. *Nat. Metab.* **3**, 1134–1136 (2021).
9. Pavlidou, E. et al. *Nutr. Metab.* **15**, 41 (2018).
10. Van Klinken, J. B., van den Berg, S. A., Havekes, L. M. & Willems Van Dijk, K. *PLoS ONE* **7**, e36162 (2012).

Acknowledgements

We express our sincere appreciation to the members of the Helmholtz Diabetes Center for valuable feedback and comments, in particular N. Dragano, P. Pflüger and C. Mencías Castillejo. Special thanks are extended to S. Haffner for help with prototype coding, J. Hasenauer for valuable input on method development, and G. Miller and M. Jimenez Munoz from the statistics consulting core

facility. Support from the German Center for Diabetes Research (DZD-Grant 2020/2021: ‘Cell free DNA as a biomarker of type 2 diabetes and diabetic complications’) and Deutsche Forschungsgemeinschaft DFG Project ‘BATenergy’ (TRR333/1, project 450149205) is gratefully acknowledged. This work is partially based on work from COST Action CA20135 ‘Improving biomedical research by automated behavior monitoring in the animal home-cage’, supported by COST (European Cooperation in Science and Technology).

Author contributions

S.L., M.G., S.K., H.E. and D.L. wrote the code and designed the software. K.A.D., J.R., C.M. and T.D.M. contributed data and helped design the application. J.R., M.K., S.G. and C.M. helped design the application. D.L. wrote the manuscript and conducted the whole project.

Competing interests

T.D.M. holds stocks from Eli Lilly and receives research funding from Novo Nordisk. T.D.M. further received speaking fees within the past 3 years from Merck, AstraZeneca, Boehringer Ingelheim, Eli Lilly and Novo Nordisk. All remaining authors declare no competing interests.

Additional information

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s42255-025-01316-8>.