

Wizualizacja danych

Wykład 7: Przegląd dobrych i złych wykresów naukowych

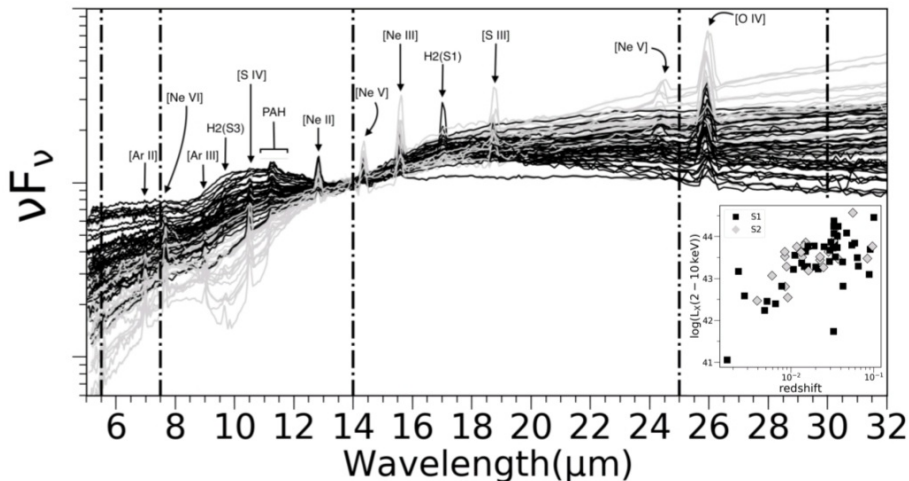
Mariusz Tarnopolski

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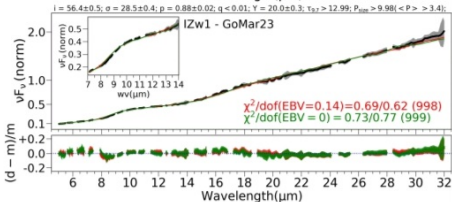
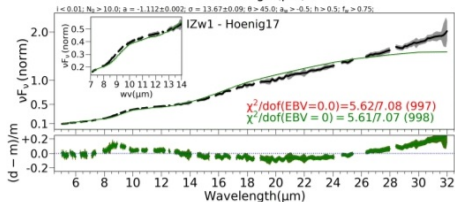
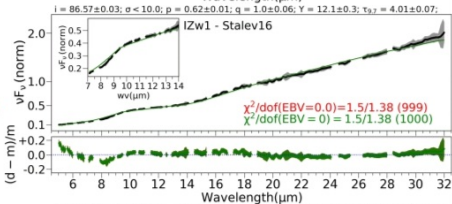
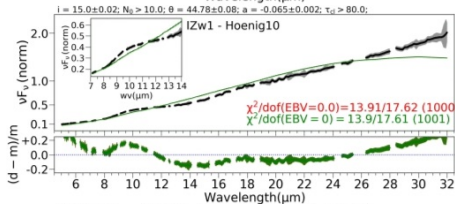
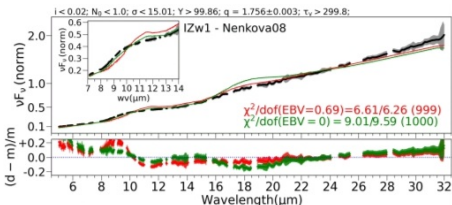
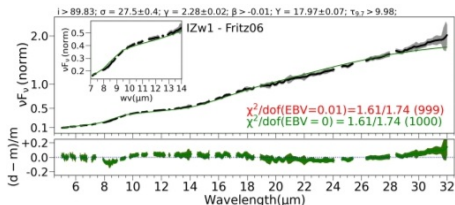
DataViz, 2024/2025

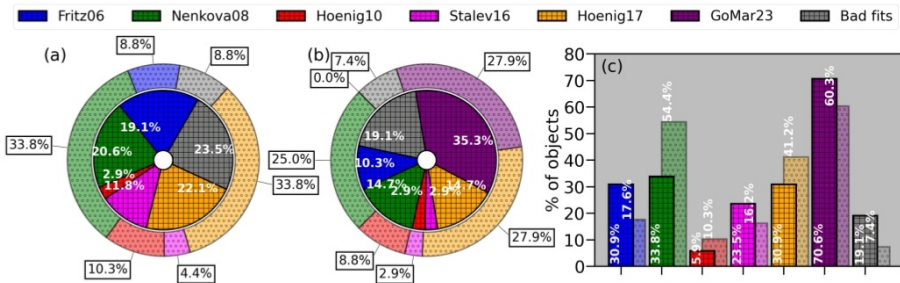


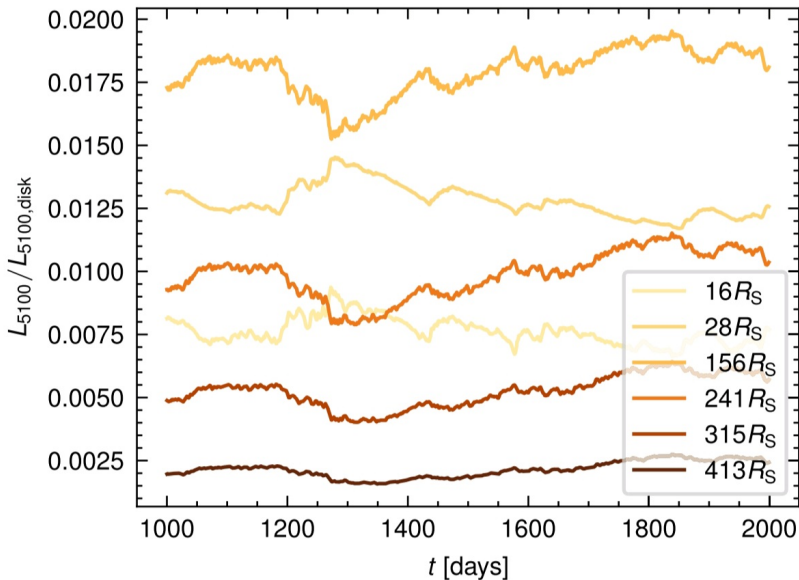
Nienajlepsze wykresy

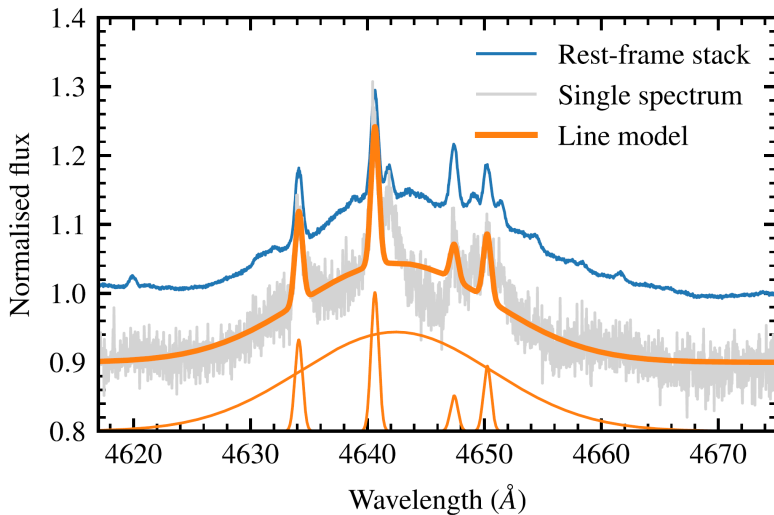


<https://doi.org/10.1051/0004-6361/202345858>









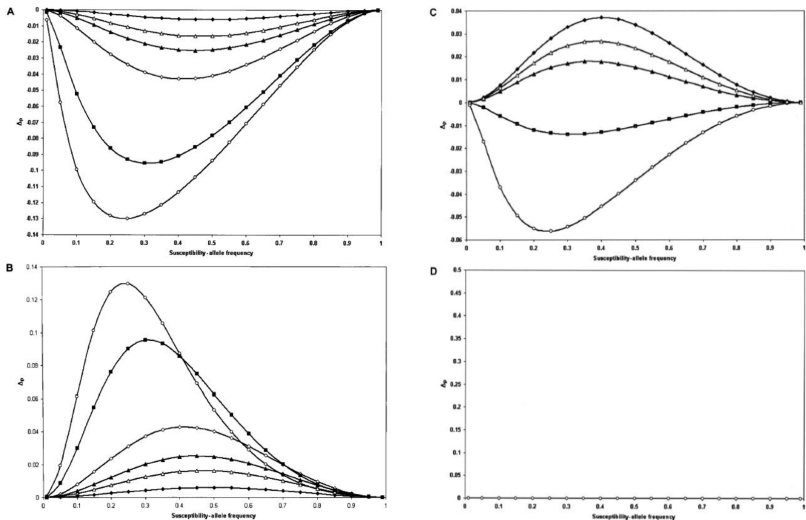
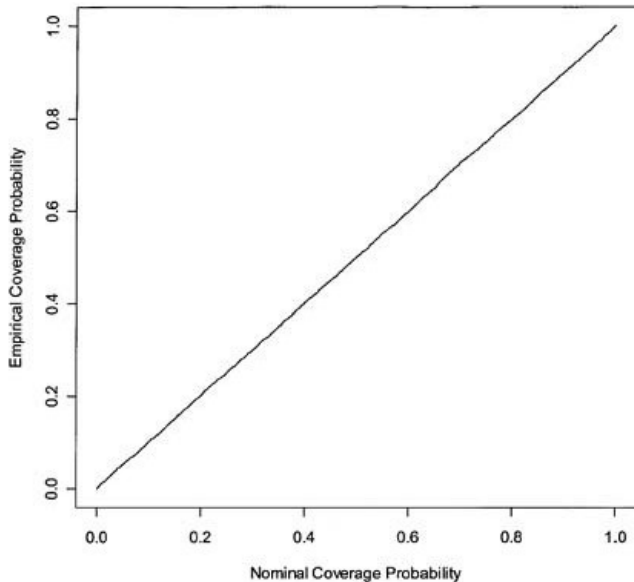
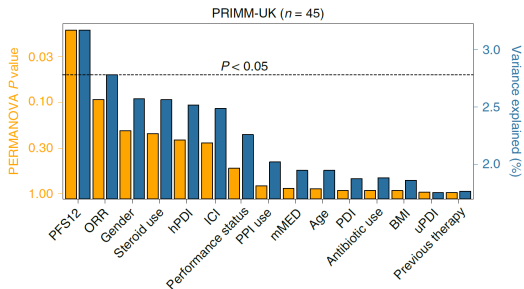
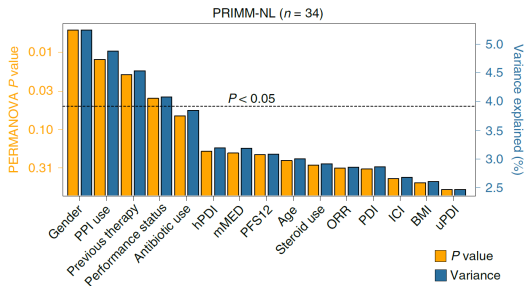


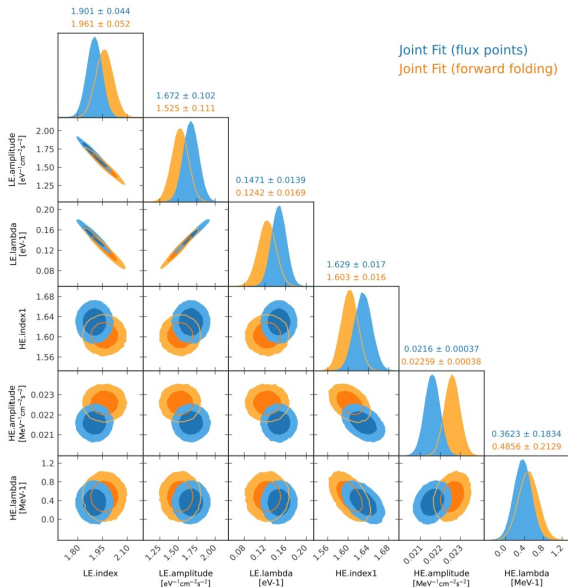
Figure 1 Δp , plotted versus the susceptibility-allele frequency for patients. A, B, and D, Data points are as follows: $\gamma = 1.1$ (blackened diamonds), $\gamma = 1.3$ (unblackened triangles), $\gamma = 1.5$ (blackened triangles), $\gamma = 2$ (unblackened diamonds), $\gamma = 5$ (blackened squares), and $\gamma = 10$ (unblackened circles). A, Dominant model. B, Recessive model. C, Additive model. Since $\gamma < 2$ would not satisfy our definition of an additive model as $\gamma = 2\beta$ and $\beta > 1$, the data points in C are as follows: $\gamma = 2.2$ ($\beta = 1.1$) (blackened diamonds), $\gamma = 2.6$ ($\beta = 1.3$) (unblackened triangles), $\gamma = 3$ ($\beta = 1.5$) (blackened triangles), $\gamma = 5$ (blackened squares), $\gamma = 2$ (unblackened diamonds). D, Multiplicative model.



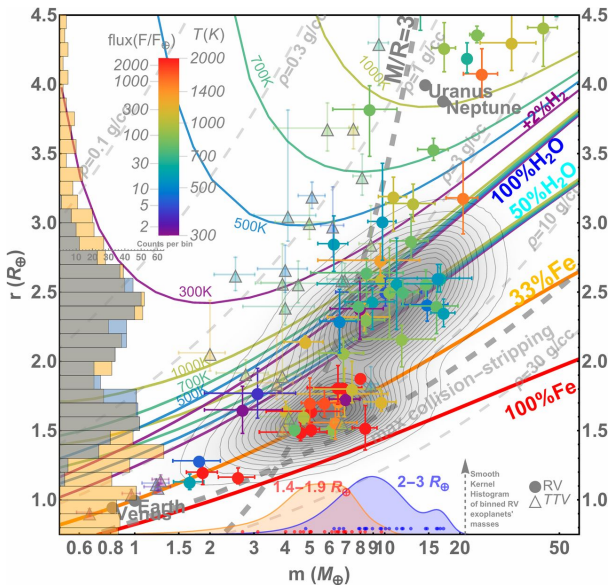
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Nieźle:

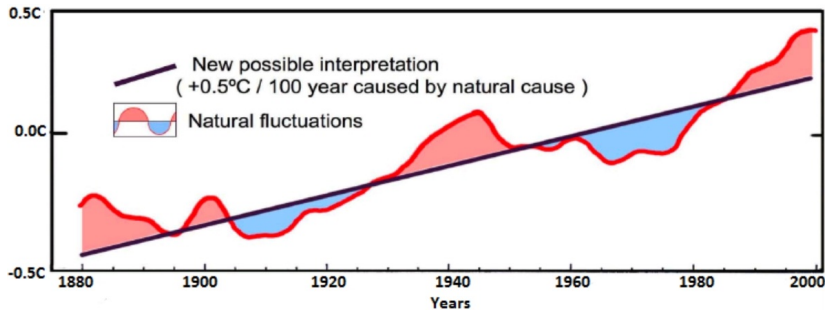


<https://arxiv.org/abs/2409.20487>

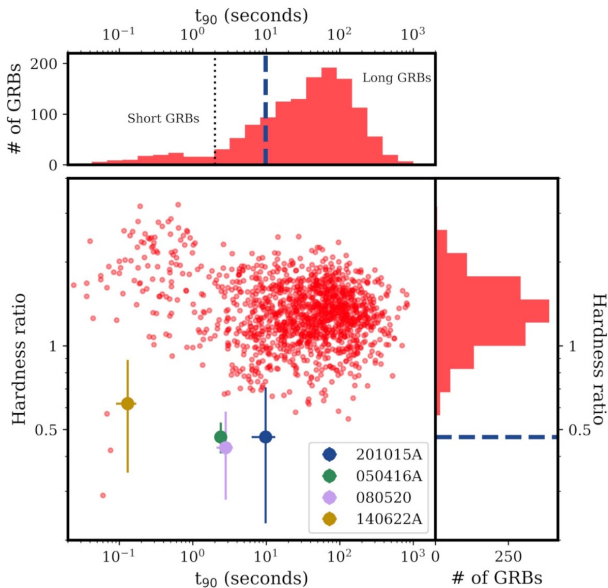


<https://doi.org/10.1073/pnas.1812905116>

Nienajgorsze wykresy

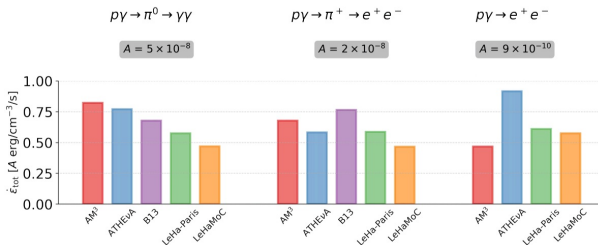


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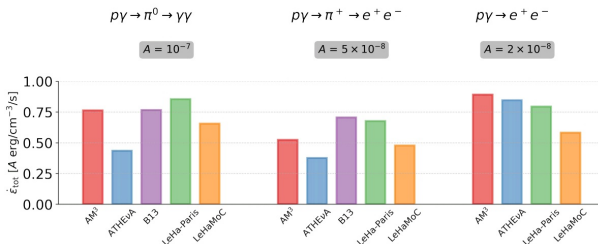


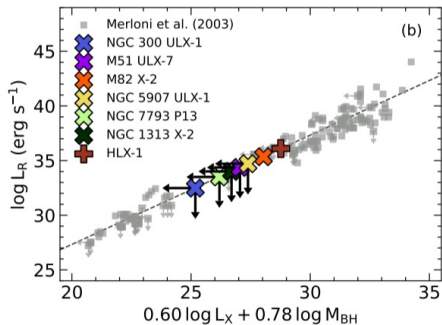
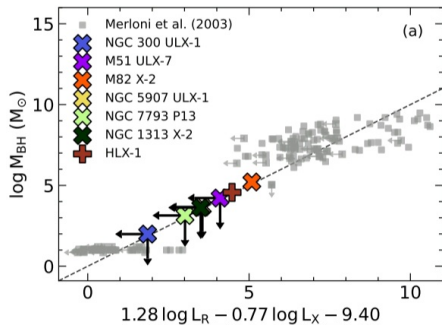
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py-MONOGB

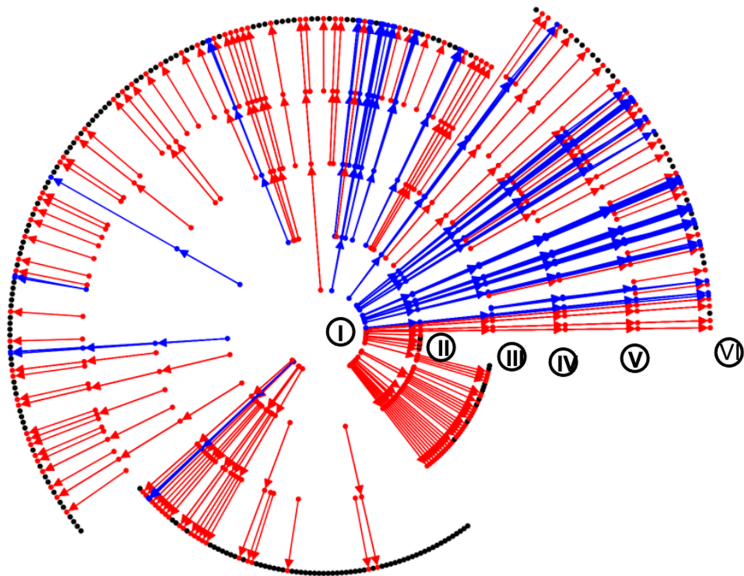


py-PLPL

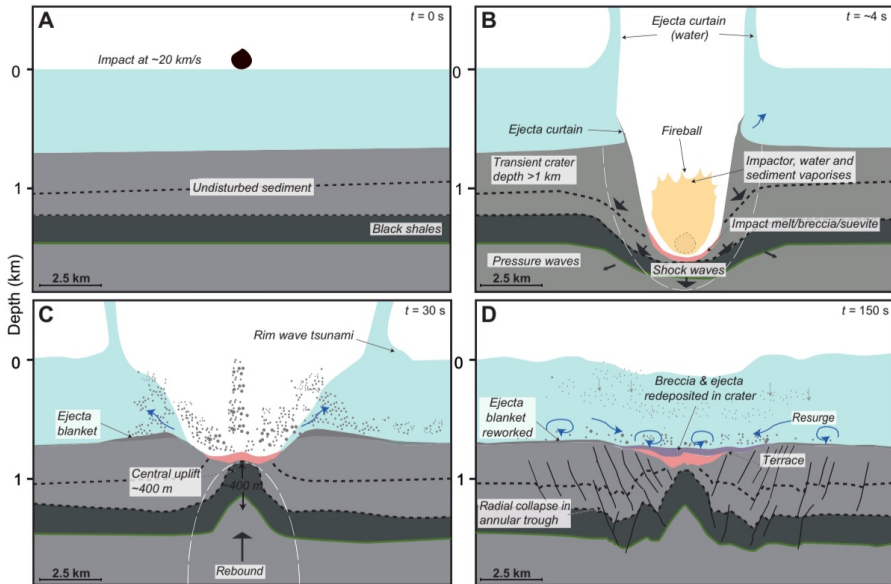




<https://arxiv.org/abs/2410.23335>



<https://doi.org/10.1051/0004-6361/202243275>



<https://doi.org/10.1126/sciadv.abn3096>

