Emadeldin Hassanin¹

y @emad_hassanin

hassanin@uni-bonn.de

R. Aldisi¹ DR Bobbili² P. May² P. Krawitz¹ C. Maj¹

¹ Institute of Genomic Statistics and Bioinformatics, University of Bonn, Bonn, Germany ² Bioinformatics Core, Luxembourg Centre for Systems Biomedicine (LCSB), Belvaux, Luxembourg

Introduction

- 1. Polygenic risk score (PRS) has been known to influence development of the prostate cancer over a life course.
- 2. PRS have recently been shown to have relative risks that depend on age, and genetic relative risks decrease with increasing age.
- 3. A recent study assessed the interplay of polygenic risk, rare pathogenic variants, and family history¹.

Objectives

We aimed to comprehensively assess the role of polygenic risk score (PRS):

- in the early-onset prostate cancer (PC) vs late-onset
- in the absence or presence of a family history of PC (FH)
- in the absence or presence of rare pathogenic variants (PV, across 5 PC susceptibility genes HOXB13, BRCA2, ATM, CHEK2, BRCA1).

Methods

Results

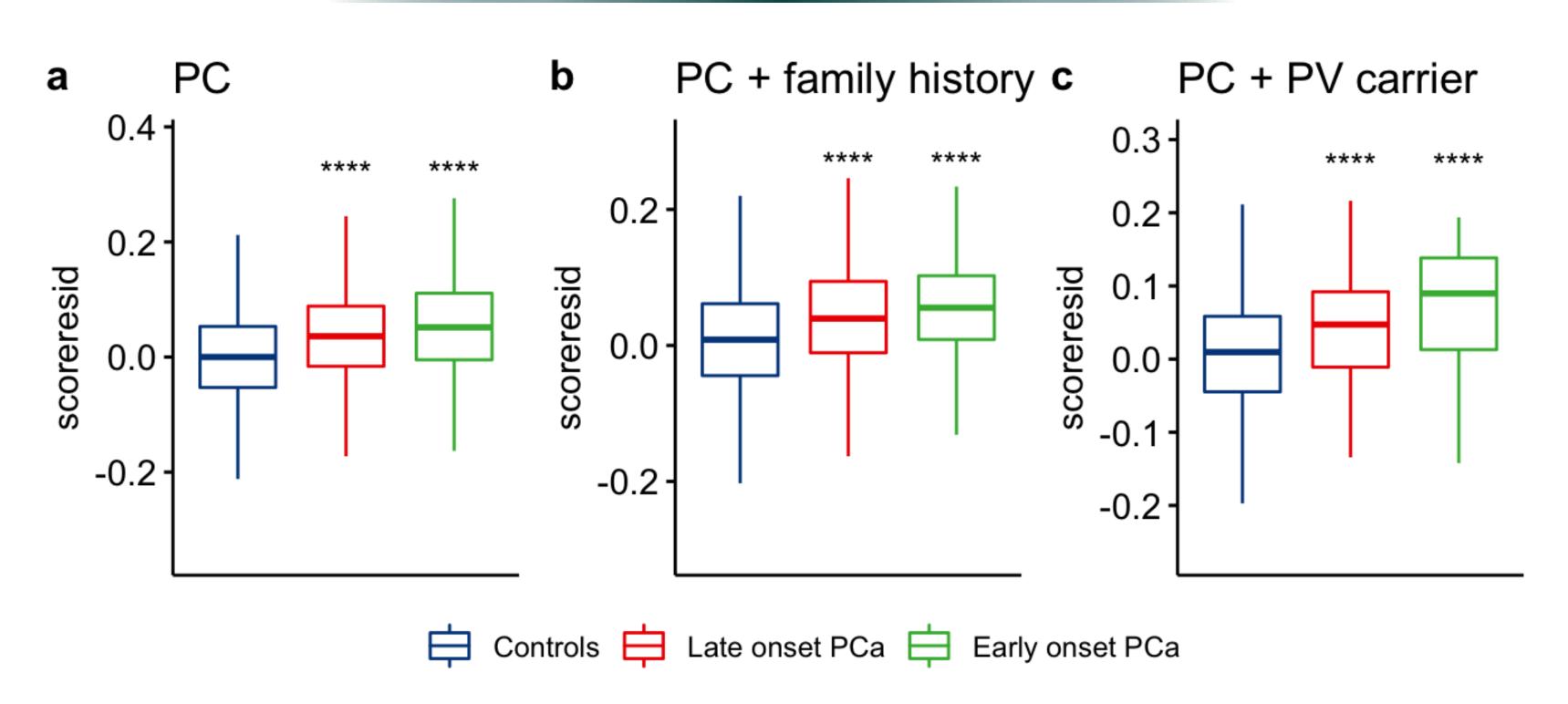


Figure 1: Boxplot of prostate cancer (PC) PRS for early-onset versus late-onset PC. PRS distribution across all PC cases (a), PC cases with PC family history (b), and PC cases with PV carrier (c)

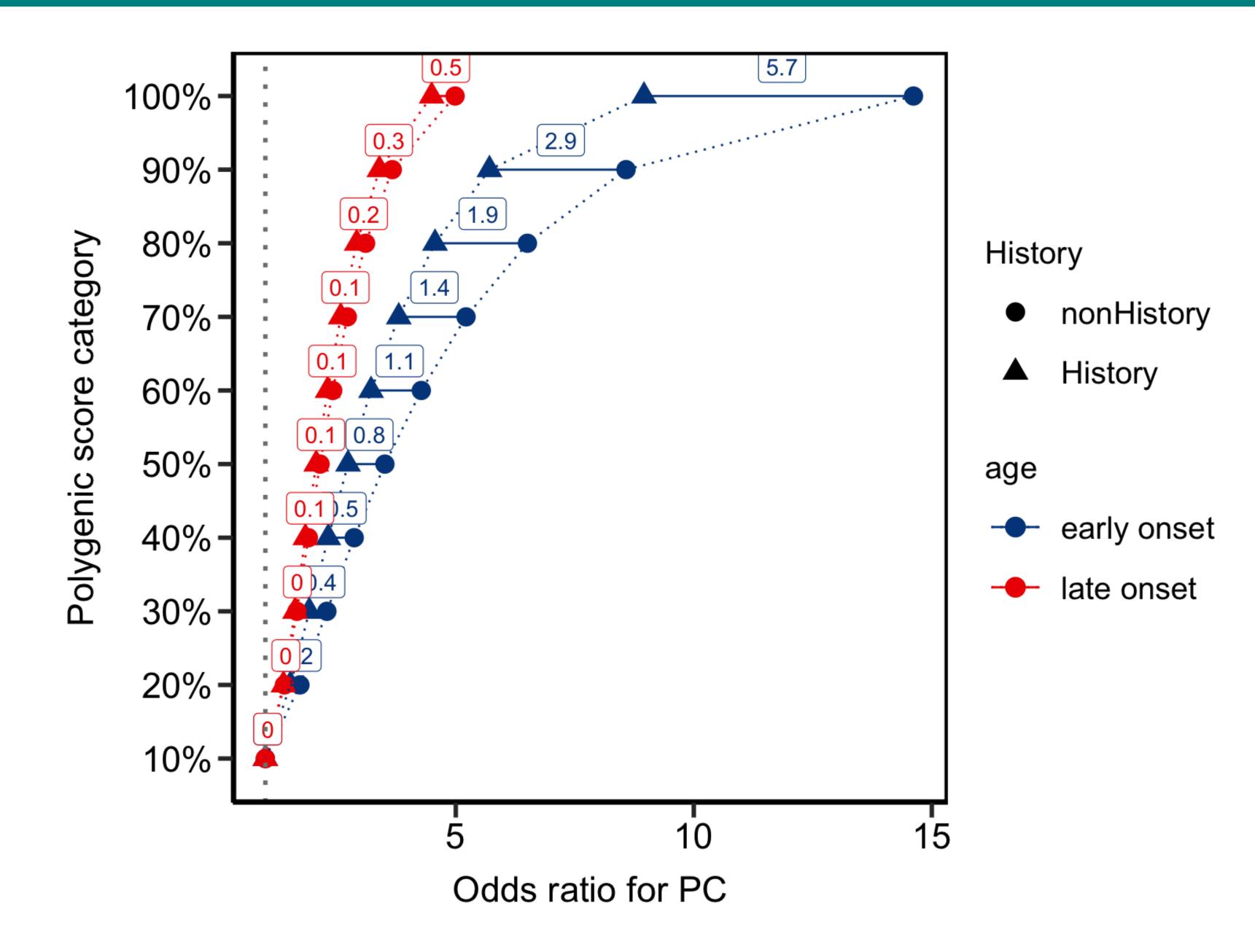


Figure 2: Risk estimates for early-onset versus late-onset CRC associated with PC PRS. Individuals stratified according to presence of family history.

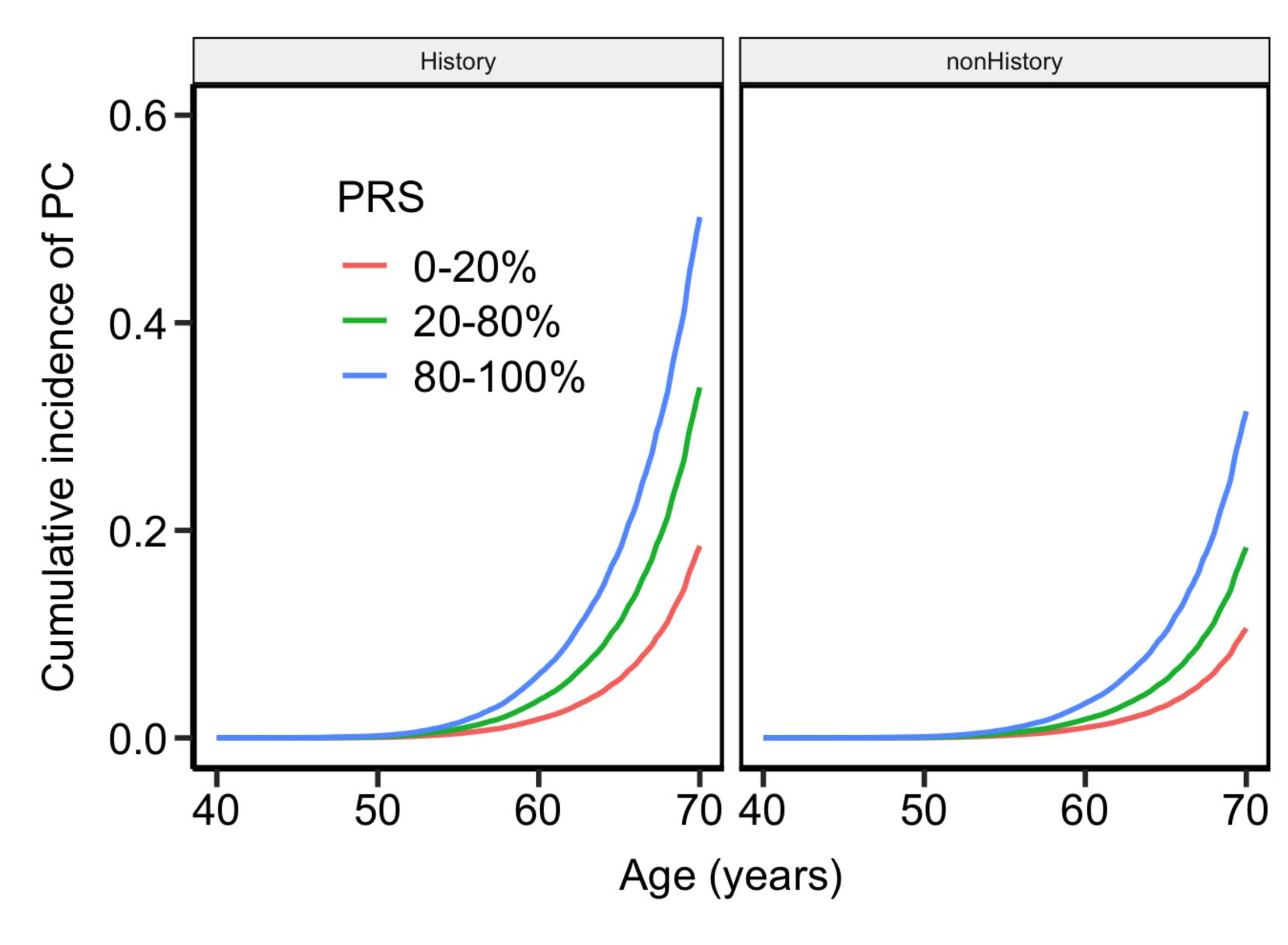


Figure 3: Absolute risk estimates of being diagnosed with PC across the age stratum by PRS percentile. Individuals stratified according to presence of family history.

References

1. Hassanin, E. *et al.* Breast and prostate cancer risk: The interplay of polygenic risk, rare pathogenic germline variants, and family history. *Genet Med* **24,** 576–585 (2022).

