



Open Research Online

Citation

Paria, Soumya (2022). Fastman: A fast algorithm for visualizing results using Manhattan plots. Postgraduate Research Poster Competition, The Open University.

URL

<https://oro.open.ac.uk/85396/>

License

(CC-BY 4.0) Creative Commons: Attribution 4.0

<https://creativecommons.org/licenses/by/4.0/>

Policy

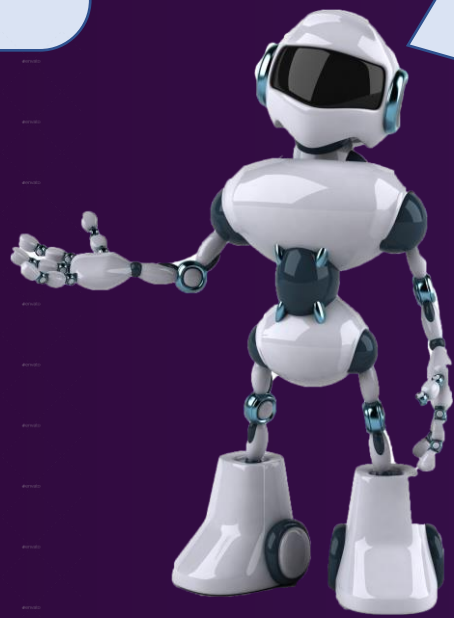
This document has been downloaded from Open Research Online, The Open University's repository of research publications. This version is being made available in accordance with Open Research Online policies available from [Open Research Online \(ORO\) Policies](#)

Versions

If this document is identified as the Author Accepted Manuscript it is the version after peer review but before type setting, copy editing or publisher branding

fastman: A fast algorithm for visualizing results using **Manhattan** plots

Hey *fastman*, what is a Manhattan plot?



Well, it's just a plot of negative log P-values vs locations of gene markers across chromosomes. It shows which genes are influencing a trait or a disease.

Then why is it called a Manhattan plot?



Humans think that the plot resembles the Manhattan skyline....

...like a group of skyscrapers rising above the smaller buildings.



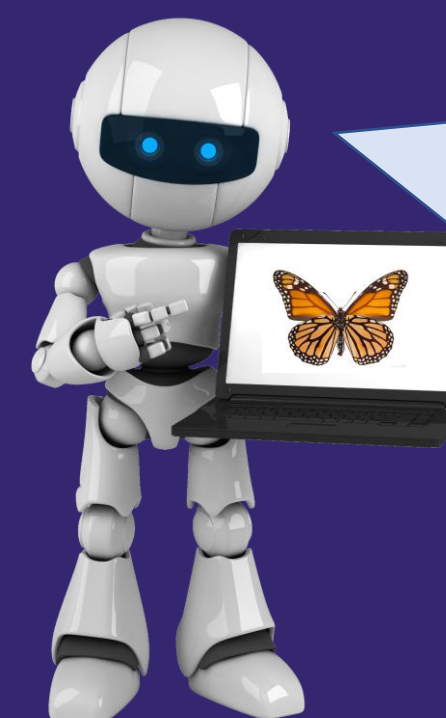
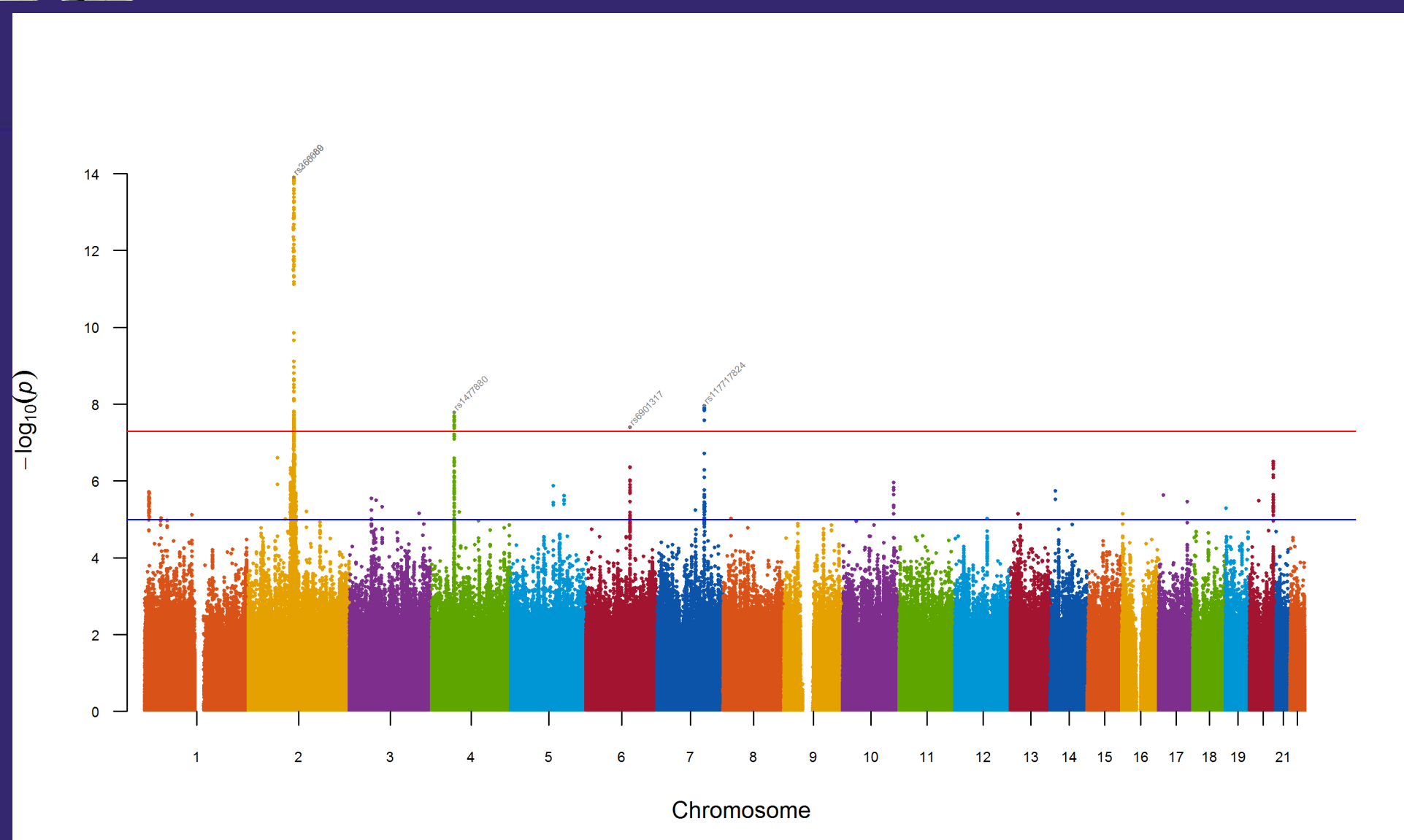
Stronger the association, smaller is the P-value, and higher is the value of its negative log. So, genes with the highest associations rise up to the top of the plot.

Let me show you my powers! Here's a sample plot that I've prepared in just 14 seconds.



Wow, that's even faster than Usain Bolt running 200 metres!! Is that human genetic data?

That is indeed human data, with 1.2 million points!! However, I can also plot results from various non-model organisms like butterflies!



I am available for public use at GitHub, please scan the QR code and you'll find me!!

