MOUSEGWAS

An R package for automated inbred and F1 mouse strains GWAS execution

https://github.com/TheJacksonLaboratory/mousegwas

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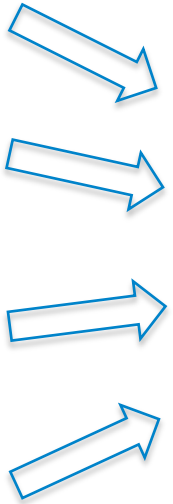
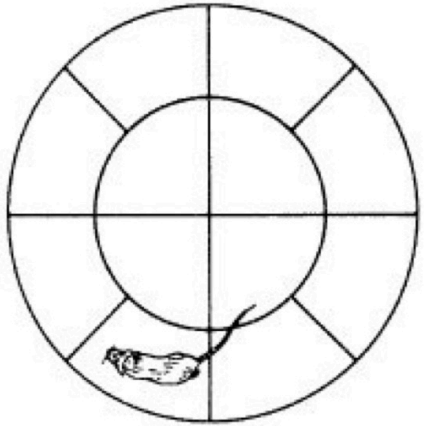
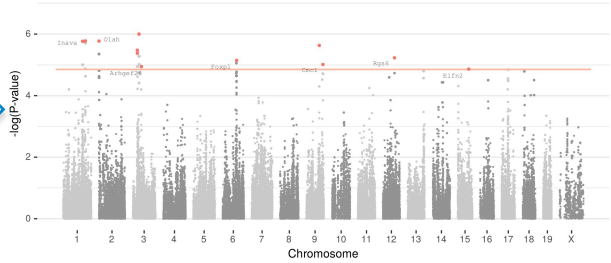
The Jackson Laboratory

Leading the search for tomorrow's cures

Motivation: GWAS as a research tool





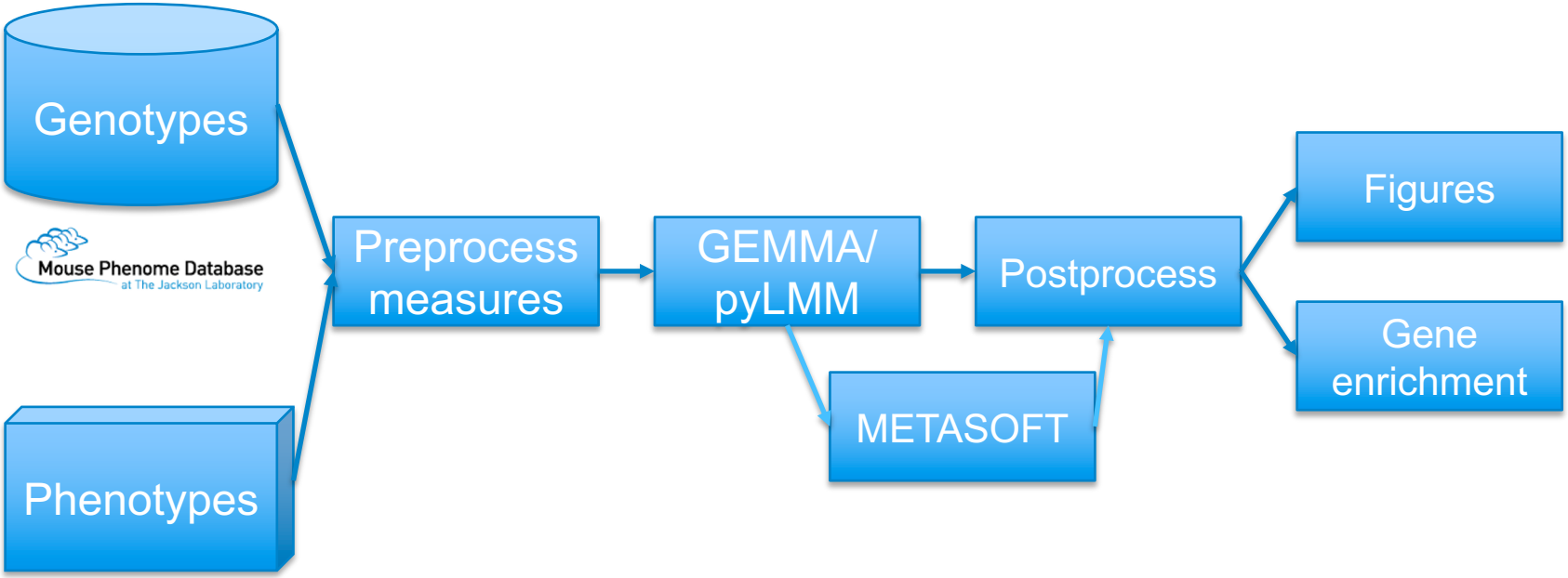


Well characterized mouse strains go through a test, GWAS is used to highlight genomic regions correlated with the phenotypes

Mouse GWAS is different than human

- Population structure is biased
- Contains repeated measures of the same strain
- Long linkage-disequilibrium blocks

Easing the process of GWAS



Options mousegwas allows

- Use GEMMA of pyLMM for GWAS
- Optional: Leave One Chromosome Out (LOCO)
- Use all individuals/ Sample some from each strain/ Average each strain
- Combine phenotypes with METASOFT, multi-variate GWAS, selecting group minimal p-value
- Use genetic markers as covariates

Input format:

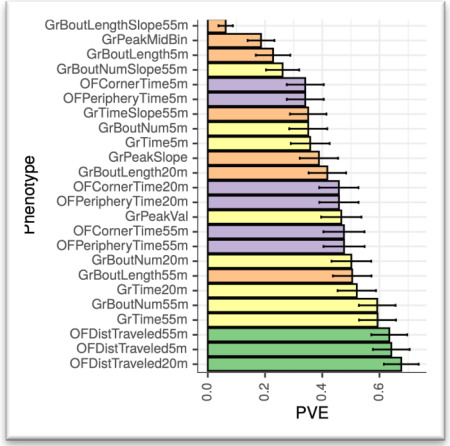
Input table

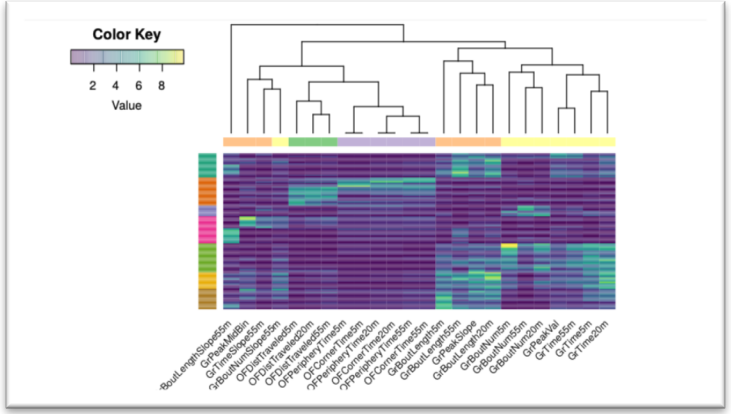
Strain	Sex	Weight	TestAge	TestDate	OFA_DistanceTraveled_first5m	OFA_DistanceTraveled_first20m
BALB/cJ	M	29	11	10/26/15	988.12	4522.7172
BALB/cJ	M	30	11	10/26/15	739.145	2014.7086
C57BL/6J	M	25.1	8.85714286	11/16/15	3562.945	8946.3269
C57BL/6J	M	26.4	8.85714286	11/16/15	2540.565	8108.016
C57BL/6J	M	24.7	8.85714286	11/16/15	3597.338	9335.455
C57BL/6J	M	24.5	8.85714286	11/16/15	2310.35	6201.162
BTBR T<+>ltpr3<tf>/J	M	32	9	12/8/15	3993.897	11574.7511
BTBR T<+>ltpr3<tf>/J	M	32	9	12/8/15	5285.544	19485.555
BTBR T<+>ltpr3<tf>/J	M	33	9	12/8/15	3990.881	11679.3283
BTBR T<+>ltpr3<tf>/J	M	32.5	9	12/8/15	4382.904	12402.6672
A/J	F	21.6	8.85714286	12/14/15	499.2504	1319.6741
A/J	F	20.8	8.85714286	12/14/15	397.5455	1314.7716
A/J	F	16.2	8.85714286	12/14/15	687.919	2736.9856
A/J	F	19.2	8.85714286	12/14/15	463.7912	930.9594
C57BLKS/J	M	25.2	8.85714286	12/21/15	1698.389	6849.767
C57BLKS/J	M	27.2	8.85714286	12/21/15	1576.2008	7729.4908
C57BLKS/J	M	29.6	8.85714286	12/21/15	1717.516	7003.072
C57BLKS/J	M	25.9	8.85714286	12/21/15	1430.847	5658.478
C3H/HeJ	F	20	9	12/22/15	1153.071	4732.0759
C3H/HeJ	F	20	9	12/22/15	1405.91	5411.497
C3H/HeJ	F	20.1	9	12/22/15	1834.498	6178.285

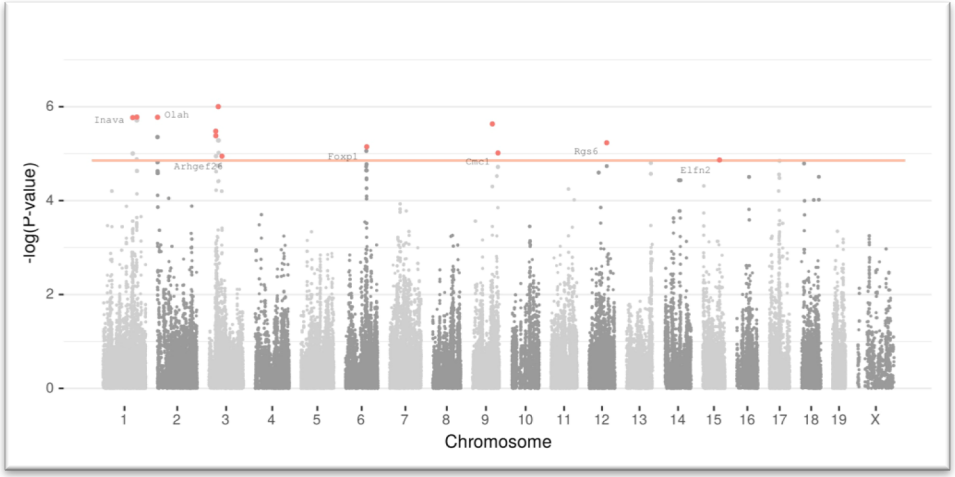
Metadata

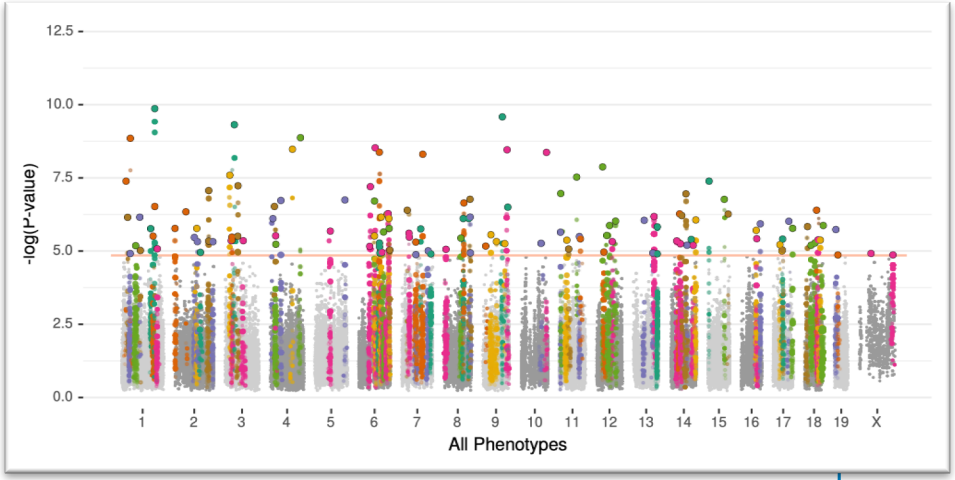
```
strain: Strain
phenotypes:
  OFA_Groom_first5m:
      papername: GrTime5m
      group: Grooming Quantity
  OFA_Groom_first20m:
      papername: GrTime20m
      group: Grooming Quantity
  OFA_Groom_first55m:
      papername: GrTime55m
      group: Grooming Quantity
  OFA_Groom_first55m_linearslope:
      papername: GrTimeSlope55m
      group: Grooming Pattern
groups:
  - Activity
  - Anxiety
  - Grooming Pattern
  - Grooming Quantity
F1:
  - B6129SF1/J:
      - C57BL/6J
      - 129S1/SvImJ
  - B6129PF1/J:
      - C57BL/6J
      - 129P3/J
```

Output figures:









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