

Survey for Diversity and Pedigree Visualization Tools for Corn Breeders Data Center at MaizeGDB

The primary mission of MaizeGDB is to serve the maize community, and the MaizeGDB team feels very fortunate to have a community dedicated to help fulfill this mission. To that end, we are asking for your input about tool development for a Corn Breeders Data Center at MaizeGDB. The anticipated tools will allow visualization of diversity, pedigrees, and network representations.

Please take a few minutes to complete a survey at MaizeGDB that will help guide this tool development process in order to create integrated views of diverse information bridging genetic, genomic, and breeding research. Your input will shape the tools that will be developed to enhance maize research.

The survey will remain open until September 10, 2015.

Your feedback is very important to get the tool development and implementation right. At the end of the survey, you will have the option to volunteer as a beta tester for the new tools. This would enable the MaizeGDB team to do better troubleshooting and ensure that the tools to be implemented will help you with your research needs.

If you have questions/comments or need technical help, please contact Taner Sen (taner.sen@ars.usda.gov, 515-294-5326).

Your Visualization Needs

1. What type of data would be most beneficial to visualize?

Check all that apply.

- SNPs in a region for a given list of lines
- Haplotype analysis in a given list of lines
- Pedigree relationships
- QTL regions
- Lines that have a common allele for a given region
- Lines containing a given SNP
- A synonym finder / search tool for line names
- Genetic distance matrices
- LD Analysis (in genetic and physical coordinates)
- Alleles in a population (local or genome-wide)
- Other: _____

2. What is your highest priority in the list above?

Top Priority #1

Mark only one oval.

- SNPs in a region for a given list of lines
- Haplotype analysis in a given list of lines
- Pedigree relationships
- QTL regions
- Lines that have a common allele for a given region
- ASynonym finder / search tool for line names
- Genetic distance matrices
- LD analysis (in genetic and physical coordinates)
- Alleles in a population (local or genome-wide)

3. How do you want this visualized? How will you use this visualization?

Visualization - Top Priority #1

4. What is your second highest priority in the list above?

Top Priority #2

Mark only one oval.

- SNPs in a region for a given list of lines
- Haplotype analysis in a given list of lines
- Pedigree relationships
- QTL regions
- Lines that have a common allele for a given region
- ASynonym finder / search tool for line names
- Genetic distance matrices
- LD analysis (in genetic and physical coordinates)
- Alleles in a population (local or genome-wide)

5. How do you want this visualized? How will you use this visualization?

Visualization - Top Priority #2

6. Any other type of data you would like to see visualized at MaizeGDB?

Maize Populations / Lines

7. Which publicly available maize inbreds/founders/populations would be most beneficial to visualize in pedigree views at MaizeGDB?

(Though there are repetitiveness in the sets below, we'd like to get a sense of the sets you most commonly use)

Check all that apply.

- 3000 inbred lines from Romay et al. (Genome Biol, 14:R55, 2013)
- Expired PVPs (Plant Variety Protection Act)
- GEM (BGMS) DH isogenic lines (360 lines, 8k SNPs)
- Goodman/Flint-Garcia panel (Flint-Garcia et al, Plant J, 2005)
- IBM RILs (Lee et al 2002 Plant Mol Biol 48:453-462)
- NAM RILs (yu et al, Genetics, 178, 539, 2008)
- NAM founder lines (Buckler et al 2009 Science 325:714-718)
- Populations used in GBS (Genotype-by-sequencing) version 2.7 from Panzea
- Inbreds used for HapMap1 (Gore et al, Science, 326, 1115, 2009)
- Inbreds used for HapMap2 (Chia et al., Nat. Genet., 44, 803, 2012)
- Germplasm used in pan-genome (Lu et al, Nature Comm, 6, 6914, 2015)
- Other: _____

8. What is your highest priority in the list above?

Mark only one oval.

- 3000 inbred lines from Romay et al. (Genome Biol, 2013)
- Expired PVPs (Plant Variety Protection Act)
- GEM (BGMS) DH isogenic lines (360 lines, 8k SNPs)
- Goodman/Flint-Garcia panel (Flint-Garcia et al, Plant J, 2005)
- IBM RILs (Lee et al, Plant Mol Biol, 2002)
- NAM RILs
- NAM founder lines (Buckler, Science, 2009)
- Populations used in GBS ver 2.7 from Panzea
- HapMap1
- HapMap2
- Germplasm used in pan-genome

9. What is your second highest priority in the list above?

Mark only one oval.

- 3000 inbred lines from Romay et al. (Genome Biol, 2013)
- Expired PVPs (Plant Variety Protection Act)
- GEM (BGMS) DH isogenic lines (360 lines, 8k SNPs)
- Goodman/Flint-Garcia panel (Flint-Garcia et al, Plant J, 2005)
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- NAM RILs
- NAM founder lines (Buckler, Science, 2009)
- Populations used in GBS ver 2.7 from Panzea
- HapMap1
- HapMap2
- Germplasm used in pan-genome

10. What publicly available lines should be prioritized for tool development at MaizeGDB?

Software you use for your research

11. What DESKTOP software do you use currently for your breeding research?

Please place the most useful software on top. A piece of software per line.

12. What ONLINE TOOLS do you use currently for your breeding research?

Please place the most useful software on top. A piece of software per line.

Comments

13. Is there anything missing in this survey that we have not covered?

About You (Optional - but much appreciated)

14. Name

15. Organization

16. E-mail

17. Phone

18. Role*Check all that apply.*

- PI
- Postdoc / Scientist
- Technician
- Graduate Student
- Undergraduate
- Other: _____

19. Organization Type*Check all that apply.*

- Academic
- Government
- Industry
- Other: _____

20. Would you be willing to provide more feedback?*Mark only one oval.*

- Yes
- No

21. Would you be willing to serve as a beta tester for the tools to be developed?*Mark only one oval.*

- Yes
- No

22. Do you self-identify yourself as a breeder?*Mark only one oval.*

- Yes
- No

23. What best describes the focus of your research program?

Mark only one oval.

- Breeding
- Biochemical and Molecular Genetics
- Cell and Developmental Biology
- Computational Biology / Bioinformatics
- Cytogenetics
- Genome Editing
- Education and Outreach
- Quantitative Genetics
- Transposons and and Epigenetics
- Plant Development

THANK YOU VERY MUCH FOR YOUR INPUT!!!

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