The need for a genome browser

Preparation of the survey

- The MaizeGDB team created and distributed the survey on behalf of the Maize Genetics Executive Committee.

- After we prepared the survey, we sent it to the Working Group and Executive Committee for suggestions and incorporated the suggestions into the survey.

- We appreciate that the Executive Committee supported the survey and promoted it among maize cooperators.

Eliminating bias from the survey

- Recommendations from Assist. Prof. Patrick Armstrong from ISU Psychology.

- Instead of asking people to circle a specific website that they use for maize genome, and then eliminating those websites in alphabetical order, so that people will be able to find the websites they are using very easily without thinking which Genome Browser the website is using.

- Combine ranking of features with rating (basically assigning weights to specify important specific feature as to the user).

Choosing the survey takers

- We sent the survey to 1,241 maize cooperators.

- Definition of a cooperators:
  - Attendees of maize meetings
  - Researchers publishing frequently on maize
  - People who specifically requested to be considered a maize cooperators from MaizeGDB.

- Privacy: we used a randomly generated key that is deleted at the end of the survey.

- Uniqueness: key system ensured that each cooperators can take the survey only once.

Survey results

- 69% of the respondents used MaizeSequence and the number is the same for Gramene users. A total of 75% use either MaizeSequence or Gramene.

- Although both sites use Ensembl as a genome browser, only 26% of the respondents acknowledged that they are using Ensembl. This result shows that the users may not be aware of the underlying software for browsers that the various websites are using.

Feature rankings

- The features are sorted as follows (rankings are shown in parentheses where a lower number indicates more support):
  - Ease of use (1.4)
  - Visuals (2.6)
  - Speed (3.2)
  - Gene content completeness (3.7)
  - Gene model selection (4.1)
  - Annotation quality (4.4)
  - Chromosome information (5.1)

- Clearly, the respondents want an intuitive genome browser that allows researchers to select the needed data in the most accessible and fastest fashion.

Conclusions

- Based on our analysis, choosing GBrowse will provide maize researchers the following strengths:
  - Ease of use, visuals, speed
  - Community development
  - Comparative genomics tools
  - Providing interlinks between MaizeGDB and Gramene will enrich the research tools with minimal cost.

Bad genome browser examples

- Among 29 comments in bad genome browser examples, 10 of them cite either MaizeSequence.org or Gramene (99%), which use Ensembl as their genome browser.

- The reason might be that MaizeSequence.org or Gramene is the most used browser for the maize cooperators (75% of the respondents use one of those websites), while Ensembl is referred by only 26% of the respondents who are using specific DNA sequence data sets.

- The respondents usually cite the perceived absence of the website as the major problem.

- Many more submission steps get information useful.

- too many choices, there should be a sense default for sequence.

Conclusions and roadmap

Roadmap for the genome browser

1. We plan to start implementing the Genome Browser right away.

2. We plan to get a copy of the database from MaizeSequence.org so that we can start working on how the sequence data will fit within the database schema of GBrowse to and get available gene models from MaizeSequence.org, Daniel Ribeiro, Schmutz, and Brandes.

3. We plan to choose 5 people to provide guidance from academia, government, and industry with at least one representative from outside of the US, and 10 people for beta testing among the cooperators.

A snapshot from the MAGI website showing MAGIv3.1_60943 region using GBrowse. Eddy Yeh and Karthik Viswanatha from the Schnable Group will assist MaizeGDB during the genome browser implementation when we encounter roadblocks.