**Planning Documentation – Ideas for Sprint 4 changes**

* Sprint 4 planning points were finalised after discussions in a team meeting on 03/01/2025.
* Useful discussion points for the next client meeting have been noted. After the next client meeting the relevance and priority of sprint 4 improvements will be decided.

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| Suggestions for improvements | Relevant discussion points for next client meeting |
| **For Panel Gene Mapper Application** | |
| Add more unit tests to panelgenemapper application. | - |
| Add automation to send an email to users when there has been a panel app database update. | Do all users have access to emails?  Would a different notification system be appropriate? |
| Add a function allowing users to set a customised interval for checking for panel app database updates. | Who will be allowed to set this interval, all users or will we need to consider permissions? |
| Improve documentation and commenting. | - |
| **Database Management** | |
| Add a function to check whether records are unique before a user can add them to the database. If they are not unique, notify user at the point of creating a new record. | Does this fit with lab processes? Are there scenarios where the exact same record could be added twice (the same record would be all fields matching another record). |
| Duplicate management processes. Add automation to check whether there are duplicate records in the database and deal with these appropriately. | How would the client like to deal with duplicate management? For example, should a list of duplicates be created for manual checking? Does the lab have capacity for this?  Alternatively, should duplicate management occur at the point of adding a record to the database? |
| Addition or removal of any database fields. | Are all of the database fields relevant? Should any be added or removed? |
| **For BED file Integration** | |
| Optimise the BED file search to run quicker. | How urgent are BED file retrievals?  How quickly would these need to be done? |
| The BED file currently displays exons in the Mane Select transcript. Add a fucnntion which allows the user to decide what transcript or transcript they would like a BED file for. | Is this relevant? Does the lab only user the BED files for the Mane Select transcript or do they need exon data for other transcripts, for example the MANE Plus Clinical transcript set. |
| Add validation checks to check   * That gene\_ensembl\_id\_GRch38" is not missing * For empty data\_list * for start and end positions in exons | - |
| **For front-end** | |
| Lists of genes included in R Codes can be long. Consider adding different views in the user interface so that lists of genes can be minimised and maximised depending on the user’s need. | Ask the client to review the current view and give feedback. |
| Add a button so that a user can initiate the check for new panel app database updates from the front end. | Gather client feedback on this feature. |
| Consider adding a summary data table. For example, so that users can see how many records are in the database, how many new records have been added over a specified time interval, how many R codes are in the database and the current version of the PanelApp database. THIS IS IN EARLY DESIGN PHASE. | Discuss whether this feature would be helpful. |