



The James Hutton Institute

Information & Computational Sciences

Germinate 3

Changelog/Migration Documentation

Version 3.4.0

March, 2017

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Version 3.3.2

New/Changed features

- ADD** Added code that allows to force table filtering programmatically.
- FIX** Fixed error on search page when searching for markers.
- FIX** Fixed position and width of context-menu for item marking when the right edge of the browser is very close to the click event.
- CHG** Synchronized item marking between tables on the same page, i.e. if there is more than one table showing the same type of markable item (e.g. accession), marking an element in one table will now select it in the other tables as well.
- FIX** Fixed an issue where the table header checkbox and the table row checkboxes were out of sync.
- CHG** Changed styling of RevealPanels.
- FIX** Fixed scroll position issue on `#news` page after clicking on one of the news item in the page's footer.
- FIX** Fixed incorrect SQL query when registering for a Germinate instance with an existing account.
- ADD** Added option to color phenotype-by-phenotype charts by year.
- ADD** Added new reusable legend widget for D3.js charts.
- ADD** Added new legend to all multi-line (climate, trials overview, line-performance, phenotype-by-phenotype, phenotype matrix) charts.
- ADD** Added explanation to phenotype matrix chart about maximum number of selectable phenotypes.
- CHG** Changed 'datasetmeta' update thread to no longer delete manual entries for external datasets, i.e. counts for internal datasets will be re-calculated every hour, counts for external datasets will be left as they are (because we can't calculate them anyway).
- ADD** Added dataset statistics to `#data-stats` page. The new chart is a grouped bar chart based on the dataset type (trial, phenotype, genotype, etc.) against the number of data points per year.
- ADD** Added selection to institutions GeoChart. When a country with data is selected, it will filter the table for you to only show institutions from this country. Selecting the empty area or a country with no data will reset the filtering.
- ADD** Added selection to taxonomy pie-chart (`#data-stats`). When the user clicks on a pie slice, s/he will be taken to the accession overview page where the table will be filtered to just show accessions with this taxonomy.
- ADD** Added selection to collecting site country chart (`#data-stats`). When the user clicks on a pie slice, s/he will be taken to the accession overview page where the table will be filtered to just show accessions from this country.

- ADD** Added accession tables to both the geographic point search as well as the geographic polygon search page.
- FIX** Fixed MySQL version checker code. It was classifying newer versions as old.
- ADD** Added download option for a specific pedigree data from the passport page.
- FIX** Fixed Markerclusterer icons not working anymore due to provider shutdown of resource (<https://github.com/googlemaps/js-marker-clusterer/issues/55>).
- ADD** Added download option for the complete pedigree to browse accessions page.
- CHG** Replaced soon to be deprecated MySQL functions with their new versions (e.g. PolygonFromText -> ST_PolygonFromText).
- CHG** Changed MySQL version checker to test-run the actual query rather than checking the version number returned from "SELECT VERSION()".
- FIX** Fixed issue where suspending a user had no effect.
- ADD** Added a completely new search page.
- ADD** Added dataset table to search page.
- CHG** Increased size of phenotype by phenotype chart.
- CHG** Changed phenotype by phenotype raw data format to include the actual phenotype (and unit) names rather than just "x" and "y" as the column headers.
- FIX** Fixed issue where phenotype data download from the phenotypic datasets selection page wasn't working.
- CHG** The small download icon in the genotype dataset selection table now downloads the genotypic data in a Flapjack-compatible tab delimited file, rather than the raw .hdf5 file.
- FIX** Fixed issue where the raw data file download of the allele frequency binning chart stopped working correctly after the page was resized.
- CHG** Added feature that allows selection of all table items across all pages (for deletion, adding, etc.).
- ADD** Added option to name the SVG file that gets downloaded from d3.js charts before starting the download.
- ADD** Added table to the #marker-details page that shows which maps the marker is on.
- ADD** Added property to config.properties that allows the customization of the main Germinate menu. Consult the documentation for an example.
- CHG** Changed the download link of the genotypes dataset table to download a tab-delimited txt file (Flapjack format) rather than the raw .hdf5 file.
- CHG** Improved code for menu item highlighting and decluttered GerminateMenu class in general.
- CHG** Re-added support for the datasets table on the #marker-details page. This now uses the data from the HDF5 file.

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- CHG** Updated Flapjack .jar file to the latest version.
- DEL** Deleted old search pages.
- CHG** Slightly changed the way table filtering works. By default we search for exact matches, i.e. no "
- CHG** Changed the way pedigrees are displayed on the passport page to a table. This allows us to show more data about a pedigree in a structured way.
- ADD** Added pedigree data table to search page.
- ADD** Added tooltip to main search box explaining how wildcard characters work.
- ADD** Added download button to all of the paginated tables on the search page.
- CHG** Changed exported data in .kml export.
- CHG** Changed file format of "parallax-genetic-map.png" to ".jpg".
- ADD** Added new automatic database update process. This requires that you're running 3.3.1 before updating to 3.3.2 (or start with 3.3.2). From now on you'll never have to run SQL queries manually ever again to update Germinate.
- ADD** Added phenotype matrix chart to trials page as well now (instead of just being on the phenotype page).
- ADD** Fixed legend highlighting of data points when user hovers over legend item.
- CHG** Changed all queries to be fully SQL99 compliant. This is required to be able to use MySQL 5.7.5 and up.
- CHG** Added "#input=PHENOTYPE" to exported phenotype files. This makes them compatible with Helium.
- DEL** Remove obsolete GrinGlobal subfolders.
- CHG** Renamed 'date' to 'date_start' and added 'date_end' column to 'datasets' table.
- FIX** Fixed issue with SVG download when the SVG itself contains too many elements. It wouldn't download properly failing with a "Network error" thrown by the browser. This has been fixed by using a different implementation to download the SVG.
- FIX** Fixed database connection leaks. Some queries weren't properly closing the database connections in special cases.
- FIX** Fixed an issue where Internet Explorer would open files in the browser rather than download them.
- FIX** Fixed issue where jumping to a specific news page from the news section at the bottom of the page wouldn't cause the pager to update the text.
- NEW** Added pagination to color-coded climate data table. The whole dataset can now be downloaded by clicking on the download button in the bottom left corner.
- CHG** Changed the way the DatabaseObjectCache is created and cleared.
- FIX** Fixed the display of the map feature type. The marker type was mistakenly displayed in its place.
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- ADD** Added config.properties option "GoogleMaps.Api.Key" to provide a Google Maps API key. This is required by Google since June 2016.
- FIX** Fixed an issue where d3 legends and tooltips weren't properly removed on page resize events.
- ADD** Added tables to store chemical compound data. These include 'compounds', 'compound-data' and 'analysismethod'.
- ADD** Added pages to show chemical compound data. These are "#compounds", "#compound-details" and "#compound-data".
- ADD** Added synonyms to "#passport" page.
- ADD** Added synonyms to "#marker-details" page.
- ADD** Added "#compound-datasets" and "#compound-data" pages. The latter contains various visualizations for compound data. This is more or less identical to the functionality that already exists for phenotypic data.
- FIX** Fixed issue with d3 selection lasso when the legend only contains one item.
- FIX** Fixed issue with d3 selection lasso and item highlighting by the legend.
- ADD** Added new compound value charts that show the individual lines with their values in a bar chart that can be sorted either by name or value.
- ADD** Added search boxes to phenotype by phenotype and compound by compound scatter plots to allow the user to search for and highlight individual accessions.
- ADD** Added compound data table to search results page.
- CHG** Improved performance of search results page by removing unnecessary initial data query before filters are applied.
- BUG** Fixed search results page table download. It was populating the columns wrongly.
- CHG** Standardized the search results page table downloads.
- CHG** Updated GWT from 2.7.0 to 2.8.0. Several Tomcat related libraries needed updating as well.
- CHG** Changed search to allow selection of search sections. The user can either search for all types of data or restrict the search to just one of them.

Migration from 3.3.1 to 3.3.2

- **IMPORTANT:** Please do not migrate to 3.3.2 from versions older than 3.3.1 without going through the individual migration steps. With this version, we introduce a new automatic migration process for the database side of things. No manual database updates will be required from this point on, unless otherwise indicated. It'll assume that you're currently running version 3.3.1.
- Move your "Text.properties" files from `instance-stuff/<your-instance>/modules/code` to `instance-stuff/<your-instance>/i18n`

- Edit your instance-stuff/<your-instance>/Germinate.gwt.xml file and change the following:
 - <entry-point class="jhi.germinate.client.core.ModuleCore" /> to
 <entry-point class="jhi.germinate.client.ModuleCore" />
 - <source path="client/core" /> to
 <source path="client" />
 - <source path="shared/core" /> to
 <source path="shared" />
- Edit your instance-stuff/<your-instance>/web.xml file and change the following:
 - jhi.germinate.server.core.util.ApplicationListener to
 jhi.germinate.server.util.ApplicationListener
- Obtain a Google Maps API key from Google and add it as the option `GoogleMaps.Api.Key` to "config.properties".
- New translatable text has been added. The following properties can be changed in your "Text.properties" file and the according translation files:

```

page.trials.phenotype.by.phenotype.coloring.year=Color by year
page.data.statistics.datasets.title=Data points per experiment type
page.data.statistics.datasets.text=This bar chart shows the number of data points per year for each of the
    experiment types. Each individual bar per group represent a year.
column.institutions.code=Code
page.data.statistics.taxonomy.text=This pie chart visualizes the percentage of accessions for each
    taxonomy. Each slice represents a taxonomy. Hovering over a slice will show the actual number of
    accessions. Clicking on a slice will take you to the accession overview page which will then just show
    the accessions with this taxonomy.
page.data.statistics.accessions.per.country.text=This chart shows the distribution of accessions. For
    each country the number of accessions collected in this country is color-coded. Clicking on a country
    will take you to the accession overview page which will then just show the accessions from this
    country.
page.geographic.search.accession.title=Accessions ordered by distance
page.geographic.search.polygon.collsite.title=Collecting sites in the polygon
page.geographic.search.polygon.accession.title=Accessions in the polygon
page.search.section.all=All data
page.search.section.accession.data=Accession data
page.search.section.attribute.data=Attribute data
page.search.section.phenotype.data=Phenotype data
page.search.section.compound.data=Compound data
page.search.section.mapdefinition.data=Map definition data
page.search.section.datasets=Datasets
page.search.section.pedigree.data=Pedigree data
page.search.section.location.data=Location data
download.format.helium=Download pedigree for Helium
page.marker.details.maps.title=Maps
page.marker.details.maps.text=This marker appears on the following maps
column.pedigree.child.gid=Child GID
column.pedigree.child.name=Child name
column.pedigree.parent.gid=Parent GID
column.pedigree.parent.name=Parent name
column.pedigree.relationship.type=Relationship type
column.pedigree.relationship.description=Relationship description
column.pedigree.pedigree.description=Pedigree description
column.pedigree.pedigree.author=Pedigree author
search.box.tooltip=Use "%" as the wildcard character, e.g. "%KINGDOM%".
column.date.set.date.end=End date
menu.data.statistics=data statistics
column.compound.id=Id
column.compound.name=Name
column.compound.description=Description
column.compound.molecular.formula=Molecular Formula
column.compound.unit.name=Unit

```

```
column.compound.monoisotonic.mass=Monoisotonic Mass
column.compound.average.mass=Average Mass
column.compound.class=Class
column.compound.data.id=Id
column.compound.data.analysis.method=Analysis Method
column.compound.data.unit.name=Unit
column.compound.data.value=Value
widget.synonyms.title=Synonyms
menu.compounds=compounds
menu.compound.data=compound data
page.compound.datasets.title=Compound datasets
page.compounds.title=Compounds
page.phenotypes.title=Phenotypes
notification.compound.dataset.no.compound=No compounds found for the selected dataset.
page.compounds.compounds.title=Select compounds
tooltip.table.header.filter.cell=Type your search term and hit enter. Use "%" as the wildcard character.
widget.d3.chart.search.field=Search for item by name
column.phenotype.short.name=Short name
```

- If you're using custom parallax-banner images, please convert your "parallax-genetic-map.png" to "parallax-genetic-map.jpg".

Version 3.3.1

New/Changed features

CHG Disabled mouse-wheel scrolling on locator map.

ADD Added option to filter datasets table by count and datapoints.

FIX Fixed issue with Maintenance-Mode.

FIX Fixed issue with spaces in file paths.

CHG Improved performance of 'germinatebase' export of whole dataset.

FIX Fixed issue with y-axis tick formats in d3.js multi-line chart.

FIX Fixed issue on admin-config page where the available pages weren't updated as expected.

ADD Added checkbox column header for item marking columns to easily mark all items.

CHG Updated FontAwesome to version 4.5.0.

CHG Major code-cleanup.

ADD Major Javadoc additions.

ADD Added pedigree information to passport page. Now uses the database tables 'pedigree', 'pedigreedefinitions', 'pedigreenotations' and 'pedigreedescriptions'.

ADD Added color picker widget to administrator configuration page to make customization of the page easier.

ADD Added "Technologies" section to the documentation. This section explains which third-party libraries (Java, JavaScript, Fonts) we use and how we use them.

ADD Added property that decides if the main website logo (top-left) contains links itself. Usually clicking the whole logo will redirect to "home", however, since we switched to SVG files, these can contain links on their own (for either the whole logo or even sections of it), so we allow to prioritize the internal links and disable the link to "home" by setting 'Germinate.Template.Logo.Contains.Link' to 'true'.

CHG The search page will now show all tabs regardless of page availability, whereas before it would only show the tabs of those types that have their details page enabled, e.g. the 'marker-details' page had to be enabled for the 'marker' search tab to show up. Now all tabs show and the table that shows the search results will only contain links to the details page if available.

CHG Changes to the admin configuration page ('#admin-config') are now persistent changes to the config.properties file. Restarting Tomcat or restarting the web-application will not erase changes made to the configuration anymore.

CHG '#news' and '#about' are now publicly visible, no matter what.

ADD Added 'Germinate.Gallery.Images.Per.Page' property to config.properties that determines how many images per page each gallery will show (default] 4).

FIX Fixed session persistency bug.

- CHG** The external data directory can now be used to not only externalize the actual 'data' folder, but also 'download', 'res' and 'apps'. Germinate will prefer the files found in that location, but fall back to the files bundled with Germinate itself. To use this feature, set the 'Germinate.ExternalDataFolder' property to the directory containing the previously mentioned folders (e.g. '/srv/data/germinate/germinate-template' which then contains 'data', etc.).
- CHG** The automatic image scaler will now work with the external data directory image folder as well.
- CHG** Restyled passport page. Moved information representation to list format when a table didn't add any functionality to it.
- DEL** Removed legacy classes related to old table structure.
- DEL** Removed Apache POI library dependencies.
- CHG** D3.js chart download context menu is now available on IE as well. However, it only shows the "download data file" option, as IE doesn't support the required functionality (or rather prohibits it).
- FIX** Client settings are no longer shared between user logins. Each user has its own settings even when the second user logs in after the first has logged out (in the same browser).
- CHG** Moved cookie creation to server.
- CHG** Removed checkbox column from datasets table if the continue button isn't available, as there is no point in selecting datasets in this case.
- FIX** Fixed group permission issue where admins weren't able to see all groups.
- CHG** Added new property 'Germinate.Template.GradientColors' that allows customization of the gradients shown on the website.
- ADD** Added parallax scrolling banners to selected pages.
- ADD** Added new property 'Germinate.Template.Show.Parallax.Banner' that determines if the parallax banner is shown or not.
- CHG** 'germinatebase.name' is now a required field and will be used for genotypic data export. It represents the BRAPI 'defaultDisplayName', a human-readable and meaningful name for the accession.
- ADD** Added data statistics page (#data-stats) with basic statistics.
- CHG** Applied some changes to the template.
- FIX** Fixed rare issue with "select" element selection where elements weren't selected if the number of items matched the visible rows and the selection happened by dragging from inside the select element to outside the select element.
- CHG** Improved performance of dataset related queries by about 33
- ADD** Added page size selection widget to paginated tables.
- CHG** Further improved the performance of dataset related queries by pre-calculating dataset sizes and storing the result in the 'datasetmeta' table. This is re-calculated every hour to ensure it's reasonably up-to-date.

CHG Initial adaptation of the Java 8 Streams API on the server.

CHG Improved performance of trials/phenotype export page (phenotypes only retrieved once in total instead of once per "tab").

NEW Added HDF5 functionalities for genotypic data export.

CHG Switched genotypic data export over to HDF5 by default.

NEW Added "Select all" buttons to multi-select boxes.

NEW Added operator selector to table filter. Users can now switch between logical "AND" and "OR" combination of query fields.

NEW Added column filtering to marker table on map-details page.

DEL Removed phenotype data export preview as it serves no good purpose. The data is already exported, so why not just download it?

DEL Removed two of the four maps (the weighted ones) on #geography as they don't really provide much new information.

ADD Added country flags to more tables containing country information.

Migration from 3.3.0 to 3.3.1

- If you're storing your genotypic data in a flat file, please convert them using Flapjack to HDF5. Run the following command to do so:

```
java -cp flapjack.jar jhi.flapjack.io.cmd.GenotypeToHdf5Converter -genotypes=<old genotype file>.txt -  
hdf5=<new hdf5 file>.hdf5
```

- Change the entry in 'datasets.source_file' to point to the newly created HDF5 file.
- New translatable text has been added. The following properties can be changed in your "Text.properties" file and the according translation files:

```
page.passport.pedigree.title=Pedigree  
notification.color.picker.at.least.one=At least one color is required.  
notification.color.picker.at.least.two=At least two colors are required.  
notification.error.writing.file=Failed to write to file on server.  
notification.inconsistency.count.result.size=Inconsistency between total number of items and count.  
page.trials.individual.not.available.for.char=Please note that the individual chart page isn't available  
for non-numeric phenotypes.  
page.about.button.add.group=Add group  
page.about.button.delete.group=Delete group  
page.geographic.search.tab.point=Point search  
page.geographic.search.tab.polygon=Polygon search  
menu.about.germinate=about germinate  
menu.about.project=about project  
page.about.project.title=About this project  
page.about.project.text=  
page.data.statistics.accessions.per.country.title=Accessions per country  
page.data.statistics.accessions.per.country.text=This chart shows the distribution of accessions. For  
each country the number of accessions collected in this country is color-coded.  
page.data.statistics.taxonomy.title=Accessions grouped by taxonomy  
page.data.statistics.taxonomy.text=This pie chart visualizes the percentage of accessions for each  
taxonomy. Each slice represents a taxonomy. Hovering over a slice will show the actual number of  
accessions.  
page.trials.overview.select.phenotypes=Select phenotypes  
page.trials.overview.select.years=Select years  
general.select.all=Select all  
column.unit.name=Unit  
column.phenotype.value=Value
```

- Make sure that 'germinatebase.name' isn't empty and contains what we call the "default display name". This will be used during all sorts of exports from Germinate to provide the user with a meaningful name of the accession.
- Run this against the database:

```

/* Change the type of `general_identifier` from `int` to `varchar` */
ALTER TABLE `germinatebase` MODIFY COLUMN `general_identifier` varchar(255) NOT NULL AFTER `id`
;

/* Allow setting the `unit_id` to NULL */
ALTER TABLE `phenotypes` MODIFY COLUMN `unit_id` int(11) NULL COMMENT 'Foreign Key to units (units.
id).' AFTER `datatype`;

/* Set `dataset_state_id` to NOT NULL (is required now) */
ALTER TABLE `datasets` DROP FOREIGN KEY `datasets_ibfk_2`;
ALTER TABLE `datasets` MODIFY COLUMN `dataset_state_id` int(11) NOT NULL DEFAULT 1 COMMENT '
Foreign key to datasetstates (datasetstates.id).' AFTER `created_by`;
ALTER TABLE `datasets` ADD CONSTRAINT `datasets_ibfk_2` FOREIGN KEY (`dataset_state_id`)
REFERENCES `datasetstates` (`id`) ON DELETE CASCADE ON UPDATE CASCADE;

/* Remove the default value of the `contact` column */
ALTER TABLE `institutions` MODIFY COLUMN `contact` varchar(255) CHARACTER SET latin1
COLLATE latin1_swedish_ci NULL DEFAULT NULL COMMENT 'The contact at the institute which should
be used for correspondence.' AFTER `country_id`;

/* Create a new table to store database versions */
CREATE TABLE IF NOT EXISTS `databaseversions` (
`id` int(11) NOT NULL AUTO_INCREMENT ,
`name` varchar(255) NOT NULL ,
`number` varchar(255) NOT NULL ,
`created_on` datetime NULL ,
`updated_on` timestamp NULL ON UPDATE CURRENT_TIMESTAMP ,
PRIMARY KEY (`id`)
);

/* Insert the latest versions */
INSERT IGNORE INTO databaseversions (id, NAME, number) VALUES (1, "Crossbill", "3.3.0"), (2, "Crossbill", "
3.3.1");

/* Allow `source_file` in the datasets table to be null */
ALTER TABLE `datasets` MODIFY COLUMN `source_file` varchar(255) CHARACTER SET latin1
COLLATE latin1_swedish_ci NULL DEFAULT NULL AFTER `date`;

/* Force the `name` column to be NOT NULL, because this will be used as the "default display name" of the
accession */
ALTER TABLE `germinatebase` MODIFY COLUMN `name` varchar(255) CHARACTER SET latin1 COLLATE
latin1_swedish_ci NOT NULL AFTER `number`;

/* Add new datasets meta table to store data counrs */
CREATE TABLE IF NOT EXISTS `datasetmeta` (
`id` int(11) NOT NULL AUTO_INCREMENT ,
`dataset_id` int(11) NOT NULL ,
`nr_of_data_objects` int(11) NOT NULL ,
`nr_of_data_points` int(11) NOT NULL ,
PRIMARY KEY (`id`),
CONSTRAINT `datasetmeta_ibfk_datasets` FOREIGN KEY (`dataset_id`) REFERENCES `datasets` (`id`)
ON DELETE CASCADE ON UPDATE CASCADE
);

/* Adds a new index to the phenotypedata table */
ALTER TABLE `phenotypedata` ADD INDEX `phenotypedata_recording_date` (`recording_date`) USING
BTREE;

/* Adds a new index to the phenotypedata table */
ALTER TABLE phenotypedata ADD INDEX `trials_query_index` (`phenotype_id`, `germinatebase_id`, `
location_id`, `trialseries_id`, `recording_date`, `treatment_id`, `dataset_id`, `phenotype_value`)
USING BTREE;

```

Version 3.3.0

New/Changed features

- FIX** Fixed accession marking mechanism. Was marking wrong items at times.
- FIX** Fixed search table highlight hiding anchor element.
- ADD** Option to show a map below the datasets table (shows associated locations).
- ADD** Added download link for markers removed from data export.
- ADD** Added another download option to d3.js charts. You can now download the data file that is used to create the chart.
- ADD** Added trials overview table.
- ADD** Added trials overview line chart.
- ADD** Added more width steps to the website template (1280px and 1600px) for higher resolution screens.
- ADD** Added export option for attributes to main accession export (below the main accession table).
- CHG** Added Filter that makes sure the browser does not cache .nocache files.
- CHG** Major rewrite of main table code. It's now much easier to use.
- CHG** Rewrite of Google Map Marker Clusterer code.
- CHG** Major rewrite of table code. AbstractBaseTable and PaginationTable now use Providers to create and render the cells.
- CHG** Moved linePerformance page to the initial trials page.
- CHG** Tweaked the web interface template.
- DEL** Deleted template image files that aren't mission critical → less images, more or less same look.
- ADD** Added dataset description to phenotype export preview table.
- ADD** <servlet> and <servlet-mapping> entries in web.xml are no longer required.
- CHG** More template style changes.
- CHG** Restricted decimal places of numbers to 2 digits where sensible.
- CHG** Changed share-widget to mirror look-and-feel of new language selector.
- ADD** Introduced new ShareWidget.java that replaces ShareButtonBar.java.
- FIX** Fixed multiple CSS issues.
- FIX** Dataset overview table showing the wrong column content.
- ADD** Germinate now uses HTML5 local storage instead of cookies (some cookies remain).
- ADD** Added pedigree database tables.

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- CHG** Updated jQuery to 2.1.4.
- CHG** Updated jQueryUI to 1.11.4.
- ADD** Added new properties entry: `Germinate.HideIdColumns` that controls if internal id columns are shown in tables.
- CHG** Updated httpclient and httpcore to newer versions.
- CHG** Major rewrite of `PaginationTable`.
- ADD** Added initial functionality to handle marking of not only accessions.
- CHG** Changed RPC signatures to use `Pagination.java` instead of a variable each for start, length and sorting, etc.
- CHG** Updated FontAwesome to 4.4.0.
- CHG** Added more database tables to conform with the MCPD.
- CHG** Removed no longer required columns from "germinatebase".
- CHG** Moved "flowering_season_start" and "growing_season_start" to "attributes".
- ADD** Markers and collecting sites can now be marked for the "shopping cart" as well as accessions.
- FIX** Fixed issue with floating table headers not loading.
- CHG** Replaced some raster image resources with vector image resources.
- CHG** logo.png and crop.png now have to be .svg files.
- FIX** Fixed issue where Germinate would not undeploy from Tomcat from time to time.
- ADD** Added pagination to dataset tables.
- ADD** Introduced caching of database query results to increase performance and decrease the load on the database while still returning up-to-date data.
- CHG** Removed restrictions for search terms on the groups item filters. Search terms can now include SQL special characters as well.
- FIX** Fixed issue with the allele frequency data export. Items were exported independent of the dataset that was selected.
- DEL** Removed table 'groupdatasets' as no longer required.
- CHG** Rewrote SQL queries formerly using 'groupdatasets' table.
- CHG** Restyling of d3.js chart options panel.
- CHG** Changed package structure to reflect new internal guideline.
- FIX** Fixed an issue with session persistence on the server.
- ADD** Added "number of data points" to the datasets table.
- ADD** Added "search" menu item to main menu. This can be disabled/enabled with a config.properties entry ("`Germinate.Template.Show.Search`").
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- ADD** Added initial table filtering feature.
- CHG** Changed PassportPage to use the new Accession data object.
- CHG** Added pagination to the attributes table on the passport page.
- CHG** Added option to show all locations on the location overview page.
- ADD** Added "read-only" mode where the user is not allowed to add/delete/update the data in the database. This can be disabled/enabled with a config.properties entry ("Germinate.Is-ReadOnly").
- ADD** Added tooltips to shopping cart indicator to explain which number represents which type of marked item.
- FIX** Fixed an issue where the context menu on markable item tables didn't show up when the actual marker checkbox was right-clicked.
- ADD** Added option to filter by just the year (in addition to full dates) in filterable tables with date columns.
- CHG** Disabled help button on pages that do not provide help information.
- FIX** Fixed multiple theming related issues on mobile devices.
- ADD** Added functionality to create groups of accessions (more types in the future) from an external software tool. This includes uploading a file with the accession identifiers. The external tool will get the name of the uploaded file in the result and can then forward the user to the Germinate web-interface where the user can review the group preview. If everything looks ok, the user can create a new group.
- CHG** Removed group editing functionality if user doesn't have permissions to actually edit the group.
- FIX** Fixed issue with shopping cart context-menu not showing when right-clicking on the actual checkbox column of a markable table.
- ADD** Added pagination to annotations/comments widget.
- FIX** Fixed issue with images not properly released on the server which caused Tomcat undeploy issues on Windows.
- ADD** Added distribution indicator to scatter plots.
- ADD** Added phenotype/trials location chart. This will show the number of phenotype/trials readings per country. If a phenotype is selected, this will show the average phenotype value per country.
- FIX** Fixed issue with phenotypic data export. It wouldn't export data for phenotypes that do not have a unit.
- CHG** It's no longer necessary (and no longer recommended) to bundle your own copy of Flapjack with Germinate. We will now bundle an up to date version of Flapjack with the basic setup.
- ADD** Added option to mark accessions from phenotype/trials charts.
- CHG** Rewrite of FileDownloadWidget and OnDemandFileDownloadWidget.
-

-
- FIX** Fixed .kml export.
- CHG** Made .kml export more efficient and stable.
- FIX** Fixed issue with duplicate gradient widgets on locations overview page.
- ADD** Added administrator configuration page (#admin-config).
- CHG** Complete rewrite of the main navigation menu to allow for sub-menus.
- ADD** Added option to download data for marked accessions from accessions overview page.
- FIX** Fixed loading indicator forcing scrollbars on tables when using Firefox.
- ADD** Added column filtering to Dataset tables.
- ADD** Added the option to download phenotypic data from the phenotypic dataset overview page (download icon per row).
- ADD** Added table options panel that allows showing/hiding the table filter headers.
- CHG** Rewrote table options panels for a more consistent look.
- FIX** Fixed "Continue" button being visible on genotype-datasets page even if genotype-export isn't available
- CHG** Improved performance of stored procedure to export germinatebase table for marked accessions.
- CHG** Right-aligned number columns.
- ADD** Added "mark all items" to selected tables. This will mark all the items from all pages of the paginated table not just the current page.
- FIX** Fixed issue with Internet Explorer where it wouldn't accept a specific (valid) jQuery call to open/close the table filter panel.
- FIX** Fixed file encoding issues when writing climate chart data files.
- CHG** Better integration of Flapjack by directly calling Flapjack's API for file manipulation instead of running the .jar file externally.
- ADD** Added "Color by dataset" to phenotype by phenotype charts.
- ADD** Added collecting site search based on user-defined polygons.
- ADD** Added units to Climate dropdown box
- FIX** Fixed issue with wrong items being selected from phenotype by phenotype chart.
- ADD** Added coloring options to phenotype matrix chart.
- FIX** Fixed issue with query location moving during query on geographic search page.
- CHG** Changed positioning of climate overlays on Google Maps.
- ADD** Added actual minimum and maximum values to Gradient legend.
- FIX** Fixed issue with maps of wrong type showing up during data export.
-

CHG Moved "Continue" button above map on datasets page.

ADD Added loading indicators to user input widgets on the groups page.

FIX Fixed issue where non-admin users weren't able to create new groups.

Migration from 3.2.0d to 3.3.0

- Install Java 8 on your server running Tomcat.
- Delete the "Flapjack" folder in your `instance-stuff/<your-project>/apps` folder.
- The "Text.properties" keys have changed from camel-case notation to dot-separated notation. Please consult the file "3.2.1-properties-mapping.tsv" for a mapping between old and new keys. The "I18NReplacer.java" class can be used to generate a file in the new format based on the old format. Please modify the paths accordingly.
- Old translatable text has been removed. The following properties can be removed from your "Text.properties" file and the according translation files:

```
column.accessions.growing.season
column.accessions.flowering.season
column.passport.contact
column.passport.status
column.passport.breeder.submitter
column.passport.contact.current
column.passport.phenotype
column.passport.state.id
column.passport.state.description
page.passport.genotype.title
page.passport.genotype.text
page.passport.breeder.title
page.passport.dus.profile.title
page.passport.passport.additional.title
column.locations.waterlog
column.locations.ph
```

- New translatable text has been added. The following properties can be changed in your "Text.properties" file and the according translation files:

```
banner.read.only=Germinate is currently operating in read-only mode. Some features have been temporarily disabled.
column.dataset.datapoints=Data points
column.locations.type.name=Location type
column.phenotype.data.treatment.description=Treatment
menu.search=search
notification.accessions.selection.empty=Please select an accession.
notification.group.group.name.exists=A group with this name already exists.
notification.group.preview.invalid.filename=Session invalidated because expected and found group members differ.
notification.group.preview.name.missing=Name missing.
notification.groups.items.added.ignored=Items added: {0}, items ignored: {1}.
notification.system.read.only=Germinate is operating in read-only mode. Changes have not been applied.
page.group.placeholder.group.name=Group name
page.group.preview.add.button=Add group
page.group.preview.create.group.title=Create a new group
page.group.preview.text=<p>This page shows the database objects that have been selected based on your selection in an external tool. Please review the selection.</p><p>When you're happy with the result, select a name for the group in the text box and hit the button to create the group.</p>
page.group.preview.title=Group preview
page.phenotypes.overview.title=Overview
page.trials.overview=Overview
page.trials.phenotype.by.phenotype.coloring.none=No coloring
page.trials.phenotype.by.phenotype.coloring.treatment=Color by treatment
page.trials.phenotype.by.phenotype.coloring.dataset=Color by dataset
general.filename=Filename
```

```

d3.alert.select.filename=Please select a filename
page.phenotypes.matrix.select.group.phenotype=Please select at least one phenotype and at least one group.
page.phenotypes.matrix.select.at.most=Please select at most {0,number} phenotypes.
page.phenotypes.matrix.select.at.most[one]=Please select at most 1 phenotype.
page.trials.matrix.title=Matrix
page.genotype.result.download.map=Download map file
page.cart.button.add.selected=Mark selected items
page.cart.button.remove.selected=Unmark selected items
page.phenotypes.geochart.all.phenotypes=All phenotypes
page.phenotypes.geochart.title=Map
column.megaenvironment.id=Id
column.megaenvironment.size=Size
page.location.treemap.label.items=Items
page.location.treemap.label.location=Locations
general.standard.deviation=Standard deviation
column.phenotype.id=Id
column.phenotype.name=Name
column.phenotype.description=Description
page.admin.config.insufficient.permissions=You don't have sufficient permissions to view this page and
    apply changes.
notification.admin.config.changes.applied=Changes have been applied successfully. Refresh the page to see
    changes in action.
page.admin.settings.gatekeeper.heading=Gatekeeper settings
page.admin.settings.social.heading=Social media settings
page.admin.settings.usage.tracking.heading=Usage tracking
page.admin.settings.template.heading=Theme template settings
page.admin.advanced.heading=Advanced settings
page.admin.warning=These settings will majorly influence the way Germinate works. Please only change them
    if you know what you are doing!
page.admin.button.save.changes=Save changes
general.confirm=Confirm
general.copy=Copy
page.admin.alert.confirm.changes=Are you sure you want to save the changes?
menu.menu=Menu
menu.germinate.info=about germinate
page.accessions.browse.download.selected.accessions=Marked accessions
notification.accessions.export.mark.at.least.one=Please mark at least one accession.
contact.us.message=Contact us: {0}
page.cart.button.add.page=Mark items on page
page.cart.button.remove.page=Unmark items on page
widget.pager.page.first=Go to first page
widget.pager.page.previous=Go to previous page
widget.pager.page.next=Go to next page
widget.pager.page.last=Go to last page
widget.table.filter.title=Toggle filtering
general.range.from=From
general.range.to=To
notification.exception.flapjack=Flapjack could not create the required file.
page.geographic.search.polygon.text=<p>The map below allows you to select a region by drawing a polygon
    around it. Once you're happy with the selection, hit the "Continue" button to get the collecting sites
    within this polygon.</p><p>You can adjust each corner point of the polygon by dragging it. It's
    also possible to add new corner points in between two existing points by dragging the semi-
    transparent circle.</p><p>Right-click a polygon to remove it from the map.</p>

```

- Change the "entry-point" attribute in your "Germinate.gwt.xml" file to:

```
<entry-point class="jhi.germinate.client.ModuleCore" />
```

- Create SVG versions of "logo.png" and "crop.png" and place them in the same folder.
- Apache Tomcat 7.0.28 or above is now required.
- Identify the listener section in your web.xml. Change the content of the "listener-class" to:

```
<listener-class>jhi.germinate.server.util.ApplicationListener</listener-class>
```

- Identify the filter section in your `web.xml`. Replace the existing filters with the following filters:

```
<filter-mapping>
  <filter-name>HeaderFilter</filter-name>
  <url-pattern />
</filter-mapping>

<!-- Add a Filter that forces the browser NOT to cache .nocache files -->
<filter-mapping>
  <filter-name>GWTCacheControlFilter</filter-name>
  <url-pattern />
</filter-mapping>
```

- Delete all `<servlet>` and `<servlet-mapping>` entries from your `web.xml` file.
- New property available in `config.properties`:

```
Germinate.AccessionDisplayColumn=<COLUMN FROM `germinatebase` TABLE>
```

This property is used to determine the main attribute of an accession that is used when "naming" the accession, i.e. whenever a name is displayed, the value of this column will be used.

- Run this against the database:

```
ALTER TABLE `datasets`
  ADD COLUMN `contact` varchar(255);

CREATE TABLE `treatments` (
  `id` int(11) NOT NULL AUTO_INCREMENT,
  `name` varchar(255) NOT NULL,
  `description` varchar(255) NULL,
  `created_on` datetime NULL,
  `updated_on` timestamp NULL ON UPDATE CURRENT_TIMESTAMP,
  PRIMARY KEY (`id`)
);

ALTER TABLE `phenotypedata`
  ADD COLUMN `location_id` INT(11),
  ADD COLUMN `treatment_id` INT(11),
  ADD COLUMN `trialseries_id` INT(11);

ALTER TABLE `phenotypedata`
  ADD CONSTRAINT `phenotypes_ibfk_locations` FOREIGN KEY (`location_id`) REFERENCES `locations` (`id`) ON UPDATE CASCADE ON DELETE SET NULL,
  ADD CONSTRAINT `phenotypes_ibfk_treatment` FOREIGN KEY (`treatment_id`) REFERENCES `treatments` (`id`) ON UPDATE CASCADE ON DELETE SET NULL,
  ADD CONSTRAINT `phenotypes_ibfk_trialseries` FOREIGN KEY (`trialseries_id`) REFERENCES `trialseries` (`id`) ON UPDATE CASCADE ON DELETE SET NULL;

ALTER TABLE `phenotypedata`
  ADD INDEX `trials_query_index` (`phenotype_id`, `germinatebase_id`, `location_id`, `trialseries_id`, `recording_date`, `treatment_id`, `dataset_id`, `phenotype_value`) USING BTREE
;

INSERT INTO treatments (name) SELECT DISTINCT(treatment) FROM trialsdata WHERE NOT ISNULL(treatment);

INSERT INTO phenotypedata (phenotype_id, germinatebase_id, phenotype_value, dataset_id, recording_date, location_id, treatment_id, trialseries_id) (SELECT phenotype_id, germinatebase_id, value, dataset_id, STR_TO_DATE(year, '%Y'), location_id, (SELECT id FROM treatments WHERE treatments.name = treatment), trialseries_id FROM trialsdata);

DROP TABLE `trialsdata`;

CREATE TABLE IF NOT EXISTS `pedigreedescriptions` (
  `id` int(11) NOT NULL AUTO_INCREMENT,
```

```

`name` varchar(255) NOT NULL,
`description` text,
`author` varchar(255) DEFAULT NULL,
`created_on` datetime DEFAULT NULL,
`updated_on` timestamp NULL DEFAULT NULL ON UPDATE CURRENT_TIMESTAMP,
PRIMARY KEY (`id`)
) ENGINE=InnoDB DEFAULT CHARSET=utf8;

CREATE TABLE IF NOT EXISTS `pedigreenotations` (
`id` int(11) NOT NULL AUTO_INCREMENT,
`name` varchar(255) NOT NULL,
`description` text,
`reference_url` varchar(255) DEFAULT NULL,
`created_on` datetime DEFAULT NULL,
`updated_on` timestamp NULL DEFAULT NULL ON UPDATE CURRENT_TIMESTAMP,
PRIMARY KEY (`id`)
) ENGINE=InnoDB DEFAULT CHARSET=utf8;

CREATE TABLE IF NOT EXISTS `pedigreedefinitions` (
`id` int(11) NOT NULL AUTO_INCREMENT,
`germinatebase_id` int(11) NOT NULL,
`pedigreenotation_id` int(11) NOT NULL,
`definition` text NOT NULL,
`created_on` datetime DEFAULT NULL,
`updated_on` timestamp NULL DEFAULT NULL ON UPDATE CURRENT_TIMESTAMP,
PRIMARY KEY (`id`),
KEY `pedigreedefinitions_ibfk_pedigreenotations` (`pedigreenotation_id`),
KEY `pedigreedefinitions_ibfk_germinatebase` (`germinatebase_id`),
CONSTRAINT `pedigreedefinitions_ibfk_germinatebase` FOREIGN KEY (`germinatebase_id`)
REFERENCES `germinatebase` (`id`) ON DELETE CASCADE ON UPDATE CASCADE,
CONSTRAINT `pedigreedefinitions_ibfk_pedigreenotations` FOREIGN KEY (`pedigreenotation_id`)
REFERENCES `pedigreenotation` (`id`) ON DELETE CASCADE ON UPDATE CASCADE
) ENGINE=InnoDB DEFAULT CHARSET=utf8;

CREATE TABLE IF NOT EXISTS `pedigrees` (
`id` int(11) NOT NULL AUTO_INCREMENT,
`germinatebase_id` int(11) NOT NULL,
`parent_id` int(11) NOT NULL,
`relationship_type` int(11) DEFAULT NULL,
`pedigreedescription_id` int(11) NOT NULL,
`relationship_description` text,
`created_on` datetime DEFAULT NULL,
`updated_on` timestamp NULL DEFAULT NULL ON UPDATE CURRENT_TIMESTAMP,
PRIMARY KEY (`id`),
KEY `pedigrees_ibfk_germinatebase` (`germinatebase_id`),
KEY `pedigrees_ibfk_germinatebase_parent` (`parent_id`),
KEY `pedigrees_ibfk_pedigreedescriptions` (`pedigreedescription_id`),
CONSTRAINT `pedigrees_ibfk_germinatebase` FOREIGN KEY (`germinatebase_id`) REFERENCES `
germinatebase` (`id`) ON DELETE CASCADE ON UPDATE CASCADE,
CONSTRAINT `pedigrees_ibfk_germinatebase_parent` FOREIGN KEY (`parent_id`) REFERENCES `
germinatebase` (`id`) ON DELETE CASCADE ON UPDATE CASCADE,
CONSTRAINT `pedigrees_ibfk_pedigreedescriptions` FOREIGN KEY (`pedigreedescription_id`)
REFERENCES `pedigreedescriptions` (`id`) ON DELETE CASCADE ON UPDATE CASCADE
) ENGINE=InnoDB DEFAULT CHARSET=utf8;

INSERT INTO attributes (name, description, datatype, created_on, updated_on) VALUES ("
flowering_season_start", "Start of the flowering season (month number)", "int", NOW(), NOW());
INSERT INTO attributes (name, description, datatype, created_on, updated_on) VALUES ("
growing_season_start", "Start of the growing season (month number)", "int", NOW(), NOW());

INSERT INTO attributedata (attribute_id, germinatebase_id, value) SELECT * FROM (SELECT id FROM
attributes WHERE name = "flowering_season_start") AS attribute_id, (SELECT id,
flowering_season_start FROM germinatebase WHERE NOT ISNULL(flowering_season_start)) AS
germinatebase;
INSERT INTO attributedata (attribute_id, germinatebase_id, value) SELECT * FROM (SELECT id FROM
attributes WHERE name = "growing_season_start") AS attribute_id, (SELECT id,
growing_season_start FROM germinatebase WHERE NOT ISNULL(growing_season_start)) AS
germinatebase;

ALTER TABLE `germinatebase`
DROP COLUMN `old_name`,
DROP COLUMN `sample_level`,

```

```

DROP COLUMN `parent_id`,
DROP COLUMN `growth_habit`,
DROP COLUMN `collector`,
DROP COLUMN `year_identified`,
DROP COLUMN `month_identified`,
DROP COLUMN `day_of_year`,
DROP COLUMN `flowering_season_start`,
DROP COLUMN `growing_season_start`;

CREATE TABLE `biologicalstatus` (
  `id` int(11) NOT NULL AUTO_INCREMENT,
  `sampstat` varchar(255) NOT NULL COMMENT 'previously known as sampstat',
  `created_on` datetime DEFAULT NULL,
  `updated_on` timestamp NULL DEFAULT NULL ON UPDATE CURRENT_TIMESTAMP,
  PRIMARY KEY (`id`)
) ENGINE=InnoDB AUTO_INCREMENT=1000 DEFAULT CHARSET=latin1;

INSERT INTO `biologicalstatus` VALUES ('100', 'Wild', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('110', 'Natural', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('120', 'Semi-natural/wild', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('130', 'Semi-natural/sown', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('200', 'Weedy', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('300', 'Traditional cultivar/landrace', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('400', 'Breeding/research material', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('410', 'Breeder's line', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('411', 'Synthetic population', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('412', 'Hybrid', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('413', 'Founder stock/base population', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('414', 'Inbred line (parent of hybrid cultivar)', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('415', 'Segregating population', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('416', 'Clonal selection', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('420', 'Genetic stock', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('421', 'Mutant (e.g. induced/insertion mutants, tilling populations)', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('422', 'Cytogenic stocks (e.g. chromosome addition/substitution, aneuploids, amphiploids)', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('423', 'Other genetic stocks (e.g. mapping populations)', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('500', 'Advanced or improved cultivar (conventional breeding methods)', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('600', 'GMO (by genetic engineering)', null, NOW());
INSERT INTO `biologicalstatus` VALUES ('999', 'Other', null, NOW());

ALTER TABLE `germinatebase`
  ADD CONSTRAINT `germinatebase_ibfk_biologicalstatus` FOREIGN KEY (`biologicalstatus_id`)
    REFERENCES `biologicalstatus` (`id`) ON DELETE NO ACTION ON UPDATE CASCADE;

CREATE TABLE `collectingsources` (
  `id` int(11) NOT NULL AUTO_INCREMENT,
  `collsrc` varchar(255) NOT NULL DEFAULT '' COMMENT 'also known as collsrc',
  `created_on` datetime DEFAULT NULL,
  `updated_on` timestamp NULL DEFAULT NULL ON UPDATE CURRENT_TIMESTAMP,
  PRIMARY KEY (`id`)
) ENGINE=InnoDB AUTO_INCREMENT=100 DEFAULT CHARSET=latin1;

INSERT INTO `collectingsources` VALUES ('10', 'Wild habitat', null, NOW());
INSERT INTO `collectingsources` VALUES ('11', 'Forest or woodland', null, NOW());
INSERT INTO `collectingsources` VALUES ('12', 'Shrubland', null, NOW());
INSERT INTO `collectingsources` VALUES ('13', 'Grassland', null, NOW());
INSERT INTO `collectingsources` VALUES ('14', 'Desert or tundra', null, NOW());
INSERT INTO `collectingsources` VALUES ('15', 'Aquatic habitat', null, NOW());
INSERT INTO `collectingsources` VALUES ('20', 'Farm or cultivated habitat', null, NOW());
INSERT INTO `collectingsources` VALUES ('21', 'Field', null, NOW());
INSERT INTO `collectingsources` VALUES ('22', 'Orchard', null, NOW());
INSERT INTO `collectingsources` VALUES ('23', 'Backyard, kitchen or home garden (urban, peri-urban or rural)', null, NOW());
INSERT INTO `collectingsources` VALUES ('24', 'Fallow land', null, NOW());
INSERT INTO `collectingsources` VALUES ('25', 'Pasture', null, NOW());
INSERT INTO `collectingsources` VALUES ('26', 'Farm store', null, NOW());
INSERT INTO `collectingsources` VALUES ('27', 'Threshing floor', null, NOW());
INSERT INTO `collectingsources` VALUES ('28', 'Park', null, NOW());
INSERT INTO `collectingsources` VALUES ('30', 'Market or shop', null, NOW());

```

```

INSERT INTO `collectingsources` VALUES ('40', 'Institute, Experimental station, Research organization,
Genebank', null, NOW());
INSERT INTO `collectingsources` VALUES ('50', 'Seed company', null, NOW());
INSERT INTO `collectingsources` VALUES ('60', 'Weedy, disturbed or ruderal habitat', null, NOW());
INSERT INTO `collectingsources` VALUES ('61', 'Roadside', null, NOW());
INSERT INTO `collectingsources` VALUES ('62', 'Field margin', null, NOW());
INSERT INTO `collectingsources` VALUES ('99', 'Other (Elaborate in REMARKS field)', null, NOW());

ALTER TABLE `germinatebase`
  CHANGE COLUMN `collsrc` `collsrc_id` int(11) NULL DEFAULT NULL AFTER `biologicalstatus_id`;

ALTER TABLE `germinatebase`
  ADD CONSTRAINT `germinatebase_ibfk_collectingsource` FOREIGN KEY (`collsrc_id`) REFERENCES
    `collectingsources` (`id`) ON DELETE NO ACTION ON UPDATE CASCADE;

ALTER TABLE `germinatebase`
  ADD COLUMN `breeder_id` int(11) NULL AFTER `institution_id`;

ALTER TABLE `germinatebase`
  ADD CONSTRAINT `germinatebase_ibfk_breeder` FOREIGN KEY (`breeder_id`) REFERENCES `
    institutions` (`id`) ON DELETE NO ACTION ON UPDATE CASCADE;

ALTER TABLE `markers`
  DROP COLUMN `other_name`,
  DROP COLUMN `close_index`,
  DROP COLUMN `32_unigene`,
  DROP COLUMN `mapped`,
  DROP COLUMN `copy_number`;

CREATE TABLE `synonymtypes` (
  `id` int(11) NOT NULL AUTO_INCREMENT,
  `target_table` varchar(255) NOT NULL,
  `name` varchar(255) NOT NULL,
  `description` varchar(255) DEFAULT NULL,
  `created_on` datetime DEFAULT NULL,
  `updated_on` timestamp NULL DEFAULT NULL ON UPDATE CURRENT_TIMESTAMP,
  PRIMARY KEY (`id`)
) ENGINE=InnoDB AUTO_INCREMENT=3 DEFAULT CHARSET=latin1;

INSERT INTO `synonymtypes` VALUES ('1', 'germinatebase', 'Accessions', 'Accession synonyms', null, NOW());
INSERT INTO `synonymtypes` VALUES ('2', 'markers', 'Markers', 'Marker synonyms', null, NOW());

CREATE TABLE `synonyms` (
  `id` int(11) NOT NULL AUTO_INCREMENT,
  `foreign_id` int(11) NOT NULL,
  `synonymtype_id` int(11) NOT NULL,
  `synonym` varchar(255) NOT NULL,
  `created_on` datetime DEFAULT NULL,
  `updated_on` timestamp NULL DEFAULT NULL ON UPDATE CURRENT_TIMESTAMP,
  PRIMARY KEY (`id`),
  KEY `synonyms_ibfk_synonymtypes` (`synonymtype_id`),
  CONSTRAINT `synonyms_ibfk_synonymtypes` FOREIGN KEY (`synonymtype_id`) REFERENCES `
    synonymtypes` (`id`) ON DELETE CASCADE ON UPDATE CASCADE
) ENGINE=InnoDB DEFAULT CHARSET=latin1;

ALTER TABLE `datasets` MODIFY `description` text NOT NULL,
  MODIFY `source_file` varchar(255) NULL;

```

Version 3.2.0d

New/Changed features

- FIX** Fixed issue with file handles not being released on Linux when using NFS mounts.
- ADD** Added new check to the registration to prevent duplicates.
- ADD** Added option to export whole chromosome for a map.
- ADD** Added more links from tables to details pages.
- ADD** Support for browser password saving.
- ADD** Added changelog information along with migration information.
- ADD** Added individual error notifications for invalid cookie/payload/session id.
- CHG** Changed SQL script, marked more columns as required.
- CHG** Updated to Font Awesome 4.3.0.
- CHG** Replaced big parts of reusable UI with UiBinder widgets.
- CHG** Updated documentation.
- CHG** Updated Toastr javascript library.
- CHG** Use "placeholder" attribute of `<input>` elements if available. If not, fall back to old solution.
- DEL** Deleted unused libraries.

Migration from 3.2.0 to 3.2.0d

- Apache Ant 1.9.1 or above is now required
- Remove the following line from `Germinate.gwt.xml` in your instance folder:

```
<inherits name="com.kiouri.sliderbar.SliderBarMVP" /> <!-- Slider bar -->
```

- Run this against the database:

```
ALTER TABLE `mapdefinitions` MODIFY `definition_start` double(11,2) NOT NULL,  
MODIFY `definition_end` double(11,2) NOT NULL;
```

- New properties required in `Text.properties`:

```
notificationRegistrationAlreadyRequestedAccess=You have already requested access to this instance of  
Germinate.  
notificationInvalidCookie=Please enable cookies to be able to use Germinate.  
notificationInvalidPayload=Request rejected by the server. Please contact the administrator.  
markersExportOptionsTabChromosomes=Chromosomes  
markersExportOptionsChromosomesText=<p>Select all the chromosomes you want to export from the list  
below.</p><p>Non-contiguous groups can be selected using <kbd>Ctrl</kbd>/<kbd>&#8984;</kbd>  
>. Use <kbd>Shift</kbd> for sequential groupings.</p>  
markersExportOptionsClosePanel=Don't use export options
```