EDIT - bug #8631

ABCD import fails to put new taxa into the classification, create mediaspecimens, etc

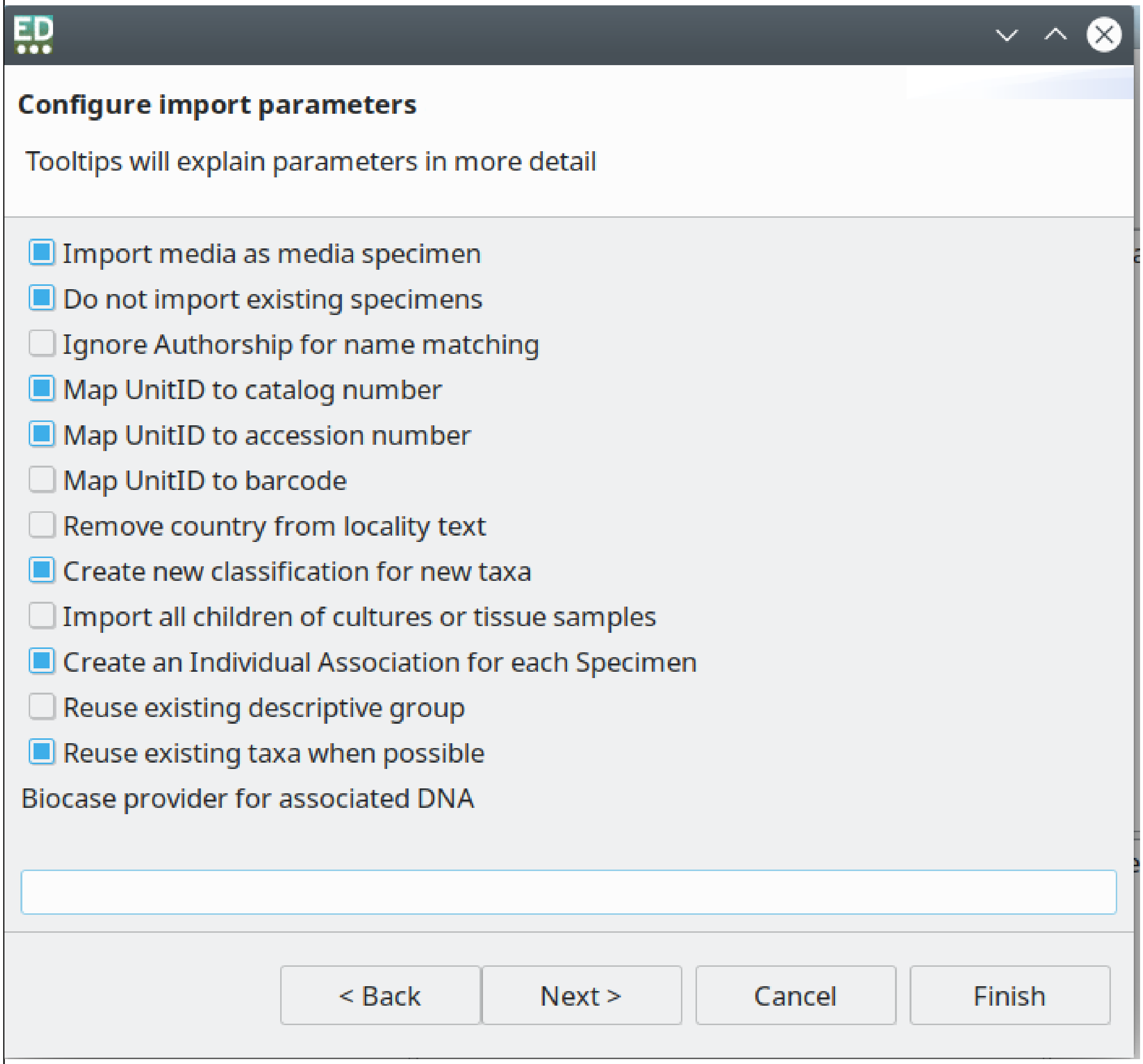
10/29/2019 03:28 PM - Andreas Kohlbecker

Status:	Closed	**Start date:**	
Priority:	New	**Due date:**	
Assignee:	Katja Luther	**% Done:**	80%
Category:	taxeditor	**Estimated time:**	0:00 hour
Target version:	Release 5.11		
Severity:	normal	**Found in Version:**	Release 5.10

Description

To reproduce:

- import Arenaria_ABCD_one_unit.xml with the below options



Configure import parameters

Tooltips will explain parameters in more detail

☑ Import media as media specimen
☑ Do not import existing specimens
☐ Ignore Authorship for name matching
☑ Map UnitID to catalog number
☑ Map UnitID to accession number
☐ Map UnitID to barcode
☐ Remove country from locality text
☑ Create new classification for new taxa
☐ Import all children of cultures or tissue samples
☑ Create an Individual Association for each Specimen
☐ Reuse existing descriptive group
☑ Reuse existing taxa when possible

Biocase provider for associated DNA

at the end the exception as described in #8630 happens.

As result of the import a classification has been created as well as the taxon "Arenaria serpyllifolia L. subsp. serpyllifolia sec. ABCD classic" but

- the taxon is not part of the classification.
- the specimen is not related to the name or taxon
- a media object was created (http://ww2.bgbm.org/herbarium/images/B/10/04/63/63/B_10_0463639.jpg) but is not associated with the specimen. A media specimen should have been created as derivative of the specimen B 10 0463639
- The DNA Sample which was fetched from a BioCase Provider is not a derivative of the specimen

BTW:

- What's the purpose of the text field close to the bottom of the dialog?

Related issues:

Related to EDIT - bug #8630: ClassCastException when ABCD import has finished	**Closed**	
Related to EDIT Platform Etablierung - task #8580: Update documentation to la...	**Closed**	**10/10/2019**
Related to EDIT - bug #8632: ABCD retrieves DNA Sample from Biocase Provider ...	**Closed**	
Related to EDIT - bug #8582: Taxon Navigator: Classification label not refres...	**Closed**	

Associated revisions

Revision f7717334 - 10/30/2019 09:54 AM - Katja Luther

ref #8631: fix errors in abcd import

Revision 92546b65 - 10/30/2019 10:21 AM - Katja Luther

ref #8631: fix ClassCastException for abcd import and NPE in abcd preferences

Revision 8a720214 - 10/30/2019 01:18 PM - Katja Luther

ref #8631: remove the possibility to search for dna when importing from abcd file

Revision 21850e02 - 11/06/2019 03:02 PM - Katja Luther

ref #8631: remove nomenclatural code selection page for file import

Revision cb45e05b - 11/11/2019 09:37 AM - Katja Luther

ref #8631: layout issues in abcd import wizard page and refresh of navigator after abcd import

Revision 905fdec1 - 11/12/2019 01:35 PM - Katja Luther

ref #8631: same layout for unit id and nomenclatural code combobox

Revision d36d2eb8 - 11/13/2019 01:47 PM - Patrick Plitzner

ref #8631 Fixed layout + merged constructors

Revision 18683dc6 - 11/14/2019 11:54 AM - Katja Luther

ref #8631: layout issues

History

#1 - 10/29/2019 03:28 PM - Andreas Kohlbecker

- Description updated

#2 - 10/29/2019 03:29 PM - Andreas Kohlbecker

- File Arenaria_ABCD_one_unit.xml added

#3 - 10/29/2019 03:29 PM - Andreas Kohlbecker

- Related to bug #8630: ClassCastException when ABCD import has finished added

#4 - 10/29/2019 03:38 PM - Andreas Kohlbecker

- Description updated

#5 - 10/29/2019 04:16 PM - Andreas Kohlbecker

- Description updated

#6 - 10/29/2019 04:45 PM - Andreas Kohlbecker

- Related to task #8580: Update documentation to latest revision of the Taxeditor added

#7 - 10/29/2019 04:46 PM - Andreas Kohlbecker

- Subject changed from ABCD import fails to put new taxa into the classification to ABCD import fails to put new taxa into the classification, create mediaspeciemens, etc

#8 - 10/29/2019 04:51 PM - Andreas Kohlbecker

- Related to bug #8632: ABCD retrieves DNA Sample from Biocase Provider even if it is not selected in the import configuration added

#9 - 10/29/2019 04:54 PM - Andreas Kohlbecker

- Description updated

#10 - 10/30/2019 09:55 AM - Katja Luther

the media was not imported because of a NPE, this is fixed.
the dna was not associated to the specimen because of wrong associationType parsing when the abcd version is different, this is fixed.

The problem of the taxon appears only for the import from file. It is a lazy loading exception while creating the nomenclatural titleCache of a team during cascading.

#11 - 10/30/2019 09:56 AM - Katja Luther

- Status changed from New to In Progress

#12 - 10/30/2019 10:26 AM - Katja Luther

- Target version changed from Unassigned CDM tickets to Release 5.11

The ClassCastException should be solved with the last commit

#13 - 10/30/2019 01:18 PM - Katja Luther

As a workaround the possibility to search for dna is disabled for file import. For the biocase seach it is still possible to add a dna biocase provider.

There is a test in cdmlib for import from file with dna search, it works.

#14 - 11/05/2019 01:44 PM - Katja Luther

- Status changed from In Progress to Resolved

- Assignee changed from Katja Luther to Andreas Kohlbecker

#15 - 11/06/2019 09:23 AM - Andreas Kohlbecker

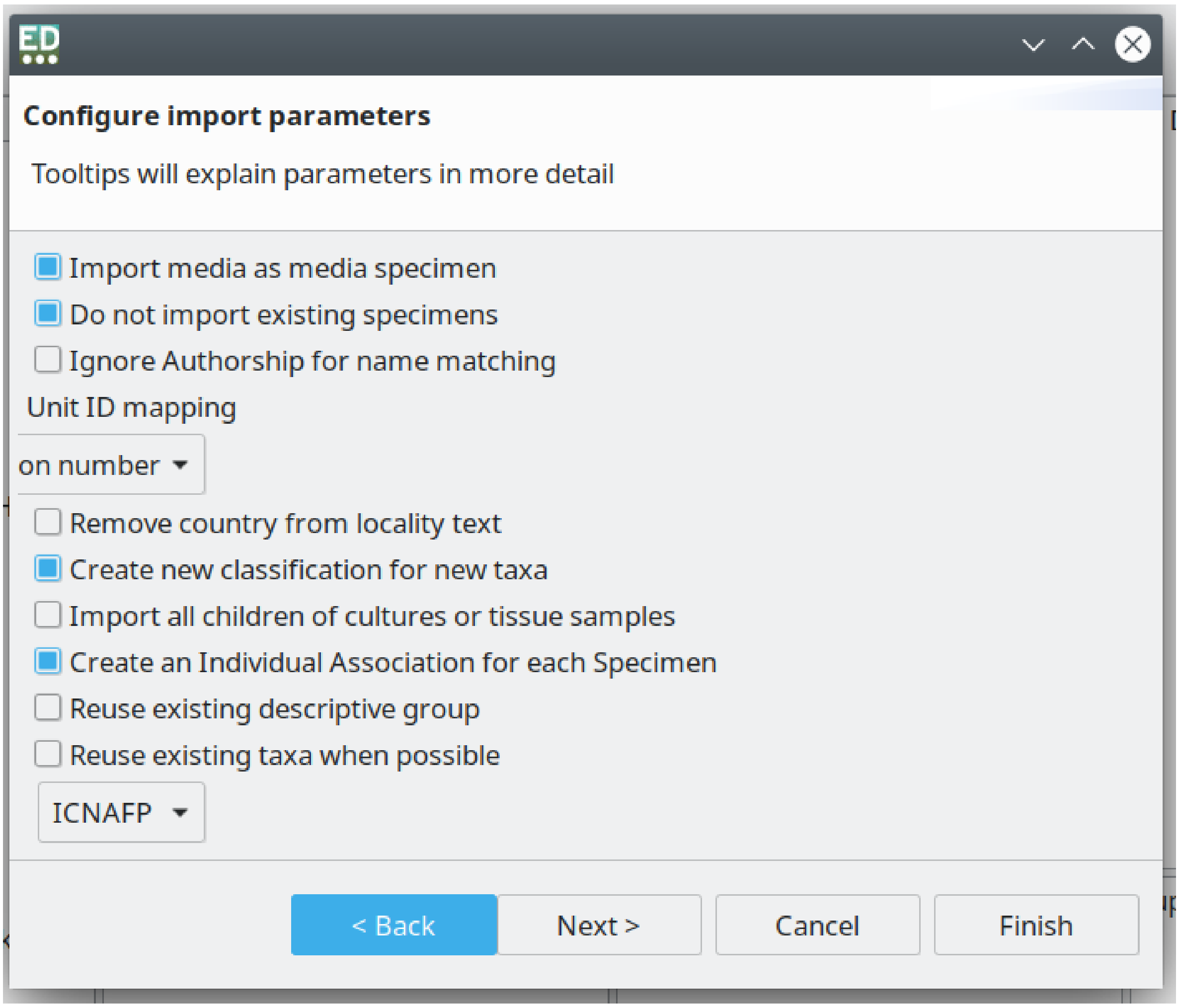
- Assignee changed from Andreas Kohlbecker to Katja Luther

There are still some problems which are not yet fixed:

- the taxon is not part of the classification.
- the specimen is not related to the name or taxon

and I found some new problems

- after the import the Taxonnavigator is not refreshes, the new classification only becomes visible after closing and re-openening this view, I will add this obeservarion to #8582
- The "Configure Import Dialog" has changed, and has two issues:
  - The select field for "Unit ID Mapping" is hardly readable and should be moved, aligned differently so that it is completely visible also in linux
  - There is a new select field offering codes, the purpose of this field is unclear, even more unclear since the next page of the import wizard allows to choose the code again.



Configure import parameters

Tooltips will explain parameters in more detail

☑ Import media as media specimen
☑ Do not import existing specimens
☐ Ignore Authorship for name matching

Unit ID mapping

on number

☐ Remove country from locality text
☑ Create new classification for new taxa
☐ Import all children of cultures or tissue samples
☑ Create an Individual Association for each Specimen
☐ Reuse existing descriptive group
☐ Reuse existing taxa when possible

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#16 - 11/06/2019 09:24 AM - Andreas Kohlbecker

- Related to bug #8582: Taxon Navigator: Classification label not refreshed & new taxa not visible added

#17 - 11/06/2019 09:24 AM - Andreas Kohlbecker

- File picture699-1.png added

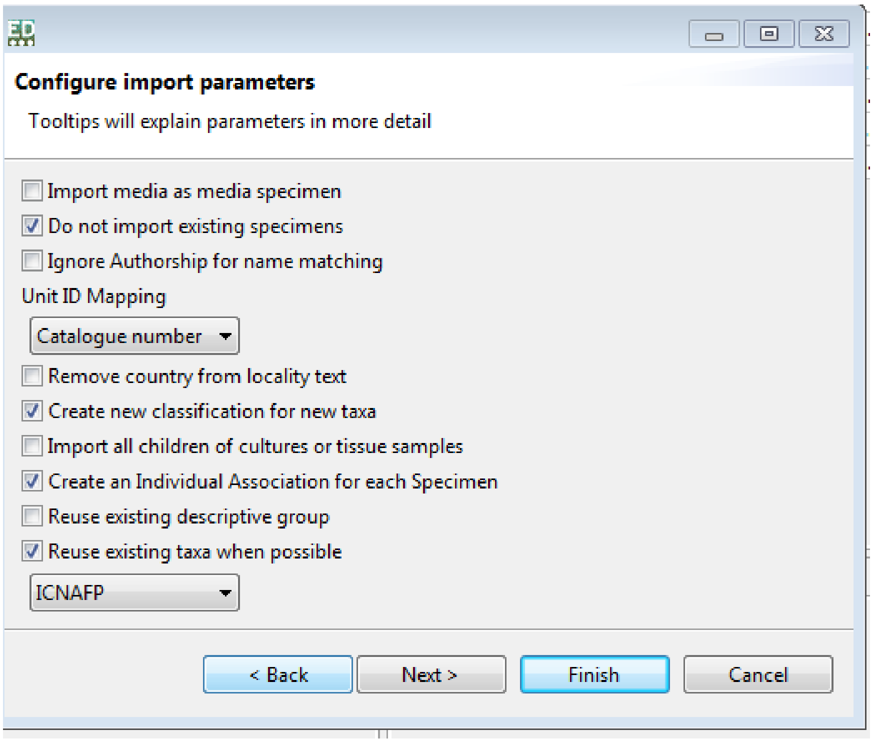
#18 - 11/06/2019 02:57 PM - Katja Luther

- File picture673-1.png added

Andreas Kohlbecker wrote:

> There are still some problems which are not yet fixed:
>
> - the taxon is not part of the classification.
> - the specimen is not related to the name or taxon
>
> and I found some new problems
>
> - after the import the Taxonnavigator is not refreshes, the new classification only becomes visible after closing and re-openening this view, I will add this obeservarion to #8582
> - The "Configure Import Dialog" has changed, and has two issues:
>   - The select field for "Unit ID Mapping" is hardly readable and should be moved, aligned differently so that it is completely visible also in linux
>   - There is a new select field offering codes, the purpose of this field is unclear, even more unclear since the next page of the import wizard allows to choose the code again.

that the field for Unit ID Mapping is hardly readable seems to be a OS problem with windows it looks like this:



Configure import parameters

Tooltips will explain parameters in more detail

☐ Import media as media specimen
☑ Do not import existing specimens
☐ Ignore Authorship for name matching
Unit ID Mapping
Catalogue number
☐ Remove country from locality text
☑ Create new classification for new taxa
☐ Import all children of cultures or tissue samples
☑ Create an Individual Association for each Specimen
☐ Reuse existing descriptive group
☑ Reuse existing taxa when possible
ICNAFP

#19 - 11/06/2019 03:02 PM - Katja Luther

the nomenclatural code selection page is removed

#20 - 11/06/2019 03:04 PM - Katja Luther

Andreas Kohlbecker wrote:

> There are still some problems which are not yet fixed:
>
> - the taxon is not part of the classification.
> - the specimen is not related to the name or taxon

I think this is related to the lazy loading exception during the import. There is now a import report at the end of the import, there these exceptions should be shown.

#21 - 11/06/2019 03:17 PM - Katja Luther

Katja Luther wrote:

> Andreas Kohlbecker wrote:
>
> > There are still some problems which are not yet fixed:
> >
> > - the taxon is not part of the classification.
> > - the specimen is not related to the name or taxon

maybe there is no "preferred" flag for one of the determinations (if there is only one determination this is the preferred determination), if this is missing the import does not create the taxon node and relation from the taxon and specimen.

#22 - 11/06/2019 03:31 PM - Andreas Kohlbecker

Katja Luther wrote:

> the nomenclatural code selection page is removed

Did you add a label to the code selection field?

#23 - 11/06/2019 03:46 PM - Andreas Kohlbecker

Katja Luther wrote:

> Andreas Kohlbecker wrote:

> > - The "Configure Import Dialog" has changed, and has two issues:
> >   - The select field for "Unit ID Mapping" is hardly readable and should be moved, aligned differently so that it is completely visible also in linux
> >   - There is a new select field offering codes, the purpose of this field is unclear, even more unclear since the next page of the import wizard allows to choose the code again.
>
> that the field for Unit ID Mapping is hardly readable seems to be a OS problem with windows it looks like this:

I don't share this view that is an OS problem. I checked a coupld of dialogs with selects in eclipse and in dBeaver and none of the dialogs has this problem.

To me it looks like the width of the select elements is determined by the code selection field (At least in QT/GTK driven desktop environments).

The way the label is added to the select is a bit special in this import dialog as in all other cases the label prepends the select:

```
label: [select]
```

#24 - 11/08/2019 10:57 AM - Andreas Müller

- % Done changed from 0 to 40

Can you please leave a note if this is easy to fix? Otherwise please move to new ticket as the layout is not really part of the original ticket description

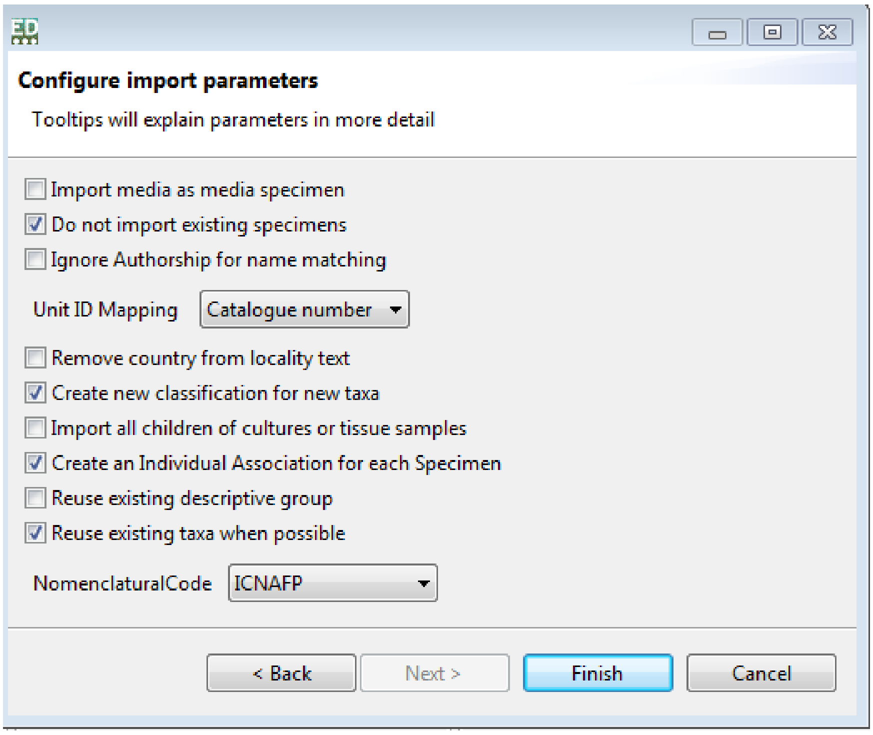
#25 - 11/08/2019 11:00 AM - Katja Luther

- File picture860-1.png added

Andreas Müller wrote:

> Can you please leave a note if this is easy to fix? Otherwise please move to new ticket as the layout is not really part of the original ticket description

the label and the combo box are now in one line:



Configure import parameters

Tooltips will explain parameters in more detail

☐ Import media as media specimen
☑ Do not import existing specimens
☐ Ignore Authorship for name matching
Unit ID Mapping: Catalogue number
☐ Remove country from locality text
☑ Create new classification for new taxa
☐ Import all children of cultures or tissue samples
☑ Create an Individual Association for each Specimen
☐ Reuse existing descriptive group
☑ Reuse existing taxa when possible
NomenclaturalCode: ICNAFP

@AK: could you please check, whether the combo box is displayed correctly on linux?

#26 - 11/08/2019 01:56 PM - Andreas Müller

- Assignee changed from Katja Luther to Andreas Kohlbecker

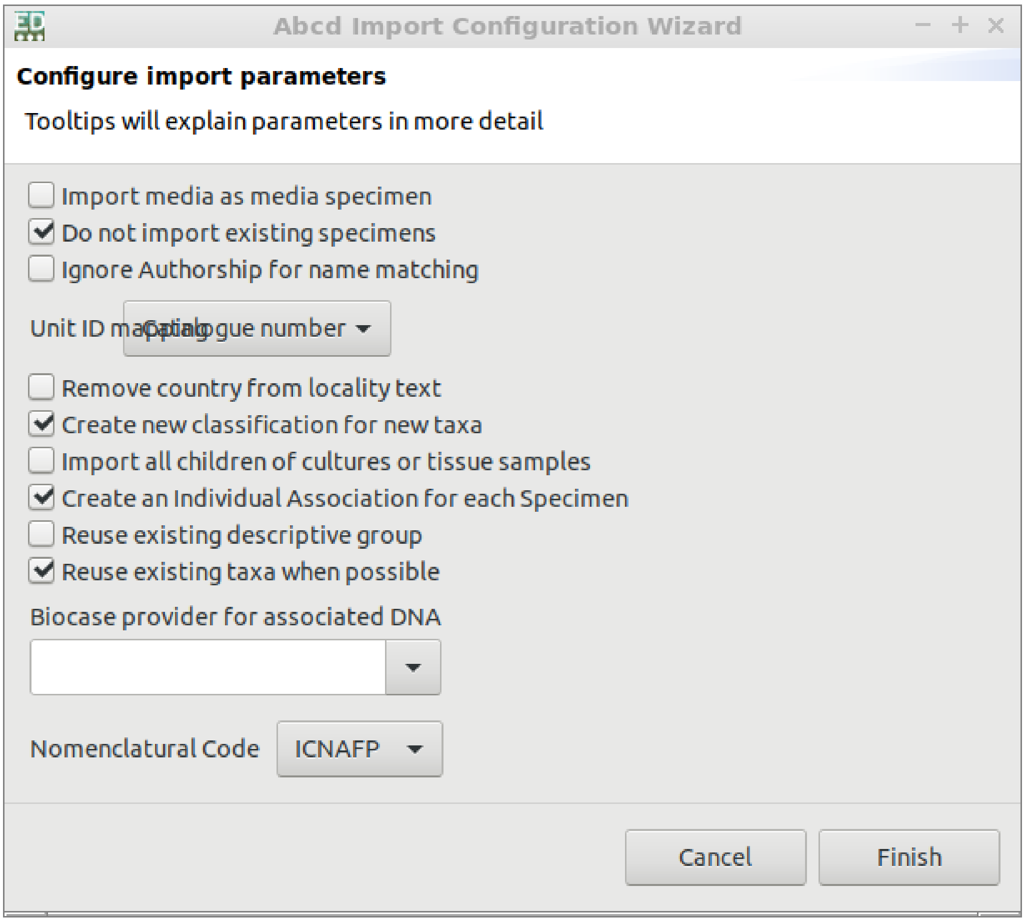
#27 - 11/09/2019 12:19 AM - Andreas Müller

- Subject changed from ABCD import fails to put new taxa into the classification, create mediaspeciemens, etc to ABCD import fails to put new taxa into the classification, create mediaspecimens, etc

#28 - 11/11/2019 11:08 AM - Patrick Plitzner

- File picture468-1.png added

This is how it looks for me. Started the editor from the IDE.



Abcd Import Configuration Wizard

Configure import parameters

Tooltips will explain parameters in more detail

☐ Import media as media specimen
☑ Do not import existing specimens
☐ Ignore Authorship for name matching

Unit ID maCatalogue number

☐ Remove country from locality text
☑ Create new classification for new taxa
☐ Import all children of cultures or tissue samples
☑ Create an Individual Association for each Specimen
☐ Reuse existing descriptive group
☑ Reuse existing taxa when possible

Biocase provider for associated DNA

Nomenclatural Code ICNAFP

#29 - 11/11/2019 01:52 PM - Andreas Müller

- Status changed from Resolved to Feedback

- Assignee changed from Andreas Kohlbecker to Katja Luther

So the layout still needs some update for linux, I guess.

#30 - 11/13/2019 12:35 PM - Katja Luther

- Assignee changed from Katja Luther to Patrick Plitzner

@Patrick could you have another look, whether it looks better now. It is difficult to check for me because with windows it looks ok.

#31 - 11/13/2019 01:48 PM - Patrick Plitzner

- Assignee changed from Patrick Plitzner to Katja Luther

I made some changes myself. Looks fine on Linux. Please test on windows.

#32 - 11/14/2019 09:55 AM - Andreas Müller

It look ok now. Only change I suggest: let the "Biocase provider for DNA" dropdown start at the same horizontal position as all other dropdowns.

@Andreas K.: Can you also check if it looks ok on your Linux?

#33 - 11/14/2019 09:55 AM - Andreas Müller

- % Done changed from 40 to 80

#34 - 11/14/2019 12:25 PM - Andreas Müller

Andreas Müller wrote:

> It look ok now. Only change I suggest: let the "Biocase provider for DNA" dropdown start at the same horizontal position as all other dropdowns.
>
> @Andreas K.: Can you also check if it looks ok on your Linux?

upps, sorry, I tested the preference page, not the file import. However, the little change in the preference would also be nice ...

#35 - 11/14/2019 01:00 PM - Andreas Kohlbecker

It looks ok in KDE!

The ticket can be closed.

#36 - 11/14/2019 01:15 PM - Katja Luther

- Status changed from Feedback to Closed

Files

picture367-1.png	59.8 KB	10/29/2019	Andreas Kohlbecker
Arenaria_ABCD_one_unit.xml	9.74 KB	10/29/2019	Andreas Kohlbecker
picture699-1.png	56.9 KB	11/06/2019	Andreas Kohlbecker
picture673-1.png	20.1 KB	11/06/2019	Katja Luther
picture860-1.png	20.2 KB	11/08/2019	Katja Luther
picture468-1.png	51.2 KB	11/11/2019	Patrick Plitzner