
UTA

Release 0.2.0a2.dev24+nda132f319b48

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UTA is a data archive and set of tools that aims to improve the precision of sequence-based descriptions of genomic variation. It will eventually contain transcripts and alignments to multiple reference genomes using multiple algorithms, as obtained from [NCBI](#), [Ensembl](#), [LRG](#), and [UCSC](#).

Contents

1.1 Overview

The UTA stores transcripts aligned to genome reference assemblies using multiple methods in order to improve the precision and accuracy by which the scientific and clinical communities describe variants.

It facilitates the following:

- enabling an interpretation of variants reported in literature against obsolete transcript records
- identifying regions where transcript and reference genome sequence assemblies disagree
- characterizing transcripts of the same gene across transcript sources
- projecting (“lifting over”) variants from one transcript to another
- identifying transcripts and genomic regions with ambiguous alignments that may affect clinical interpretation
- querying for multiple transcript sources through a single interface

1.2 Installation

building from scratch

installing locally

1.3 Database

1.3.1 Schema

1.3.2 Loading UTA

These docs are in flux as the database loading process matures.

Overview

Loading occurs in three distinct stages:

1. extraction and translation from data sources into intermediate files;

2. loading from intermediates into UTA;
3. generating new exon alignments within UTA.

The extraction/translation scripts, which are specific for each source, are in `uta/sbin/`. Each script reads from one source and writes one or more intermediates in formats that are specified in `uta/formats/`. The intermediate file formats are independent of source.

Loading is largely driven by `loading/Makefile`.

Updated 2014-08-29 Tested with Ubuntu 14.04, x86_64, PostgreSQL 9.3.4

Preparing a PostgreSQL cluster and database

You may specify certain PostgreSQL options using environment variables or command line options. For readability, these instructions use environment variables:

```
export PGDATA=/local/home/reece/var/pg/9.4
export PGHOST=localhost
export PGPORT=5432
export PGDATABASE=uta_dev
```

First, create the PostgreSQL cluster if you do not have one already installed:

```
initdb -D $PGDATA
perl -i.bak -pe "s/#port = 5432/port = $PGPORT/" $PGDATA/postgresql.conf
pg_ctl -D $PGDATA -l logfile start
```

By default, PostgreSQL specifies local “trust” authentication in `pg_hba.conf` for local connections.

Then, create users and a `uta` database:

```
createuser uta_admin
createuser uta_public
createdb -O uta_admin uta_dev
```

Install UTA

The scripts necessary to build the UTA database are in the UTA repo.

```
mkvirtualenv uta
hg clone ssh://hg@bitbucket.org/biocommons/uta uta_dev
cd uta_dev
make develop
# TODO: error the first time (re: distribute package). Second time was clean. Figure this out.
make develop
```

Prepare intermediate files

Sequences

UTA requires sequence data for every sequence that is referenced in the intermediate files. Fasta files (with `.fa`, `.fna`, `.faa`, or `.fasta` filename extensions) should be placed at the root of a single directory. The path is specified in `etc/global.conf`.


```
[sequences] fasta_directory = /locus/data/core-rest/2014-01/sequences
```

NCBI

Data from NCBI are pulled using tools in a separate repo. Briefly:

- Clone <https://bitbucket.org/biocommons/mirrors-ncbi>
- Type *make update*

When this is completed, you will have a dated snapshot of NCBI data used by UTA.

- Make a symlink to the source data directory:

```
cd loading/aux ln -s ../../mirrors-ncbi # adjust as necessary
```
- The loading makefile will pull data from that source as necessary

Ensembl

LRG

Preparing to load the whole kielbasa

```
make main-data
```

This will take a long time. 36 hours maybe.

Preparing test data

These data are used for testing and therefore committed with the repo. You probably don't need to rebuild them.

```
make test-data
```

Data Loading

The general command to load data is:

```
cd loading
make uta-build DATA=<dataset> CONF=<confname>
```

DATA specifies a directory of intermediate files in loading/<dataset> to be loaded

CONF specifies a config file in ../etc/ for connection parameters

Testing Loading

uta/loading/test contains a set of intermediate files to test the loading process. These files are part of the UTA repository.

For testing, type:

```
make uta-build DATA=test CONF=test
```

If that fails:

```
psql -p $PGPORT -d <db> -c 'drop schema utal cascade'
make cleanest
```

and retry.

Create and load a database

```
make uta-build DATA=main CONF=dev
```

Push to RDS

The current practice is to dump UTA, then restore to Amazon RDS for the public instance (uta.invitae.com).

```
:: sname=uta_20150813 make dumps/$sname.pgd.gz # takes ~5 minutes make push-dev-$sname
```

The dump and restore each take ~5 minutes. If you don't care about the intermediate, you can pipe directly of course.

1.4 ChangeLog

1.4.1 0.2 Series

0.2.0a1 (2015-08-13)

changes since 0.1.7 (2014-05-10)

Bug Fixes

- Removed previous Ensembl data; <0.3% of previous sequences were inconsistent with newer ensembl releases

Changes

- Added liftover mechanism to bootstrap new schemas from existing data
- Standardize on “NCBI” as origin name
- When RefSeq transcript exon structures differ between chromosome and patch versions, use chromosome version [0926cf34e173]
- Use explicit sequence sources when loading sequences
- Bumped schema version to 1.1 for addition of associated_accessions and tx_similarity_v

New Features

- New data: ensembl-79, refseq 2015-07-31
- Added RefSeq NR (non-coding) transcripts
- Added geneacs (associated accessions)
- Added transcript similarity view [40a4e734d606] with multiple similarity metrics (*experimental*)

- Added Change Log to documentation
- Developed and documented release flow w/tools
- Implement gene-based data subsets for testing loading
- Explicitly set cds_{start,end}_i to None when not defined in txinfo (for non-coding transcripts) [e82011d1b02c]

Other Changes

- Added uta subcommand and make rule to update materialized views [b1f2ef185320]
- Add load-origin from tsv file; update ensembl Makefile rules [dc421df5ef19]
- Added “mega-test” and “the-whole-kielbasa” test targets
- Added indexes to tx_def_summary_mv [c1cda1cfd4c9]
- Enforce FK relationship from exon_set.tx_ac to transcript.ac [ad5309895b5c]
- Facilitate restartability in ensembl-fetch by creating canonical gene order and batching fetches
- Standardize on schema name as uta_1_1 for dev, then rename on release
- Updated code to use new eutils [#171, d831e02f51fa]
- Update to use bioutils instead of bdi [769eea9241e4]
- Updated to use the aligner from uta-tools-align (f.k.a. locus-lib-bio) [a1f492a32f5e]

1.4.2 0.1 Series

0.1.7 (2014-05-10)

changes since 0.1.6 (2014-01-03)

Bug Fixes

New Features

Changes

Security

Other Changes

- use testing.postgresql package rather than existing db for tests [7511b226b3cb]
- #157: commented out align2() method and updated remaining tests in uta.alignment.py [5bdc11f4d45b]
- #157: fixed eutils and genomeutils doctests [d46df3d530f0]
- fixed sqlalchemy tests (finally) [c0031f5e7fbf]
- updated package metadata [a93a4d931fe9]
- bermuda 2014-03 rc5 [d8fd0fa68f60]
- bermuda 2014-03 rc4 [48f3313cb0aa]

- bermuda 2014-03 rc3 [4269d160b881]
- u0 cigars should be semi-delimited [15ee84daefbc]
- merged bermuda1 branch [fe5563ca7be9]
- #147 - can generate test DB or full DB; replaced old version with this one. [0c6c09c4ee4b]
- #147 - incremental checkin; full psql to sqlite works; gcp tests in hgvs pass when using this DB. Still need to create the test DB. [6d4304a2580e]
- added additional header info; added observations [d78405e52a22]
- bermuda-table: fixed bug in human-readable indel coordinates [2fc0fdfa8337]
- bermuda-2014-03 rc 1 [f7290b00a690]
- lots of bermuda work incl. running (but broken) full table [ce0f95070c1b]
- resurrected matchmaker code for ensembl lookup [e93a6eb4471d]
- bermuda2 sql commit/rearrangement [f5fbc045518e]
- commit before rfur-bermuda merge [2e89dac43914]
- added missing dependencies; pull test conf file from TEST_CONF if defined [f1c1906136ba]
- fixed alt_ac bug in tx_3way_v [779176e3064a]
- added eutils to setup.py [80978678ac53]
- sync with default [0ad684c152c5]
- modularized loading (during a reloading test) [cabcff9788d3]
- Makefile sync with sibling projects [297340df627b]
- added trival indel at end discount; updated trival criteria [757124836c56]
- fixed alt_ac in bic exonsets (missing underscore) [6f58c4f333b8]
- close branch with misplaced commits, after grafting to default [2a251272d9c9]
- added stats str to cigar_stats return [7dd970443e12]
- uppercase loaded and aligned sequences [de0804f1528f]
- added misc/uta0-uta1-cigar-cmp [334bce71eed3]
- set role for align_exons (missed because it bypasses the ORM) [23757cca5b3a]
- uppercase loaded and aligned sequences [9b74f39d4847]
- added misc/uta0-uta1-cigar-cmp [f99db269c985]
- set role for align_exons (missed because it bypasses the ORM) [65e0d8f4918f]
- added cigar_stats_is_trivial [49f9e8308dec]
- added bermuda1 changes [7c6a79c0042d]
- added indices; grant-permissions changes [e009003d3009]
- bermuda: materialize WITH NO DATA [76db3edb6afb]
- loading.py: grant permissions to PUBLIC, not uta_public (duh) [839ba03570e0]
- added session authorization to loading.py (and etc/global.conf) [8818b2563744]
- allow multiple conf files [fd36bbe4ab9f]

- updated grant-permissions cli subcommand; removed obsolete sql/grant-public-permissions.sql [a03a7ab00f2a]
- bic data updates to fix headers and cds_start_i; minor loading code updates to handle bic [f44b70588960]
- #28 - fix headers; modify script to use exonset/txinfo writers to ensure consistency. [f345adec505e]
- in-place bic data updates (Rudy will handle scripts); minor loading code updates to handle bic [4ea9106943d5]
- restructured materialized views; added refresh script [12ae8b971a90]
- #37 - exonset, txinfo files, & fasta files for BIC txs. [eb71b7f00a9f]
- #28 - minor fix to script; METHOD=LRG in exonset file. [ba80d13e52cb]
- #28 - removed LRG_347 and LRG_163 fasta files (NR transcripts) from the bundle; not in the txinfo and exonset files anyway. [13455060b9e3]
- added sql/grant-public-permissions.sql [2dd98f7f92e7]
- store acmg uncompressed (easier copy loading) [75cf356e8bfb]
- added load-sequences to cli [ea0f63cbd27f]
- updated doc link on README [166cba527720]
- auto merge [de41e5ec0125]
- #120 - quick and dirty script to compare uta0/uta1 cigars [430e78a347f5]
- #28 - added fastas; includes 2 fastas (347 & 163) for public transcripts whose data is missing from the LRG TXT export, & thus from the tx info & exonset files. [e6566bbdfe7a]
- #28 - fixed a duplication in the exonset file that comes about when a TX in the TXT export have 2 diff LRG proteins associated (only occurred for LRG_321). [e6f1e0561401]
- #28 - updated inputs based on LRG fix for genomic exon coords on indels for transcripts on negative strands relative to GRChr37. lrg.exonset.gz - METHOD=LRG_download (set in the script). [cafeccb5bd4a]
- updated bermuda-related sql [fbca3f65ccd3]
- updated bermuda views [690bb3fd0c17]
- removed stale scripts in sbin/ [f81c3a0ae714]
- added bermuda_v and lots of other views, mat views, and functions [6797ee052ed9]
- pull fasta directory from conf; add -sql option hack; update loading/README [637b274818bb]
- #28 - script to fetch exon/txinfo; corresponding outputs. These look OK per the inputs from LRG, but the genomic coords for exons with indels relative to GRChr37 don't match... there may be an error in the LRG outputs. Needs review prior to DB import. [e5e640a842a0]
- forgot to commit grant changes [47c0fe04750f]
- added grant-permissions to cli; added SERPINE1 gene and NC_ seqinfo filtering to test data [3551c6dbf0d8]
- update ensembl origin name and ncbi exonset suffix (missed in previous commit) [e0c628ca4f56]
- seqinfo-filter: allow regexp based filtering (for NCs primarily) [f86dd2c8f5f3]
- uta0-fetch: write fasta file [ab77e5c193a5]
- add cds_md5 to transcript model and compute on loading [2a1e4567564e]
- added loading/README; cleaned up minor filename and script inconsistencies [dd713f1d3f86]
- provide additional feedback during loading txinfo and exonset files [372deb640868]
- moved uta/db/loading.py to uta/loading.py; removed redundant schema declaration with tables [faea54fc6c2c]

- skip existing txinfo where the transcript already exists [94765dce7553]
- added format filters and used to create more comprehensive loading test sets; added seq+seq_anno updating [1dbb0cc1b80f]
- restructured loading/ for test and main [36d5cb8747ff]
- updated loading diagram and added PDF (doc/misc-figures.pdf) [294526dd38df]
- added n_exons to exon_set_exons_v and transcript_exons_v [7dc5bf387cf1]
- fixed bug in ucsc-fetch-exonsets [e099e256efe7]
- ensembl-fetch: skip redundant transcripts; write as .tmp files, then rename [aa60762aa856]
- adding loading/test-data/ncbi.seqinfo.gz (missed from previous commit) [b30330657ca3]
- re-added Seq & SeqAnno to schema; updated testdb loader [539f4527ea6d]
- added doc/misc-figures.odg [61b2bcf97546]
- updated ensembl-fetch to write sequences and catch errors (like undefined transcripts) [503877415cb1]
- first draft of ensembl-fetch [bd54ef964608]
- merged and modified Rudy's uta0 extraction code [5693b707f3d0]
- Generate uta0 tx & exonset files [b7541cd8f47c]
- updated test-data with larger set of genes and transcripts [caef61089d88]
- added testdb setup ("make -C loading testdb") [98b3871869db]
- moved sql to top level [1507c0b9f47f]
- removed fetch-align-tasks [338bb23474c6]
- finished switch to Kevin's aligner (and other minor changes) [6d72928ef63a]
- removed web [7b710b3f5d34]
- implemented alignment with locus_lib_bio; dropped older alignment scripts [9bcb85bf9859]
- added time remaining (based on average speed) to align stats [3dc50158d9ca]
- added exon alignment – cooking with gas now! [551a5c2ce3c3]
- loads full data sets from ncbi and ucsc! [24fd33f0ea44]
- loads genes, txinfo, exonsets for first 100 genes alphabetically [2c9c0afd67ed]
- auto merge [52e5fb383c09]
- #40 - updated script to allow optional creation of a test DB [58f193e75e2e]
- schema overhaul, again: no seq support, inlined accessions (no-dedup); updated gene loading (others pending) [ff1a7c2436c7]
- added ucsc-fetch-exonsets [5504e34b1530]
- allow genes from stdin [4a4823449858]
- updated ncbi-fetch for genes, genomic exon sets, and transcript info [4e0440afc8e9]
- finished (?) ncbi-fetch-exonsets [d6b36293c2a1]
- added seqinfo and exonset tools [7a75302621d4]
- use transcript hash as PK [9a37befc7519]
- moved bin/* to sbin/ for consolidation [5c439b96e155]

- added colored logging [[f57de62adec4](#)]
- merged grand-reorg branch [[b6c407bb9ac9](#)]
- last schema update for reorg [[b7b2751fa4e0](#)]
- improved consistency of align/alignment/aln/alt (in favor of alt) and transcript/tx [[8c6c1621ca6b](#)]
- schema refactor, again [[85a10e9bbd27](#)]
- updated tests; uta.models still failing – will fix after model updates [[b3bb51f5ef46](#)]
- dropped engine from cli call signatures (it was redundant) [[67ab29f01ab4](#)]
- added uta.connect() function [[f0a6bbe31cad](#)]
- removed old test data [[a81451e99620](#)]
- eliminated lib/ to structure more a like typical python package [[92a8a298c16d](#)]
- full eutils loading worked [[91da2fda8369](#)]
- huge loader improvements; more testing needed [[9c4de875f047](#)]
- implemented gene loading via eutils [[6ab9dfcfb9c8](#)]
- schema updates; improved schema creating handling for postgresql [[5bb499e21247](#)]
- implemented gene loading [[36116a5a2242](#)]
- updated sqlalchemy database for new schema (DDL check okay!) [[211a393586ab](#)]
- #61 - update test target to find tests and run coverage [[da94a3188b42](#)]
- updated README with pypi info [[7693ea034dfd](#)]
- simple change to trigger dev branch build, maybe [[b13f95bf5ebe](#)]
- add link to drone.io test status; upload only bdist_egg and sdist (bdist causes install problems) [[5ee38833e845](#)]

0.1.6 (2014-01-03)

changes since 0.1.5 (2014-01-03)

Bug Fixes

New Features

Changes

Security

Other Changes

- more doc and ci-test fixes [[8d6dd89831d9](#)]

0.1.5 (2014-01-03)

changes since 0.1.3 (2014-01-03)

Bug Fixes

New Features

Changes

Security

Other Changes

- fixed doc building and dropped upload_sphinx (in favor of upload_docs); moved docs to doc/source [4dbc0f653939]

0.1.3 (2014-01-03)

changes since 0.1.2 (2013-12-30)

Bug Fixes

New Features

Changes

Security

Other Changes

- misc doc updates, incl. version [9f356eb03f8d]

0.1.2 (2013-12-30)

changes since 0.1.1 (2013-12-30)

Bug Fixes

New Features

Changes

Security

Other Changes

0.1.1 (2013-12-30)

changes since 0.1.0 (2013-12-30)

Bug Fixes**New Features****Changes****Security****Other Changes**

- updated setup.py “license” attribute [6ef392a5eb58]
- s/locusdevelopment/invitae/ [9aa5579f84cd]
- removed license from ez_setup.py and sphinx_pypi_upload.py [0d922f3819c7]

0.1.0 (2013-12-30)

changes since 0.0.3 (2013-10-21)

Bug Fixes**New Features****Changes****Security****Other Changes**

- added Apache license and code boilerplate to all source files and scripts [3d692ea0d5a2]
- update default host to uta.invitae.com CNAME [605e6e399e5f]
- updated README; added sbin/uta-shell [c3931dda575b]
- #58: migrated uta to publicly-accessible RDS instance and updated uta defaults [d609a81d1ec9]
- updated sbin/uta-pg-to-sqlite to include protein_hash and meta tables [bade1ac7f98c]
- added sbin/fastq-hash-to-tsv [af8cdea82e96]
- updated uta-pg-to-sqlite script to embed version number and name file (name no longer accepted from commandline) [cc8598eedc8]
- uta-pg-to-sqlite: order records and output loading info [785501f0e8d4]
- use uta0 database by default (rather than reece’s db) [59d60c55cc35]
- #62: synchronized setup files among UTA program components [4319672439a1]
- updated README.rst [a2b81a989aff]
- added jenkins target to makefile [7f509a0b2a0e]
- bring back ez_setup [1b8cec6df88a]

- Makefile: new rule ve-test to execute tests in a fresh ve (as in with jenkins) [779fc64e42d9]
- removed localhost UTA_DB_URL setting in Makefile [e2948fc5577c]
- changed NC_000014.10 to NC_000014.8 [8a0f92bd39ea]
- added get_tx_seq() method [38424d1df2d9]
- removed mapping code that now lives in hgvs [e353859717a1]
- doc/ updates (incomplete) [4323c2a0fec1]
- fetch-tx-* scripts: include gene name in response [c8b55ca6bcf5]
- start feature branch [32732d3ea403]
- fixed start <= end for negative coordinates [432b799d29db]
- corrected NC number for ch14 in genomeutils [e8aea8436a46]
- fixed ci_to_human with additional logic checks [f547aa8355dc]
- updating intron mapping coordinates [16bcb4919240]
- format edits [bb25bc960fe3]
- tests and bug fixes for offsets and strands [06d5e4a0fcdf]
- transcriptmapper with offsets [4dc927d62610]
- first offset commit [6d7f936c0304]
- updated webservice index.html help [221cbbb5dfec]
- fixed strand bug in webservice api hgvs to genomic coords [d475267ab253]
- Created a web directory and moved the webservice in there for future expansion. Created a help page and additional API call for NM to genomic coords. Restructured the API links and versioned the URLs [6725c420f067]
- added NEFL-dbSNP to the tests [c887969c51a6]

1.4.3 0.0 Series

0.0.3 (2013-10-21)

changes since 0.0.2 (2013-10-15)

Bug Fixes

New Features

Changes

Security

Other Changes

- fixed uta.__version__, I think [71ea26442ebe]
- minor setup.py and Makefile changes; +x on bin/uta-webservice [045b6c412919]

- fixed and commented out DNAH11 tests; see TODO [[1b9fe0bd9edb](#)]
- changed logic for db connection info (set UTA_DB_URL=postgresql://localhost/) [[ffa815074d8d](#)]
- don't run test_uta_db_sa_models.py (not ready yet) [[8073d4465978](#)]
- added sbin/dbsnp-rs-summary-to-tsv [[250fe0dc69df](#)]
- catch errors related to webservice calls [[d5675d6acead](#)]
- added uta-webservice and requirements [[35b847867c8f](#)]
- added tests for HGVSMapper.hgvsg_to_hgvsc [[527cbaf6cd27](#)]
- updated Makefile and setup.py [[33b25cca8f3e](#)]

0.0.2 (2013-10-15)

changes since 0.0.1 (2013-10-09)

Bug Fixes

New Features

Changes

Security

Other Changes

- implemented HGVSMapper.hgvsg_to_hgvsc with tests [[a508efd70568](#)]
- update hgvsmapper and add DNAH11 tests [[137912d1b76f](#)]
- comment out doctests that require db connection [[3441affbcb39](#)]
- raise InvalidIntervalError for intervals outside transcript bounds [[6ad61ee30739](#)]
- updated README with installation instructions [[482fce4e5917](#)]
- removed stray import IPython [[90a5caac6aea](#)]
- changed max_extent default to False; updated TranscriptMapper and tests to use max_extent [[a3d0adc5eec7](#)]
- rewrote intervalmapper for min/max extent support, with tests [[6e8dc808c42b](#)]

0.0.1 (2013-10-09)

changes since 0.0.0 (2013-06-30)

Bug Fixes

New Features

Changes

Security

Other Changes

- don't use ez_setup due to setuptools conflicts with other locus projects [43571336cc9e]
- update README with HGVSMapper instructions [95f166a41888]
- specifying hgvs-0.0.2 in dependency_links [aa07e408bdb0]
- testing specifying hgvs-pre in dependency_links [8fcd3a52d92b]
- updated setup.py [e8ea75c7ed49]
- fixed make test [14c04a585bbd]
- incorporated HGVSMapper [ab241c8d090a]
- fixed pkg_dir for sdist [fc92498a6e59]
- reverted assertion [a5cf9207ef3b]
- removed bundled distribute_setup.py [85c8b31997f6]
- removed hgvs dependency; added ez_setup [f0e4942e44d3]
- assertion for start==end==0; doc updates [66088ddbd4be]
- added cds<->ci conversion [e01dbdcb5338]
- added example to README and updated misc/garcia-setup.py [6d5153945396]
- mostly passes John Garcia's tests [877664636b0e]
- minor commenting and addition of _debug_info in TranscriptMapper [f18ed7daaac2]
- minor doc updates; fixed make test bug [5ab50f868238]
- added support for sphinx_upload [2b5f3204c619]
- fix package_dir setting [daf2c3d8e8ea]

1.5 License

uta is released under the [Apache License 2.0](#), the text of which appears below:

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Additional Resources

- [UTA Code Repository and Issue Tracker](#)

Indices and tables

- `genindex`
- `modindex`
- `search`