

MolecularMatch Conditions 2018 Update

In 2013, MolecularMatch integrated SNOMED-CT as our technology's primary condition (disease) dataset. For months and years after, oncologists and scientists at MM added a layer of curation so that it fits with modern cancer diagnoses. This included editing and adding new conditions and synonyms, and creating genetic composite conditions. Since then, SNOMED has improved in relation to oncology. Also, several open-source disease datasets have been launched. Matching patients to trials, drugs and assertion evidence guidelines depends on an accurate diagnoses and consistent interpretation between healthcare systems. Therefore in 2018, we upgraded our condition system, accomplishing the goals of:

1. Allowing cohesive code-based searching to improve EHR/Payer/LIMS integrations.
 2. Updating to the most modern data ontologies.
 3. Expanding operations outside of cancer.
 4. Data validation (duplicates merging) with medical oversight.
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MolecularMatch NLP entity extraction and search engines run on ontologies. These include our conditions and findings, our in-house developed [molecular ontology](#) and our global clinical trial aggregation. As our experience with data aggregation has grown, we've developed a protocol that allows for easy integration of big data to enhance our search engines. This high-level protocol is:

1. Acquire datasets in their native form on update intervals.
 2. Identification strategy and merging to allow diverse inputs and avoid duplicates.
 3. Incorporate into MMPower for broad use.
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Condition Data Incorporated into MM

Condition terms are now searchable by prefix_code (e.g. `SNOMEDID_12345`).

Search Prefix	Dataset Name	Records Count
SNOMEDID	Systematized Nomenclature of Medicine -- Clinical Terms	313,940
ICD10	10th rev. of the International Statistical Classification of Diseases	94,127

Custom Conditions and Genetic Composites

Only a handful of genetic composite conditions exist in the public datasets, like "EGFR positive NSCLC". At MM, we've created many more composites, which are necessary in our NLP engine for coalescing meaning from medical documents.

Screenshot of internal MM tools for creating composite conditions.

The screenshot shows the 'Data Management' interface with tabs for Conditions, Clinical Findings, Anatomies, Stages, OncoTree, SNOMED, ICD10, DiseaseOntology, and Processes. The 'Conditions' tab is active, showing a list of conditions with columns for Name, Composite, Custom, and Suppress. A search bar is at the top left. On the right, a form for creating a new condition is visible, with fields for Name, Alias, and a 'Clear Alias' button. Below the form, there's a section for 'Associated Tags' with a table of terms and checkboxes for Custom and Suppress. The bottom of the interface shows pagination information: 'Page 1 of 3' and 'Displaying 1 - 25 of 72'.

Name	Composite	Custom	Suppress
BCH-ABL1			
B lymphoblastic leukaemia/lymphoma with TEL-AML1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
B lymphoblastic leukaemia/lymphoma with t(1;19)(q23;p13.3)	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
B lymphoblastic leukaemia/lymphoma with t(5;14)(q31;q32)	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
B lymphoblastic leukaemia/lymphoma with t(v;11q23); MLL rearranged	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
BRAF mutated colorectal cancer	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
BRAF mutated melanoma	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Carney's Triad	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Childhood myelodysplastic syndrome	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Classical Hodgkin lymphoma type PTL	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
EGFR mutated GBM	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
ER+ HER2- PIK3CA Breast cancer	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
FLT3 AML	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
GIST - NF1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
GIST KIT exon 11	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
GIST KIT exon 13	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>

Term	Custom	Suppress
PIK3CA	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Neoplasm of breast	<input checked="" type="checkbox"/>	<input type="checkbox"/>
ERBB2 Loss	<input checked="" type="checkbox"/>	<input type="checkbox"/>
ESR1	<input checked="" type="checkbox"/>	<input type="checkbox"/>

Lets Use It!

These codes can now be used in the whole MM ecosystem. From the application search, to API queries, to EHR integration.

App Search

http://app.molecularmatch.com/search/ICD10_D45

http://app.molecularmatch.com/search/SNOMEDID_12345

http://app.molecularmatch.com/search/DOID_0121

http://app.molecularmatch.com/search/ONCOTREE_AML

API Queries

See specs on

```
#####  
# Trials Search -- save this as a .sh file  
#####
```

```
# to run include apiKey as first argument
# $ chmod 777 file.sh
# $ ./file.sh apiKey

curl -X POST 'https://api.molecularmatch.com/v2/search/trials' \
--data "apiKey=$1" \
--data-urlencode 'filters=[ \
    {"facet":"ICD10","term":"ICD10_D45"}, \
    {"facet":"STATUS", "term":"Enrolling"}, \
    {"facet":"TRIALTYPE", "term":"Interventional"} \
    ]'

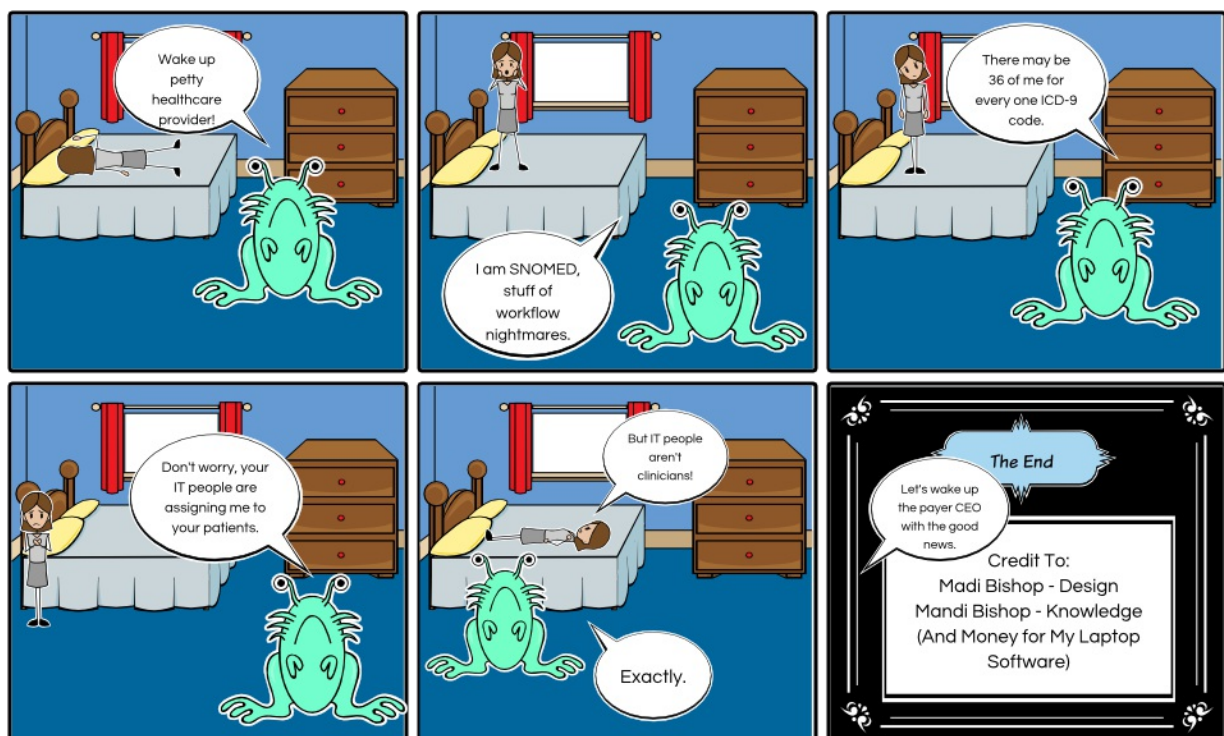
curl 'https://api.molecularmatch.com/v2/search/trials' \
--data "apiKey=$1" \
--data-urlencode 'filters=[ {"facet" : "SNOMEDID", "term" : "03387111"}]'
```

EHR Integration

Contact Us at info@molecularmatch.com for a demonstration of how to integrate with an EHR, payer system or LIMS.

Mapping Trouble?

No mapping effort is perfect. Work with us to make sure you are getting the results you expect for your patients.



Create your own at StoryboardThat.com

From: <http://healthstandards.com/blog/2014/04/21/snomed-problems/>