Probabilistic Name and Address Cleaning and Standardisation

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Project web page: **http://datamining.anu.edu.au/linkage.html**

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Outline

- Data cleaning and standardisation
- Record linkage and data integration
- Our approach
  - Cleaning
  - Tagging
  - Segmentation
- Hidden Markov models for data segmentation
- Experimental results
- *Febrl* – Freely extensible biomedical record linkage

Data cleaning and standardisation (I)

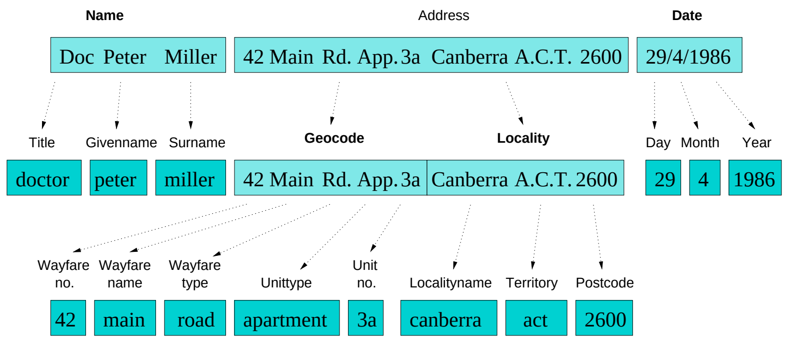
- Real world data is often *dirty*
  - Missing values
  - Typographical and other errors
  - Different coding schemes
  - Outdated data
- Names and addresses are especially prone to data entry errors
- Cleaned and standardised data is needed for
  - loading into databases and data warehouses
  - data mining and other data analysis studies
  - record linkage and data integration

Record linkage and data integration

- The task of linking together information from one or more data sources representing the same entity
- If no *unique identifier* is available, *probabilistic linkage techniques* have to be applied
- Applications of record linkage
  - Remove duplicates in a data set (internal linkage)
  - Merge new records into a larger master data set
  - Create customer or patient oriented statistics
  - Compile data for longitudinal studies

Data cleaning and standardisation is an important first step for successful record linkage

Data cleaning and standardisation (II)



- Remove unwanted characters and words
- Expand abbreviations and correct misspellings
- Segment data into well defined *output fields*

Our approach

1. Data cleaning
   - Remove unwanted characters and words
   - Correct various misspellings and abbreviations
2. Data tagging
   - Split into a list of words, numbers and separators
   - Assign one or more tags to each element of this list
3. Data segmentation
   - Assign list elements to *output fields*
   - Use *hidden Markov models* (HMMs) or rules

Data cleaning

- Assume the input *component* is one string
  (name or address – dates are processed differently)
- Convert all letters into lower case
- Use *correction lists* which contain pairs of `original:replacement` strings
- An empty `replacement` string results in removing the original string
- Correction lists are stored in text files and can be modified by the user
- Different correction lists for names and addresses

Data tagging

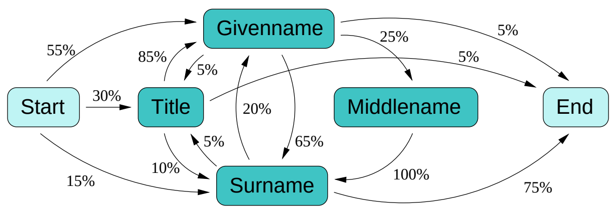
- Split cleaned string at whitespace boundaries into a list of words, numbers, characters, etc.
- Using *look-up tables* and some had-coded rules, each element is tagged with one or more *tags*
- Example:
  - Uncleaned input string: *“Doc. peter Paul MILLER”*
  - Cleaned string: *“dr peter paul miller”*
  - Word and tag lists:

```
['dr', 'peter', 'paul', 'miller']
['TI', 'GM/SN', 'GM',    'SN'   ]
```

Data segmentation

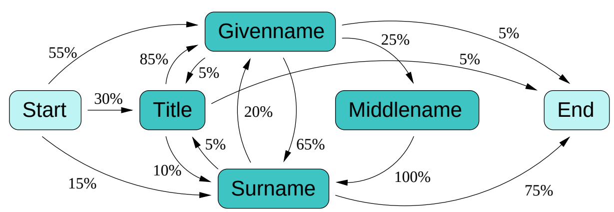
- Using the tag list, assign elements in the word list to the appropriate *output fields*
- Rules based approach (e.g. *AutoStan*)
  - Example: *“if an element has tag ‘TI’ then assign the corresponding word to the ‘title’ output field”*
  - Hard to develop and maintain rules
  - Different sets of rules needed for different data sets
- Hidden Markov model (HMM) approach
  - A machine learning technique (supervised learning)
  - Training data is needed to build HMMs

Hidden Markov model (HMM)



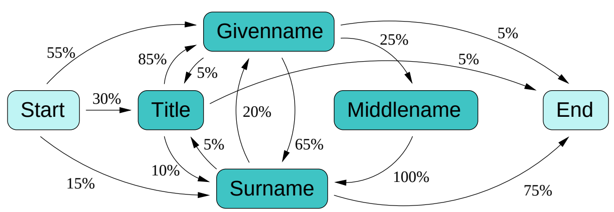
- A HMM is a *probabilistic* finite state machine
  - Made of a set of *states* and *transition probabilities* between these states
  - In each state an *observation* symbol is emitted with a certain probability distribution
  - In our approach, the observation symbols are *tags* and the states correspond to the *output fields*

HMM probability matrices



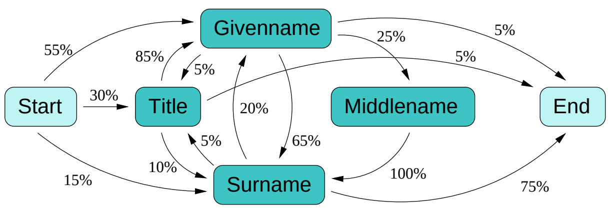
	State					
Observation	*Start*	Title	Givenname	Middlename	Surname	*End*
TI	–	96%	1%	1%	1%	–
GM	–	1%	35%	33%	15%	–
GF	–	1%	35%	27%	14%	–
SN	–	1%	9%	14%	45%	–
UN	–	1%	20%	25%	25%	–

HMM data segmentation



- For an observation sequence we are interested in the most probable path through a given HMM
  (in our case an observation sequence is a *tag list*)
- The *Viterbi* algorithm is used for this task
  (a dynamic programming approach)
- *Smoothing* is applied to account for unseen data
  (assign small probabilities for unseen observation symbols)

HMM segmentation example



- Input word and tag list

  `['dr', 'peter', 'paul', 'miller']`

  `['TI', 'GM/SN', 'GM', 'SN' ]`

- Two example paths through HMM

```
Start -> Title (TI) -> Givenname (GM) ->
        Middlename (GM) -> Surname (SN) -> End
Start -> Title (TI) -> Surname (SN) ->
        Givenname (GM) -> Surname (SN) -> End
```


HMM training (I)

- Both transition and observation probabilities need to be trained using *training data*
  (maximum likelihood estimates (MLE) are derived by accumulating frequency counts for transitions and observations)
- Training data consists of records, each being a sequence of `tag:hmm_state` pairs
- Example (2 training records):

```
# '2 richard street lewisham 2049 new_south_wales'
NU:wfnu,UN:wfna1,WT:wfty,LN:loc1,PC:pc,TR:ter1

# '42 / 131 miller place manly 2095 new_south_wales'
NU:unnu,SL:sla,NU:wfnu,UN:wfna1,WT:wfty,LN:loc1,PC:pc,TR:ter1
```


HMM training (II)

- A *bootstrapping* approach is applied for semi-automatic training
  1. Manually edit a small number of training records and train a first rough HMM
  2. Use this first HMM to segment and tag a larger number of training records
  3. Manually check a second set of training records, then train improved HMM
- Only a few person days are needed to get a HMM that results in an accurate standardisation
  (instead of weeks or even month to develop rules)

Address standardisation results

- Various NSW Health data sets (millions of records)
  - *HMM1* trained on 1,450 Death Certificate records
  - *HMM2* contains *HMM1* plus 1,000 Midwifes Data Collection training records
  - *HMM3* is *HMM2* plus 60 unusual training records
- *AutoStan* rules (for ISC) developed over years

	HMM/Method			
Test Data Set (1,000 records each)	HMM 1	HMM 2	HMM 3	Auto Stan
Death Certificates	95.7%	96.8%	97.6%	91.5%
Inpatient Statistics Collection	95.7%	95.9%	97.4%	95.3%

Name standardisation results

- NSW Midwifes Data Collection (1990 - 2000)
  (around 963,000 records, no medical information)
- 10-fold cross-validation study with 10,000 random records (9,000 training and 1,000 test records)
- Both rule based and HMM data cleaning and standardisation
  - Rules were better because most names were simple (not much structure to learn for HMM)

	Min	Max	Average	StdDev
HMM	83.1%	97.0%	92.0%	±4.7%
Rules	97.1%	99.7%	98.2%	±0.7%

Outlook - Febrl

- HMM approach is comparable with traditional rule based approach (but easier to develop and maintain)
- Implemented in *Febrl* **http://febrl.sourceforge.net**
  (Freely extensible biomedical record linkage)
  - Open-source, *Python*, multi-platform
- Currently under development are
  - probabilistic record linkage routines
  - new *fuzzy indexed look-up* mechanisms
  - parallel techniques for standardisation and linkage
  - predictive modelling for increased linkage quality