Department of Modern Languages
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# Morphological Disambiguation using Probabilistic Sequence Models

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*Academic dissertation to be publicly discussed, by due permission of the Faculty of Arts at the University of Helsinki in auditorium FOO (in lecture room QUUX), on the $XY^{th}$ of February at 12 o'clock.*

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*Nobody is going to read your PhD thesis*

*Ancient Proverb*

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# Notation

**Acronyms**

| | |
|---|---|
| CRF | Conditional Random Field |
| HMM | Hidden Markov Model |
| MEMM | Maximum-Entropy Markov Model |
| NB | Naïve Bayes |
| PGM | Probabilistic Graphical Model |
| POS | Part-of-Speech |
| MAP | Maximum a posteriori |

**Mathematical Notation**

| | |
|---|---|
| $x[i]$ | The element at index $i$ (starting at 1) in vector or sequence $x$. |
| $\mathbb{R}_n^m$ | The space of $m \times n$ real valued matrices. |
| $x[1:t]$ | Prefix $(x_1,\ ...,\ x_t)$ of vector or sequence $x = (x_1,\ ...,\ x_T)$. |
| $X^t$ | The cartesian product of $t$ copies of the set $X$. |
| $M^\top$ | Transpose of matrix $M$. |
| $M^+$ | The More-Pennrose pseudoinverse of matrix $M$. |
| $f(x;\theta)$ | Function $f$, paramerized by vector $\theta$, applied to $x$. |
| $x \mapsto f(x),\ x \overset{f}{\mapsto} f(x)$ | A mapping of values $x$ to expressions $f(x)$. |
| $\|v\|$ | Norm of vector $v$. |
| $\hat{p}$ | Estimate of probability $p$. |

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# Chapter 1

# Introduction

# Chapter 2

# Morphology

## 2.1 The Structure of Words

Many linguistc units are rather controversial. What is the definition of a sentence? Do sentences even exist in spoken language? Is there such a thing as a phoneme?

The concept of a word is, however, among the among the more universally accepted. The reason for this may be that there is in fact a fairly easy and readily applicable test for what is a word: X is a word if X can be used as an answer to a question. For example

- You said you saw a what yesterday?
- Dog. I saw a dog.

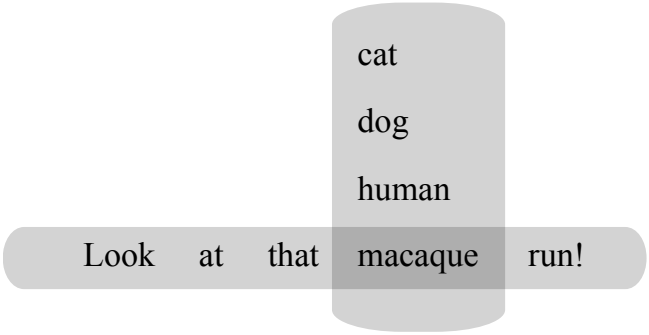
Although, singular nouns in English usually take a compulsory article, exceptional contexts where they are uttered without an article are acceptable for many language users. Therefore, it is plausible to stipulate that singular nouns are words in English. For most languages, this criterion can be used to find most words that language users intuitively group under the concept word. Even this criterion, however, fails for polysemous languages. Nevertheless, it very useful for many languages.

Of course, orthographic words are much easier to identify than spoken language words in many writing systems. Simply look for entities separated by punctuation and white-space. This, however, does not work for some languages such as Chinese where word spaces are not indicated in written text. Because this thesis exclusively deals with written language and because I have performed experiments on European languages whose orthographies mark word boundaries, I will gloss over the difficulties of locating word boundaries although this is an interesting problem from the points of view of both linguistics and engineering.

Morphology is the sub-fields of linguistics that investigates the structure of words. For example the knowledge that appending a suffix “s” to a singular English nouns makes it plural is morphological knowledge. Of course this rule is not entirely correct because some nouns form plurals in some other way (e.g. “foot/feet”) and yet other nouns have no plural form (e.g. “music”).

Because words consist of phonemes or orthographic symbols, the structure of words cannot be investigated without considering the phonological system of a language. If we had to form the singular inessive of the the non-existent Finnish noun “looka”, we would say “lookassa”, not “lookassä” because vowel harmony, a phonological co-occurrence restriction, prohibits the latter form.

Figure 2.1: The syntagmatic and paradigmatic axes of language.




## 2.2 Languages with Rich Morphology

- Typological classification of languages.
- “Large label sets”.

## 2.3 Morphological Analyzers

- Finite-state morphology (Koskenniemi, 1984), (Kaplan and Kay, 1994).

# Chapter 3

# Machine Learning

This section outlines the basic methodology followed in machine learning approaches to Natural Language Processing. I will briefly discuss machine learning from a general point of view and then present supervised machine learning in more detail using linear regression as example. I will then elaborate on the different kinds of classifiers applied in NLP; both unstructured and structured.

### 3.0.1 Overview

**Statistical and Rule-Based NLP** Approaches to Natural Language Processing can be broadly divided into two groups: rule-based and machine learning approaches. Rule-based approaches utilize hand crafted rules for tasks such as text labeling or machine translation. Machine learning approaches solve the same set of problems using data driven (usually statistically motivated) models and samples from the problem domain, which are used to estimate model parameters.

This thesis focuses on extending machine learning techniques to the domain of morphologically complex languages, where they have been applied less frequent than for morphologically more straightforward languages like English. I want to emphasize that the thesis should not be seen as an attack against the rule-based paradigm for Natural Language Processing which has proven to be very successful in treatment of morphologically complex languages . This thesis is simply an investigation into extension of machine learning techniques. Truly successful language processing systems should probably combine rule-based and statistical techniques.

Machine learning and hand crafted rules have their respective merits and short-comings and these are dependent on the task to some extent. For example, in the domain of machine translation, rule-based methods can give syntactically correct results . However, statistical machine translation systems are in general better at lexical choice .

**Supervised and Unsupervised ML** Machine learning is can be divided into two fields supervised and unsupervised. Supervised machine learning uses a training material of labeled training examples. An example would be a set of images with associated key words, where the task is to build a system which can associate previously unseen images with appropriate key words.

Supervised machine learning is typically employed for tasks such as labeling (that is classification) and translation. Typical examples of tasks include Part-of-Speech labeling and speech recognition where

annotations consist of POS labels for the words in some text and written sentences corresponding to an acoustic speech signal respectively.

In contrast to supervised machine translation, unsupervised approaches exclusively utilize unannotated data. Unsupervised machine learning is most often used for various kinds of clustering tasks, that is grouping sets of examples into subsets of similar examples.

Finally, semi-supervised (and weakly supervised) systems use an annotated training set with in combination with a, typically, very large unannotated training set to improve the results beyond the maximum achievable by either approach in isolation.

In Natural Language processing, supervised learning approaches are most often used (for example ...). Unsupervised approaches, however, can also be useful for e.g. exploratory data analysis (...).

This thesis focuses on supervised machine learning.

## 3.1 Supervised Learning

In this section, I will illustrate the key concepts and techniques in supervised Machine Learning using the simple example of linear regression. I will explain the plain linear regression model and show how it can be fitted using training data. I will then briefly present ridge regression which is a regularized version of linear regression.

I chose linear regression as example because it is a simple model yet can be used to illustrate data driven techniques. Moreover, the model has several tractable properties such as smoothness and convexity. Additionally, it can be seen as the simplest example of a linear classifier which is a category of models encompassing

### 3.1.1 Basic Concepts

**Linear Regression** As a simple example, imagine a person called Jill who is a real estate agent. She is interested in constructing an application, for use by prospective clients, which would give rough estimates for the selling price of a property. Jill knows that a large number of factors affect housing prices but there are a few very robust quantifiable predictors of price that are easy to measure.

Jill decides to base the model on the following predictors:

1. The living area.
2. The number of rooms.
3. The number of bathrooms.
4. Size of the yard.
5. Distance of the house from the city center.
6. Age of the house.
7. Amount of time since the last major renovation.

Jill decides to use the simplest model which seems reasonable. This model is *linear regression* which models *the dependent variable* house price as a linear combination of the independent variables listed above and parameter values in $\mathbb{R}$. The linear regression model is probably not accurate. It fails in several regards. For example, increasing age of the house probably reduces the price up to a point but very old houses can in fact be more expensive then newly built houses especially if they have been renovated lately. Although, the linear model is unlikely to be entirely accurate, Jill is happy with it because the intention is just to give a ball park estimate of the price for the average prospective client.

To formalize the linear regression model, let us call the dependent variable price $y$ and each of the independent variables living area, number of rooms and so on $x_i$. Given a vector $x = (x[1], ..., x[n])^\top \in \mathbb{R}^n$, which combines the independent variables[1], and a parameter vector $\theta \in \mathbb{R}^n$ the linear regression model is given in Equation 3.1.

$$y(x; \theta) = x^\top \theta \tag{3.1}$$

Two questions immediately arise: How to compute the price given parameters and predictors and how to compute the parameter vector $\theta$. These questions are common for all supervised learning problems also when using other models than the linear regression model.

**Inference** The first question concerns *inference*, that is finding the most likely value for the dependent variable given the independent variables. In the case of linear regression, the answer to this question is straightforward. To compute the price, simply perform the inner product in Equation 3.1. The question is, however, not entirely settled because one might also ask for example how close to the actual price the estimate $y$ is likely to be. A related question would be to provide an upper and lower bound for the price so that the actual price is very likely to be inside the provided bounds. To answer these questions, one would have to model the expected error.

Inference is very easy and also efficient in the case of linear regression. With more complex model such as structured graphical models used in this thesis, it can however be an algorithmically and computationally more challenging problem. The principle is still the same: Find the $y$ which is most likely given the input parameters.

**Estimation** The second question concerns *estimation of model parameters* and it is more complex than the question of inference. First of all, Jill needs training data. She also needs to decide upon an *estimator*, that is, a method for estimating the parameters $\theta$.

In the case of house price prediction, Jill can simply use data about houses she has brokered in the past. She decides to use a training data set $\mathcal{D} = \{(x_1, y_1), ..., (x_T, y_T)\}$, where each $x_t = (x_t[1]...x_t[n])$ is a vector of independent variable values (living area, age of the house and so on) and $y_t$ is the dependent variable value, that is the final selling price of the house. Now Jill needs to make a choice. How many training examples $(x_t, y_t)$ does she need? The common wisdom is that more data is always better, however, this has bearing on how the parameters need to be estimated. In any case, the number of data points in the training data should ideally be higher than the number of parameters that need to be estimated. When one cannot accomplish this, one encounters the so called *data sparsity problem*.

[1] In reality, each of the predictors would probably be transformed to give all of them the same average and variance. Although this ii not required in theory, it tends to give a better model **?**.

**Data Sparsity** Whereas getting sufficient training data is fairly easy in the case of housing prices, it is vastly more difficult to accomplish with more complicated models in natural language processing. Therefore, one central question in this thesis is how to counteract *data sparsity*.

**Cost Functions** The objective in estimation is to find a parameter vector $\theta$ which in some sense minimizes the error of the house price predictions $y(x_t;\theta)$ when compared to the actual realized house prices $y_t$ in the training data. The usual minimization criterion used with linear regression is the least square sum criterion given in Equation 3.2. It is minimized by a parameter vector $\theta$ which gives as small square errors $|y_t - y(x_t;\theta)|^2$ as possible.

$$\theta = \underset{\theta' \in \mathbb{R}^n}{\arg\min} \sum_{x_t \in \mathcal{D}} |y_t - y(x_t;\theta')|^2 \tag{3.2}$$

The square sum is an example of a *cost function* (also called the objective function). A cost function assigns a non-negative real cost for each parameter vector. Using the concept of cost function, the objective of estimation can be reformulated: Find the parameter vector $\theta$ that minimizes the cost of the training data.

**The Exact Solution** In the case of linear regression, there is a well known exact solution for $\theta$ which utilizes linear algebra. The solution is given in Equation 3.3. The matrix $X \in \mathbb{R}_n^T$ is defined by $X_{t,i} = x_t[i]$ and its More-Pennrose pseudoinverse $X^+ \in \mathbb{R}_T^n$ is defined as $X^+ = (X^\top X)^{-1} X^\top$. The vector $Y \in R^T$ is simply the vector of realized house prices $y_t$. The solution $\theta$ exists only when none of the independent variables are linear combinations of each other in the training data.

$$\theta = X^+ Y \tag{3.3}$$

**Iterative Estimation** Although the linear regression model is simple enough so that it can be estimated exactly, the same does not hold for most more complex models such as the Conditional Random Field investigated in this thesis. Moreover, the exact solution might often not be the one that is desired. Often the training data is quite sparse, that is there is too little of it compared to the amount of parameters that need to be estimated. Therefore, the model may *over-fit* the training data and fail to generalize well to examples not included in the training data.

**Regularization** Due to the problem of over-fitting, a family of heuristic techniques called *regularization* is often employed. They aim to transform the original problem in a way which will penalize both deviance from the gold standard and "complexity" of the solution $\theta$. Regularization can be seen to convey the same idea as Occam's Maxim which states that a simpler explanation for a phenomenon should be preferred when compared to a more complex explanation yielding equivalent results. Of course, this does not explain what is meant by a "complex" parameter vector $\theta$.

To illustrate simple and complex parameter vectors, examine a case of linear regression where the dependent variable $y$ and the predictors $x_i$ have mean $0$ and variance $1$ in the training data. This may seem restrictive but in fact any linear regression problem can easily be transformed into this form by applying an affine transformation $z \mapsto az - b$. When doing inference, this affine transformation can simply be reversed by applying $z \mapsto a^{-1}(z + b)$. The simplest parameter vector $\theta$ is clearly the zero vector $\theta = (0...0)^\top$. It

corresponds to the hypothesis that the predictors $x_i$ have no effect on the dependent variable $y$. According to this hypothesis, the prediction is always the average of the dependent variable values in the training data.

The zero solution to a linear regression problem is simple but also totally biased. Because we are assuming that the independent variables $x_i$ explain the dependent variable $y$, a model that completely disregards them is unlikely to give a good fit to the training data. By introducing a regularization term into the cost function, we can however encourage simple solutions while at the same time also preferring solutions that give a good fit. There are several ways to accomplish this but the most commonly used are so called $L_1$ and $L_2$ regularization. These are general regularization methods that are employed in many models in machine learning.

The $L_1$ regularized cost function for linear regression is given in Equation 3.4. $L_1$ regularization, also called LASSO regularization **?**, enforces solutions where many of the parameter values are $0$. These are also called sparse parameters. It is suitable in the situation where the model is over specified, that is, many of the predictors might not be necessary for good prediction. The expression is a sum

$$\theta = \underset{\theta' \in \mathbb{R}^n}{\arg\min} \sum_{x_t \in \mathcal{D}} |y_t - y(x_t; \theta')|^2 + \lambda \sum_i |\theta[i]| \tag{3.4}$$

The $L_2$ regularized cost function is given in 3.5. $L_2$ regularization is also called Tikhonov regularization. In contrast to $L_1$ regularization, it directly prefers solutions with small norm. A linear regression model with Tikhonov regularization is called a ridge regression model.

$$\theta = \underset{\theta' \in \mathbb{R}^n}{\arg\min} \sum_{x_t \in \mathcal{D}} |y_t - y(x_t; \theta')|^2 + \lambda \|\theta\|^2 = \underset{\theta' \in \mathbb{R}^n}{\arg\min} \sum_{x_t \in \mathcal{D}} |y_t - y(x_t; \theta')|^2 + \lambda \sum_i |\theta[i]|^2 \tag{3.5}$$

The coefficient $\lambda \in \mathbb{R}^+$ is called the *regularizer*. The regularizer determines the degree to which model fit and simplicity affect the cost. A higher $\lambda$ will increase the cost for complex models more than a lower one. When $\lambda$ increases, the optimal parameter vector $\theta$ approaches the zero vector and when it decreases $\theta$ approaches the parameters that fit the training data as closely as possible. This is called under-fitting.

The regularizer is a so called *hyper-parameter* of the regularized liner regression model. It is easy to see that increasing $\lambda$ will automatically increase the cost. Therefore, there is no direct way to estimate its correct magnitude simply using the training data. Instead *held-out data* can be used. Held-out data is labeled data that is not used directly for estimating model parameters. If the model over-fits the training data, that is generalizes poorly to unseen examples, the held-out data will have a high cost. However, it will also have a high cost if the model under-fits, that is, performs poorly on all data. Held-out data can therefore be used to find an optimal values for the regularizer $\lambda$. Often one tries several potential values and chooses the one that minimizes the cost of the held-out data. Usually, one uses the unregularized cost function for the held-out data.

**Iterative Estimation** Regularization is an additional reason for introducing iterative estimation methods instead of exact estimation. There are several choices of regularization methods and some of them might not result in optimization problems that have closed form solutions[2]. When an exact solution cannot be

[2] In the case of regression, non-linear *kernel functions* also result in optimization problems that don't have a closed form solution. I will elaborate this when discussing logistic regression.

computed, or it is undesirable, numerical methods can be used to estimate model parameters.

Because the cost of the training data is a function of the model parameters, one can apply analytical methods to try to find optimal parameter values. These methods include for example Newton's method which is an iterative procedure that can be used to find the zeros of a differentiable function or local extrema of a twice differentiable function. Approximations of Newton's method, so called Quasi-Newton methods **?**, have also been developed because Newton's method requires evaluation and inversion of the Hessian matrix of a function. This is a very costly operation for functions where the domain has high dimension. Quasi-Newton methods use approximations of the inverse Hessian.

A simpler method called gradient descent can be applied to functions that are only once differentiable.[3] In general, gradient descent converges toward the optimum more slowly than Newton's method, however, the computation of one step of the iterative process is much faster when using gradient descent. Therefore, it may be faster in practice.

All gradient based methods rely on differentiability of the cost function. For the models used in this thesis, differentiability holds. Gradient based methods work in the following general manner. Let $L_{\mathcal{D}} : \mathbb{R}^n \to \mathbb{R}$ be the cost of the training data $\mathcal{D}$.

1. Start at a random point $\theta_0$ in the parameter space.
2. Determine the direction of steepest descent of the cost function. This is the negative gradient $-\nabla L_{\mathcal{D}}(\theta_t)$ at point $\theta_t$.
3. Determine a suitable step size $\alpha_t \in \mathbb{R}_+$.
4. Take a step of length $\alpha_t$ in direction $v_t$ to get to the next point in the parameter space $\theta_{t+1}$, that is $\theta_{t+1} = \theta_t - \alpha_t \nabla L_{\mathcal{D}}(\theta_t)$.
5. If the difference in cost $|L_{\mathcal{D}}(\theta_{t+1}) - L_{\mathcal{D}}(\theta_t)|$ is smaller than a threshold $\rho$, set $\theta = \theta_{t+1}$. Otherwise, set $\theta_t = \theta_{t+1}$ and return to line 2.

The main difference between first and second order methods is the computation of the step size $\alpha_t$. Second order methods can take longer steps when the cost is plateauing. Thus they typically take fewer steps in total. In first order methods such as gradient descent, $\alpha_t$ can be constant, a decreasing function of $t$ or can also be determined by a line search in the direction of $-\nabla L_{\mathcal{D}}(\theta_t)$ **?**. For example $\alpha_t = t^{-1}$ may work[4].

As the meta-algorithm above suggests, gradient based optimization algorithms are local in the sense that they always move in the direction of steepest descent of the cost function that is toward a local optimum. Therefore, they will in general not find the global optimum of the cost function. By choosing a *convex* cost function it is possible to avoid getting stuck at local optima. All local optima of convex functions are in fact global optima.

Convexity is, however, not enough to guarantee convergence to a global optimum. First of all, a global optimum might not exist[5]. Convergence could also be too slow thus leading to premature termination of the training procedure. This is specifically a problem for first order methods.

[3] Essentially the same procedure can also be applied to functions that are not differentiable but are only guaranteed to have a sub-gradient **?**.

[4] In general, stepsize $(\alpha_t)_{t\in\mathbb{N}}$ that resemble the harmonic sequence, that is $\sum \alpha_t^2 < \infty$ and $\sum \alpha_t = \infty$, guarantee convergence of gradient descent to an minimum of the cost function (if it exists) for a wide variety of functions **?**

[5] This can happen if the domain of the cost function is not compact. Unfortunately, it usually is not.

**Online Estimation** The optimization methods discussed up to this point have been so called *batch methods*. The derivatives of the cost function is computed over the entire training data and parameters are updated accordingly. Batch methods can be slow and subsequent training when new training examples become available is computationally intensive. *Online algorithms* are an alternative to batch methods, where the cost is instead computed for a randomly chosen training example and the parameters are the updated accordingly **?**. In practice, online methods can give fast convergence. Moreover, re-training is relatively efficient when new training examples become available.

*Stochastic gradient descent* is a well known online estimation algorithm. It has vastly superior convergence properties when compared to regular gradient descent **?** but is identical in all other respects except that it is an online estimation algorithm instead of a batch algorithm. The algorithm processes one random training example at a time. It uses the gradient $\nabla L_{\mathcal{D}[i]}(\theta)$ of the cost over the single training example $\mathcal{D}[i]$ to approximate the gradient $\nabla L_{\mathcal{D}}(\theta)$ for the entire training data $\mathcal{D}$.

## 3.2 Classifiers

The main topic of this thesis is morphological tagging. It can be seen as a structured *classification task* where each word in a sentence is assigned one morphological label[6]. Classification is a fundamental supervised machine learning task where the objective is to learn a mapping from objects like words, sentences, documents or images onto discrete classes such as morphological labels (Noun+Sg+Nom) or sentiments (Positive sentiment versus Negative Sentiment).

Classification resembles regression. The output of a classifier is, however, not a single real value $y$ but a distribution over the set of nominal classes.

Probabilistic classifiers can broadly be divided into two groups, namely generative and discriminative. Generative classifiers learn a joint distribution $p(x, y)$ over labels $y$ and input examples $x$. Given an example $x$, a distribution over classes $y$ can be computed using the marginal probability of example $x$, which is $p(x) = \sum_{y' \in Y} p(y', x)$. The probability distribution over classes is defined by $p(y|x) = p(y, x)/p(x)$.

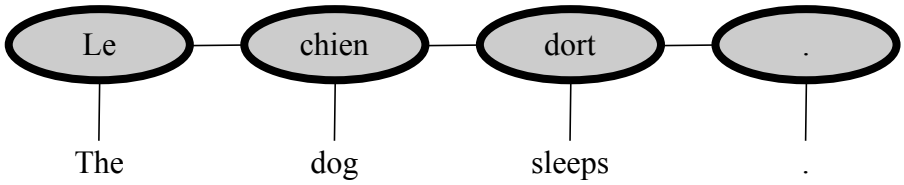
## 3.3 Structured Classifiers

There are tasks in natural language processing that cannot be adequately formulated as supervised classification tasks in the simple way that has been discussed earlier. Examples of tasks that require more sophisticated methods are syntactic parsing and translation between languages. One could think of parsing as a labeling task where the objective is to label a sentence with the appropriate syntactic tree. Likewise, the translation of a sentence could be seen as its label.

It is, however, easy to see that these approaches are deeply flawed. Firstly, there is an infinite number of syntactic trees and indeed an infinite number of sentences of finite length. Therefore, the label set would have to be infinite as well. Secondly, the data sparsity problem would be unmanageable. Just in order to see most relatively frequent syntax trees for moderately long English sentences, say twenty words long, we would need an unfathomable amount of training data.

[6] which may have internal structure as is seen in Section 7.13.

Figure 3.1: A translation from English to French




Instead of a simplistic classification approach, *structured* classifiers can be employed. Structured classifiers relate parts of the complex label such as a translation, syntax tree or sequential labeling with the input. They also learn how to piece together complex labels from simple constituents. A very simple (and probably very bad) translation software could learn how to translate isolated English words into French words and then learn how to combine French words into sentence as shown in Figure 3.1. Note that although both “Le” and “La” are perfectly good translations for “The”, only “Le” is usually possible before “chien”, which is a masculine French word.

In general, structured classifiers rely on two models, the unstructured and structured model. The unstructured model learns to relate simple labels such as words in a translation or nodes in a syntax tree with the input. In contrast, the structured model learns how to combine simple labels into complex labels such as entire translations or syntax trees. In practice, some models make a stricter division then other models.

Structured models are the main subject matter of this thesis and I will present two structured models, the Hidden Markov model and the Conditional random field in detail in Chapters **??** and **??**.

## 3.4 The Aim of Research – Improving the State of the Art

Like most language technological research, the work documented in this thesis aims at improving existing solutions for language processing. Specifically, my work is targeted at improving morphological taggers for morphologically rich languages. It is not entirely easy to define what constitutes an improvement to the field of morphological tagging or indeed any sub-field of language technology. Nevertheless, most researchers would probably agree that the following kinds of changes are improvements compared to existing approaches:

1. Improving labeling accuracy.
2. Speeding up estimation.
3. Speeding up tagging.
4. Reducing model size.
5. Clarifying the underlying theoretical foundations.
6. Simplifying implementation of taggers.
7. Uncovering best practices for building taggers.

Items 1 though 4 in the list above are *quantifiable* improvements. It is possible to perform experiments to measure the labeling accuracy, tagging speed, estimation speed and model size given by different morphological taggers and derive conclusions about the respective merits of the taggers. In contrast, the rest of the items in the list cannot be measured as easily.

Although, most probably would agree that clarifying theoretical foundations of a field is a substantial contribution, it may not be as easy to agree upon what constitutes a clarification. This could for example be dependent on the background of individual researchers. Similarly, one model might be more straightforward to implement than another model using some programming language, however, this can very well depend on the specific programming language and available libraries to some degree.

Because quantifiable improvements are easier to ascertain, this thesis focuses on demonstrating such improvements compared to other state of the art approaches. Nevertheless, I will also aim to show that the model demonstrated in the thesis is conceptually simpler than other state of the art approaches.

Although quantifiable improvements are easier to demonstrate than other improvements, there are still caveats. First of all, it is impossible to compare machine learning models directly. One can only compare implementations of the models. Because of differences between platforms even different implementations of the exact same model can have radically different run time on the same data. Moreover, bugs in the implementation of different models can reduce the accuracy or have sporadic effects on run time.

Besides practical concerns like dependence on implementation, there are also theoretical issues that interfere with measuring performance of different models. It is easy to say that the accuracy of one system is better than another system on *a specific data set*. This does, however, not imply that the accuracy is better on *all data sets*. In formal terms, we can only conduct experiments on samples of the distribution of all texts in a given language. Therefore, our experiments will yield results only in a probabilistic sense: it is likely that the labeling accuracy of one system is better than the accuracy of another, if the accuracy was better on the sample used for testing.

Using large test sets and test sets compared from a variety of different genres will probably give more reliable results. This is, however, also to some extent a debatable matter. Some methods are very accurate on the same genre that they were trained on but perform worse on other genres. Other methods instead perform well on average but, as a trade-off, cannot reach as high accuracy on a specific text domain. It is not easy to say which kind of system is preferable. This trade-off is called the bias variance trade-off **?** and it has bearing on measuring the performance difference of systems.

When using a high variance system, accuracy on different texts varies a lot. When instead using a system with high bias, the accuracy tends to vary much less.

When comparing two systems, it is not sufficient to simply look at the performance of the systems on a test set. If we measure the performance of the systems on a particular test, one of them will almost certainly perform better than the other regardless of whether there is an actual difference in the performances of the systems. The probability of exactly equal performance is simply very small.

The larger the test sets are, the more accurately the results of experiments will on average reflect the true performance of the systems. This is easy to see, because ultimately the test set will represent the entire domain. Unfortunately, the amount of test material is usually restricted and producing more test data might not be feasible[7].

[7] Especially when using standard data sets, one is restricted to the given amount of test data

An approach that is often used is splitting the test data into segments and performing several experiments – one for each segment. If one system outperforms the other system on most segments with a large margin, then we are more confident in saying that there is in fact a difference in the performance of the systems. If on the hand each system outperforms the other on roughly half of the segments, we might be inclined to doubt whether there is any real difference in performance between the systems. The higher the variance between the results, the larger the margins between the systems need to be in order for us to be able to conclude that there is a difference in performance. This argument can be made rigorous using statistical tests which measure the significance of the difference in performance of two systems.

The usual set up of statistical significance testing is to make a null hypothesis $H_0$ that the average performance of two systems is the same. After this a test statistic is computed. The test statistic is simply a real number whose value indicates the significance of the difference in performances between the systems. If the statistic is high enough, the null hypothesis can be discarded in favor of the alternative hypothesis that there is a genuine difference in performance between the systems. The test statistic incorporates information about the difference in performance of the systems on test data all segments as well as the variance of the performances.

In the work conducted presented in this thesis, I have used the Wilcoxon signed-rank test **?** to ascertain the significance of results. I use it instead of the T-test because it is not dependent on the fact that the distribution of differences in performance are normally distributed[8]. In practice it is less sensitive than the T-test.

[8] In practice it might be a fairly accurate assumption that the differences are normally distributed. This often holds for measurements **?**.

# Chapter 4

# Part-of-Speech Tagging

## 4.1 Background

## 4.2 Statistical Part-of-Speech Taggers

Morphological disambiguation and part-of-speech tagging are interesting tasks from the perspective of machine learning because they represent labeling tasks where both the set of inputs and outputs are unfathomably large. Since each word in a sentence $x = (x_1, \ ..., \ x_T)$ of length $T$ receives one label, the complete sentence has $n^T$ possible labels $y = (y_1, \ ..., \ y_T)$ when the POS label set has size $n$.

The exact number of potential English sentences of any given length, say ten, is difficult to estimate because all strings of words are not valid sentences[1]. However, it is safe to say that it is very large – indeed much larger than the combined number of sentences in POS annotated English language corpora humankind is likely to ever produce. Direct ML-estimation of the conditional distributions $p(y \mid x)$, for POS label sequences $y$ and sentences $x$, by counting is therefore impossible.

Because the POS labels of words in a sentence depend on each other, predicting the label $y_t$ for each position $t$ separately is not an optimal solution. Consider the sentence "The police dog me constantly although I haven't done anything wrong!".

The labels of the adjacent words "police", "dog", "me" and "constantly" help to disambiguate each other. A priori, we think that "dog" is a noun since the verb "dog" is quite rare. This hypothesis is supported by the preceding word "police" because "police dog" is an established noun–noun collocation. However, the next word "me" can only be a pronoun, which brings this interpretation into question. The fourth word "constantly" is an adverb, which provides additional evidence against a noun interpretation of "dog". In total, the evidence points toward a verb interpretation for "dog".

The disambiguation of the POS label for "dog" utilizes both so called *unstructured* and *structured* information. The information that "police dog" is a frequent nominal compound is unstructured information, because it refers only to the POS label (the prediction) of the word "dog". The information that verbs are much more likely to be followed by pronouns than nouns is a piece of structured information because it refers to the combination of several POS labels. Structured information refers to the combination of predic-

[1] Moreover, it is not easy to say how many word types the English language includes.

tions. Both kinds of information are very useful, but a model which predicts the label $y_t$ for each position in isolation cannot utilize structured information.

Even though structured information is useful, structure is probably mostly useful in a limited way. For example the labels of “dog” and “anything” in the example are not especially helpful for disambiguating each other. It is probably a sensible assumption that the further apart two words are situated in the sentence, the less likely it is that they can significantly aid in disambiguating each other. However, this does not mean that the interpretations of words that are far apart cannot depend on each other – in fact they frequently do. For example embedded clauses introduce long range dependencies inside sentences.

It is said that machine learning is sophisticated counting of co-occurrences. This statement applies extremely well to POS tagging. Counting is an adequate approach to capturing correlations between the labels of words inside a small window (in the league of five words), because most adjacent words indeed do depend on each other is some way. However, sophisticated counting fails for larger windows, because the number of meaningful dependencies in large windows is negligible in comparison to the space of possibilities.

## 4.3 Morphological Disambiguation

# Chapter 5

# Hidden Markov Models

AN INTRO

## 5.1 Example

I will illustrate Hidden Markov Models using an example. Imagine a person called Jill who is hospitalized and occupies a windowless room. The only way for her to know what is happening in the outside world is to observe a nurse who passes her room daily[1].

Suppose, Jill is interested in weather phenomena and she decides to pass time by guessing if it is raining outside. She bases her guesses on whether or not the nurse is carrying an umbrella. In other words, she predicts an unobserved variable, the weather, based on an observed variable, the nurse's umbrella.

There are several probabilistic models Jill might use. The simplest useful model assigns probability $1$ to the event of rain, if the nurse carries an umbrella, and assign it the probability $0$ otherwise. This simplistic model would certainly give the correct prediction most of the time, but Jill believes that she can do better.

Jill knows that people often carry an umbrella when it is raining. She also knows that they rarely carry one when the weather is clear. However, people sometimes do forget their umbrella on rainy days, perhaps because they are in a hurry. Moreover, people sometimes carry an umbrella even when it is not raining. For example the weather might be murky and they might anticipate rain. Therefore, Jill decides to reserve some probability, say $0.2$, for the event that the nurse is carrying an umbrella when the weather is clear. She reserves an equal probability for the event that the nurse arrives at work without an umbrella although it is in fact raining.

Without additional information, this more complicated model will give exactly the same MAP predictions as the simplistic one. Knowledge of meteorology, however, also factors in. Let us suppose Jill is a weather enthusiast and she knows that the probability of rain is $0.25$ a priori, making the probability of clear weather $0.75$. She also knows that the probability of rain increases markedly on days following rainy days at which time it is $0.7$. Similarly, the probability of clear weather increases to $0.9$ if the weather was clear on the previous day. Figure 5.1 summarizes these probabilities.[2]

[1] To make things simple, imagine the nurse never gets a day off.

[2] Since the author of this thesis has very little knowledge about meteorology, these probabilities are likely to be nonsense. The overall probability of rain and clear weather is, however, chosen to be the steady state of the Markov chain determined by the probabilities of transitioning between states. Consistency is therefore maintained.

| $\iota$ | |
|---|---|
| CLEAR | 0.75 |
| RAIN | 0.25 |

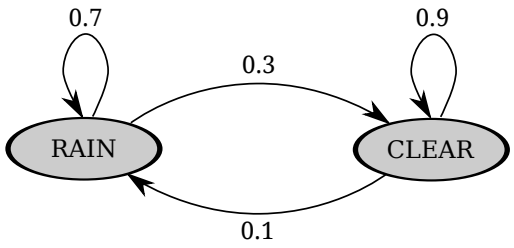
| $T$ | CLEAR | RAIN |
|---|---|---|
| CLEAR | 0.9 | 0.1 |
| RAIN | 0.3 | 0.7 |

| $E$ |  |  |
|---|---|---|
| CLEAR | 0.8 | 0.2 |
| RAIN | 0.2 | 0.8 |

Figure 5.1: Foo FIXME

Let us assume that Jill observes the nurse for one week. She sees the nurse carry an umbrella on all days except Tuesday. The MAP prediction given by the simplistic model is that Tuesday is clear and all other days are rainy. The more complex model will, however, give a different MAP prediction: the probability is maximized by assuming that all days are rainy. Under the more complex model, it is simply more likely that the nurse forgot to bring an umbrella on Tuesday.

Figure 5.2: Foo




The model Jill is using for weather prediction is called a Hidden Markov Model. It can be used to make predictions about a series of events based on indirect observations.

The HMM is commonly visualized as a directed graph. Each hidden state, for example Rain and Clear, represents a vertex in the graph. Transitions from one hidden state to another are represented by arrows labeled with probabilities. Figure 5.2 shows a graph representing the transition structure of the HMM outlined in Figure 5.1.

## 5.2 Formal Definition

Abstracting from the example above, an HMM is a probabilistic model that generates sequences of state-observation pairs. At each step $t$ in the generation process, the model generates an observation by sampling the *emission distribution* $\varepsilon_{y_t}$ of the current state $y_t$. It will then generate a successor state $y_{t+1}$ by sampling the *transition distribution* $\tau_{y_t}$ of state $y_t$. The first hidden state $y_1$ is sampled from the *initial distribution* $\iota$ of the HMM.

Since the succession of days is infinite for all practical purposes, there was no need to consider termination in the example presented in Figure 5.2. Nevertheless, many processes, such as sentences, do have finite duration. Therefore, a special *final state* $f$ is required. When the process arrives at the final state, it stops: no observations or successor states are generated.

Following Rabiner (1989), I formally define a *discrete* HMM as a structure $(Y,\ X,\ i,\ T,\ E,\ F)$ where:

1. $Y$ is the set of hidden states ($Y = \{\mathrm{CLEAR}, \mathrm{RAIN}\}$ in the example in Figure 5.1).

2. $X$ is the set of emissions, also called observations ( $X = \{$  ,  $\}$ in the example in Figure 5.1).

3. $\iota : Y \to \mathbb{R}$ is the initial state distribution, that is the probability distribution determining the initial state of an HMM process (array $\iota$ in Figure 5.1).

4. $T$ is the collection of transition distributions, $\tau_y : Y \to \mathbb{R}$, that determine the probability of transitioning from a state $y$ to each state $y' \in Y$ (array $T$ in Figure 5.1).

5. $E$ is the collection of emission distributions $\varepsilon_y : X \to \mathbb{R}$, which determine the probability of observing each emission $o \in X$ in state $y \in Y$ (array $E$ in Figure 5.1).

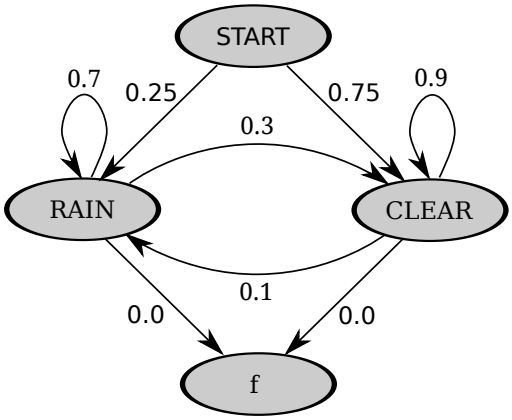
6. $f \in Y$ is the final state. The state $f$ emits no observations and there are no transitions from $f$.

The definition of HMMs in this thesis differs slightly from Rabiner (1989) since I utilize final states. Final states were used in for example **?**. Absorbing states **?** could also be used. FIXME.

Figure 5.3 is a more accurate description of the HMM in Figure 5.1 than Figure 5.2. The image has been augmented with initial distribution and a final state.

Because the progression of days is infinite for all practical purposes, the probability of transitioning to the final state $f$ in example 5.2 is 0 regardless of the current state. Hence, the probability of any single sequence of states and emissions is 0. Still, the probability of an initial segment of a state sequence may still be non-zero[3].

Figure 5.3: Foo




An HMM models a number of useful quantities:

1. The *joint probability* $p(x, y; \theta)$ of a observation sequence $x$ and state sequence $y$. This is the probability that an HMM with parameters $\theta$ will generate the state sequence $y$ and generate the observation $x_t$ in every state $y_t$.

2. The *marginal probability* $p(x; \theta)$ of an observation sequence $x$. This is the overall probability that the observation sequence generated by an HMM is $x$.

[3]The probability of an initial segment up to position $t$ can be computed using the forward algorithm, which is presented in Section 5.3.1.

3. The *conditional probability* $p(y \mid x; \theta)$ of a state sequence $y$ given an observation sequence $x$. That is, how likely it is that the model passes through the states in $y$ when emitting the observations in $x$ in order.

4. The *marginal probability* $p(z, t,\ x; \theta)$ *of state* $z$ *at position* $t$ when emitting the observation sequence $x$. That is, the probability of emitting observation sequence $x$ under the single constraint that the state at position $t$ has to be $z$.

To formally define these probabilities, let $\theta = \{\iota,\ T,\ E\}$ be the parameters of some HMM with observation set $X$ and hidden state set $Y$, $x = (x_1,\ ...,\ x_T) \in X^T$ be a sequence of observations and $y = (y_1,\ ...,\ y_T, y_{t+1} = f) \in Y^{T+1}$ a sequence of hidden states. Note, that the last state in $y$ has to be the final state $f$. Then the joint probability $p(x, y; \theta)$ of $x$ and $y$ given $\theta$ is defined by Equation (5.1).

$$p(x, y; \theta) = p(y; \theta) \cdot p(x \mid y; \theta) = \left( \iota(y_1) \cdot \prod_{t=1}^{T} \tau_{y_t}(y_{t+1}) \right) \cdot \prod_{t=1}^{T} \varepsilon_{y_t}(x_t) \tag{5.1}$$

Equation (5.1) is a product of two factors: the probability of the hidden state sequence $y$, determined by the initial and transition probabilities, and the probability of the emissions $x_t$ given hidden states $y_t$ determined by the emission probabilities.

FIXME: Talk about language models and stuff.

There is no limit on the number of hidden states in $Y$ that can emit a given observation. Therefore, it is quite possible that several state sequence $y \in Y^{T+1}$ can be generate the same sequence of observations $x \in X^T$. The marginal probability $p(x; \theta)$ of an observation sequence $x$ can be found by summing over all state sequences that could have generated $x$. It is defined by Equation (5.2).

$$p(x; \theta) = \sum_{y \in Y^{T+1},\ y_{T+1} = f} p(x, y; \theta) \tag{5.2}$$

Possibly the most important probability associated to the HMM is the conditional probability $p(y \mid x; \theta)$ of state sequence $y$ given observations $x$. This is an important quantity because maximizing $p(y \mid x; \theta)$ with regard to $y$ will give the MAP assignment of observation sequence $x$. It is defined by Equation (5.3).

$$p(y \mid x; \theta) = \frac{p(x, y; \theta)}{p(x; \theta)} \tag{5.3}$$

It is noteworthy, that $p(y \mid x; \theta) \propto p(x, y; \theta)$ because the marginal probability $p(x; \theta)$ is independent of $y$. Therefore, $y$ maximizes $p(y \mid x; \theta)$ if and only if, it maximizes $p(x, y; \theta)$. This facilitates inference.

Finally, the posterior marginal probability of state $z$ at position $t$ given the observation sequence $x$ is computed by summing, or marginalizing, over all state sequence $y$, where $y_t = z$. It is defined by Equation (5.4)

$$p(z, t,\ x; \theta) = \sum_{y' \in Y^{T+1},\ y'_t = z,\ y'_{T+1} = f} p(x, y'; \theta) \tag{5.4}$$

## 5.3 Inference

Informally, inference in HMMs means finding a maximally probable sequence of hidden states $y$ that might have emitted the observation $x$. As Rabiner (1989) points out, this statement is not strong enough to suggest an algorithm.

Maximally probable is an ambiguous term when dealing with structured models. It could be taken to mean at least two distinct things. The MAP assignment $y_{MAP}$ of the hidden state sequence is the most probable joint assignment of states defined by Equation (5.5) and depicted in Figure 5.4a.

$$y_{MAP} = \arg\max_{y \in Y^T} p(y \mid x; \theta) \tag{5.5}$$

Another possible definition would be the *maximum marginal* (MM) assignment. It chooses the most probable hidden state for each word considering all possible assignments of states for the remaining words. The MM assignment $y_{MM}$ is defined by Equation (5.6). Figure 5.4c shows the marginal for one position and state.

$$y_{MM} = \arg\max_{y \in Y^T} \prod_{t=1}^{T} p(y_t, t \mid x; \theta) \tag{5.6}$$

As Merialdo (1994) and many others have noted, the MAP and MM assignments maximize different objectives. The MM assignment maximizes the accuracy of correct states per observations whereas the MAP assignment maximizes the number of completely correct state sequences. Both objectives are important from the point of view of POS tagging. However, they are often quite correlated and, at least in POS tagging, it does not matter in practice which of the criteria is used (Merialdo, 1994). Most systems, for example Church (1988), Brants (2000), Halácsy et al. (2007), have chosen to use MAP inference.

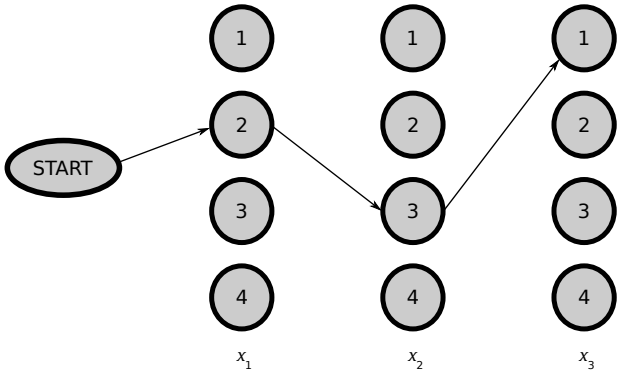
Although, MM inference is more rarely used with HMMs, computing the marginals is important both in unsupervised estimation of HMMs and discriminative estimation of sequence models. Therefore, an efficient algorithm for MM inference, the *forward algorithm*, is presented below.

There are a number of strongly related algorithms for both exact MAP and MM inference. The work presented in this thesis, uses the Viterbi algorithm for MAP inference and the forward-backward algorithm for MM inference (Rabiner, 1989). *Belief propagation*, introduced by Pearl (1982), computes the MM assignment and can be modified to compute the MAP assignment as well. For sequence models, such as the HMM where hidden states form a directed sequence, belief propagation is very similar to the forward-backward algorithm. It can, however, be extended to cyclic graphs (Weiss, 2000) unlike the Viterbi algorithm.

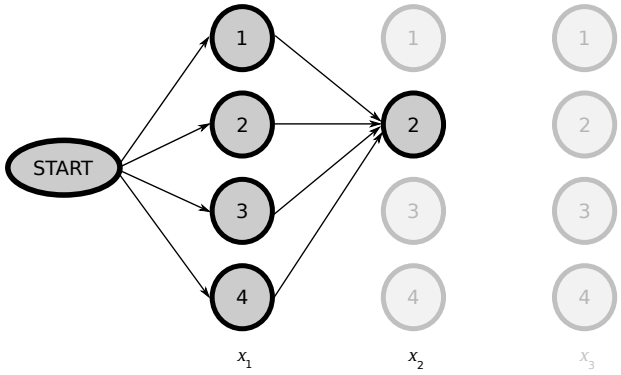
Since cyclic models fall beyond the scope of this thesis and both the Viterbi and forward-backward algorithms are amenable to well known optimizations, which are of great practical importance, I will not discuss belief propagation belief propagation further. Koller and Friedman (2009) gives a nice treatment of belief propagation and graphical models at large.

Before introducing the Viterbi and forward-backward algorithm, it is necessary to investigate the forward algorithm, which is used to compute the marginal probability of an observation and also as part of the forward-backward algorithm. The forward algorithm and Viterbi algorithm are closely related.

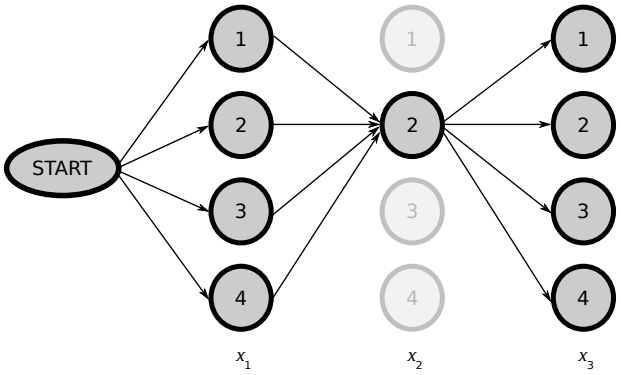
Figure 5.4: foo.




(a) Trellis and path.




(b) Forward path prefixes.




(c) Marginal paths.

### 5.3.1 The Forward Algorithm

Equations (5.5) and (5.6) reveal, that both MAP and MM inference require knowledge of the entire observation $x$. In the weather prediction example, observations are, however, always infinite. What kind of inference is possible in this case?

Even when we only know a prefix $x[1:t]$ (of length $t$) of the entire observation $x$, we can still compute the *belief state* (Boyen and Koller, 1998) of the HMM given the prefix. The belief state is in fact not a single state, but rather a distribution over the set of hidden states $Y$. It tells us how likely we are to be in state $z$ at time $t$, when we have emitted the prefix $x[1:t]$.

To compute the belief state at position $t$, we first need to compute the *forward probabilities* for each state $z \in Y$. The forward probability $\mathrm{fw}_{t,z}(x)$ of state $z$ at position $t$ is the probability of emitting prefix $x[1:t]$ and ending up in state $z \in Y$. For example, given an infinite observation $\{$  ,  ,  , ...$\}$, the forward probability $\mathrm{fw}_{3,\mathrm{RAIN}}$ is the probability that the third day is rainy, when the nurse carried an umbrella on the first and second days, but did not carry one on the third day.

I am going to make a technical but useful definition. The *prefix probability* of observation sequence $x = (x_1, \ldots, x_T)$ and state sequence $y = (y_1, \ldots, y_t)$ at position, where $t < T + 1$ is given by Equation (5.7).

$$p(x, y; \theta) = \left( \iota(y_1) \cdot \left( \prod_{u=1}^{t-1} \tau_{y_u}(y_{u+1}) \right) \cdot \prod_{u=1}^{t} \varepsilon_{y_u}(x_u) \right), \; t \leq T \tag{5.7}$$

When $t = T$, this is very similar to the joint probability of $x$ and $y$, but the final transition is missing.

Conceptually, the forward probability is computed by summing over the probabilities of all path prefixes up to position $t$, where the state at position $t$ is $z$, see Figure 5.4b. Formally, the forward probability is defined by Equation (5.8).

$$\mathrm{fw}_{t,z} = \sum_{y \in Y^t, \; y_t = z} p(x, y; \theta) \tag{5.8}$$

Comparing Equations (5.8) and (5.1) shows that the forward probability in a sense represents the probability of a prefix of observation $x$.

The belief state and posterior marginal distribution may seem similar. They are, however, distinct distributions because the belief state disregards all information about observation $x$ after position $t$. In contrast, the marginal distribution encompasses information about the entire observation. For example the marginal probability of RAIN at position 3 is likely to depend strongly on whether or not Jill observes the nurse carry an umbrella on the fourth day. However, this will have no impact on the belief state.

Figure 5.5 demonstrates a naive approach to computing the forward probabilities. Simply list all relevant state sequences, compute the probability of each sequence and sum the probabilities. Unfortunately, the naive approach fails for large $t$ because the number of distinct state sequences depends on the sequence length in an exponential manner.

The complexity of the naive algorithm is $|Y|^t$, which is infeasible. For example, $f_{20,\mathrm{RAIN}}(x)$ requires us to sum approximately 20 million probabilities and $f_{30,\mathrm{RAIN}}(x)$ entails summation of approximately 540 million probabilities. Since observation sequences in domains such as natural language processing frequently reach lengths of $100$, a more efficient approach is required.

The belief state can be computed in linear time with regard to $t$ and quadratic time with regard to $|Y|$ using the *forward algorithm* (Rabiner, 1989), which is in fact simply a recursive application of the right

Figure 5.5: foo

| $y_1$ | $y_2$ | $y_3$ | $p$ |
|---|---|---|---|
| CLEAR | CLEAR | CLEAR | $(0.75 \cdot 0.8 \cdot 0.9 \cdot 0.2) \cdot 0.9 \cdot 0.8 \approx 0.078$ |
| RAIN | CLEAR | CLEAR | $(0.25 \cdot 0.2 \cdot 0.3 \cdot 0.2) \cdot 0.9 \cdot 0.8 \approx 0.002$ |
| CLEAR | RAIN | CLEAR | $(0.75 \cdot 0.8 \cdot 0.1 \cdot 0.8) \cdot 0.3 \cdot 0.8 \approx 0.012$ |
| RAIN | RAIN | CLEAR | $(0.25 \cdot 0.2 \cdot 0.7 \cdot 0.8) \cdot 0.3 \cdot 0.8 \approx 0.007$ |
|  |  |  | |
| | | | $\approx 0.098$ |

distributive rule of algebra

$$a_1 \cdot b + ... + a_n \cdot b = (a_1 + ... + a_n) \cdot b$$

for real numbers $a_1$ up to $a_n$ and $b$.

Instead of computing the probability separately for each path, the forward probabilities for longer paths are computed incrementally using the forward probabilities of shorter paths. Examine Figure 5.5. By grouping rows one and two, as well as three and four into pairs, it is easy to see that

$$\text{fw}_{3,\text{CLEAR}} = (\text{fw}_{2,\text{RAIN}} \cdot \tau_{\text{RAIN}}(\text{CLEAR}) + \text{fw}_{2,\text{CLEAR}} \cdot \tau_{\text{CLEAR}}(\text{CLEAR})) \cdot \varepsilon_{\text{CLEAR}}(\text{  })$$

Generalizing, we get the recursion in Equation (5.9).

$$\text{fw}_{t,z} = \begin{cases} \iota(z) \cdot \varepsilon_z(x_1) & , t = 1 \\ \left( \sum_{z' \in Y} \text{fw}_{t-1,z'} \cdot \tau_{z'}(z) \right) \cdot \varepsilon_z(x_t) & , 1 < t \leq T \\ \sum_{z' \in Y} \text{fw}_{T,z'} \cdot \tau_{z'}(f) & , t = T+1,\ z = f. \end{cases} \tag{5.9}$$

The remaining forward probabilities $\text{fw}_{T+1,z}$, where $z \neq f$ are defined to be $0$.

The forward probability $f_{T+1,f} = p(x; \theta)$. In fact one of the principal applications for the forward algorithm is computing the marginal probability of an observation. The other central application is in the forward-backward algorithm, which computes the state marginals.

The forward algorithm is outlined in Algorithm 5.1. Assuming that accessing the data structures `x`, `i_prob`, `e_prob`, `tr_prob` and `trellis` is constant time, the complexity of the algorithm is dominated by the three nested loops on lines 27–37. This shows that the complexity of the forward algorithm is linear with regard to the length of the sequence and quadratic with regard to the size of the hidden state set.

Although, the forward algorithm depends linearly on the observation length, its quadratic dependence on the size of the hidden state set is problematic from the perspective of morphological disambiguation of morphologically complex languages, where the size of the hidden state set is measured in the hundreds or thousands for regular HMMs. When using second order HMMs presented below, the state set can grow to tens of thousands or millions, which can slow down systems to a degree that makes them infeasible in

practice. I will present partial solutions to these problems below.

### 5.3.2 The Viterbi Algorithm

Whereas the forward algorithm incrementally computes the marginal probability of an observation $x$, the Viterbi algorithm incrementally computes the MAP assignment for observation $x$.

A naive approach to finding the MAP assignment is to list all the hidden state paths, compute their probabilities and pick the one with the highest probability. Similarly as for the forward algorithm, the complexity of this approach is exponential with regard to the length of observation $x$.

Just as in the case of forward probabilities, the MAP assignment of hidden states for a prefix of the observation $x$ can be computed incrementally. Formally, the MAP assignment for a prefix $x[1 : t]$ is defined by equation (5.10) utilizing the joint prefix probability of $x$ and a state sequence $y$ of length $t$. Intuitively, it is the sequence of hidden states $y_{t,z}$ which maximizes the joint probability and ends at state $z$.

$$y_{t,z} = \underset{y \in Y^t,\ y_t = z}{\arg\max}\ p(x,\ y; \theta) \tag{5.10}$$

Comparing this equation with the definition of the forward probability $f_{t,z}$ in Equation 5.8, we can see that the only difference is that the sum has been changed to $\arg\max$.

I will now show that the MAP prefix $y_{t,z}$ can be computed incrementally in a similar fashion as the forward probability $f_{t,z}$. Suppose that $y_{t+1,z'} = (y_1,\ ...,\ y_t = z,\ y_{t+1} = z')$. I will show that $y_{t+1,z'}[1 : t] = y_{t,z}$. Let $y'$ be the concatenation of $y_{t,z}$ and $z'$. If $y_{t+1,z'}[1 : t] \neq y_{t,z}$, then

$$\begin{aligned} p(x,\ y_{t+1,z'}; \theta) &= p(x,\ y_{t+1,z'}[1 : t]; \theta) \cdot \tau_z(z') \cdot \varepsilon_{z'}(x_{t+1}) \\ &< p(x,\ y_{t,z}; \theta) \cdot \tau_z(z') \cdot \varepsilon_{z'}(x_{t+1}) \\ &= p(x, y'; \theta) \end{aligned}$$

This contradicts the definition in Equation (5.10)[4].

We now get Equation (5.11), which gives us a recursion.

$$y_{t+1,z} = \underset{z \in Y}{\arg\max} \begin{cases} \iota(z) \cdot \varepsilon_z(x_1) & , t = 1 \\ y_{t-1,z'} \cdot \tau_{z'}(z) \cdot \varepsilon_z(x_t) & , 1 < t \leq T \\ y_{T,z'} \cdot \tau_{z'}(f) & , t = T + 1,\ z = f. \end{cases} \tag{5.11}$$

### 5.3.3 Beam Search

As seen in the previous section, the complexity of the Viterbi algorithm depends on the square of the size of the hidden state set. This can be problematic when the set of hidden states is large, for example when the states represent POS tags in a very large label set or when they represent combinations of POS tags. When tagging, a morphologically complex language, the state set may easily encompass hundreds or even thousands of states.

*Beam search* is is a heuristic which prunes the search space explored by the Viterbi algorithm based on the following observation: in many practical applications, the number of hidden states which emit a given

[4] As long as we suppose that there is exactly one MAP prefix.

Algorithm 5.1: The forward algorithm in Python 3.

```
def forward(x, i_prob, e_prob, tr_prob):
    """
        x       - The observation as a list.
        i_prob  - Initial state distribution.
        e_prob  - Emission distributions.
        tr_prob - Transition distributions.

        Return the trellis of forward probabilities.
    """

    assert(not x.empty())

    trellis = {}

    # Indexing in python starts at 0.
    x_1 = x[0]
    T   = len(x) + 1

    # Set final state F. States are consequtive integers
    # in the range [0, F].
    F = len(i_prob) - 1

    # Initialize first trellis column.
    for z in range(F):
        trellis[(1,z)] = i_prob[z] * e_prob[z][x_1]

    # Set all except the final column.
    for t in range(2, T):
        trellis[(t, z)] = 0

        x_t = x[t - 1]

        for z in range(F):
            for s in range(F):
                trellis[(t, z)] = trellis[(t - 1, s)] * tr_prob[s][z]

            trellis[(t, z)] *= em_prob[z][x_t]

    # Set the last column.
    for z in range(s_count):
        trellis[(T + 1, z)] = trellis[(T, z)] * tr_prob[z][F]

    return trellis
```

observation with appreciable probability is small. This is true even when the total number of hidden states is very large. For example, when the states represent POS labels, a given word such as “dog” can usually only be emitted by a couple of states (maybe Noun and Verb in this case).

When the Viterbi algorithm maximizes (5.11) for $y_{t+1,z}$, a large number of histories $y_{t,z}$ can, therefore, be ignored.

Often a constant number, the *beam width*, of potential histories are considered in the maximization. The complexity of the Viterbi algorithm with beam search is $o(|Y| \cdot \log |Y|)$. The log factor stems from the fact that the histories need to be sorted before maximization.[5]

In addition to histories, the possible hidden states for output can also be filtered. The simplest method in to use a so called tag dictionary. These techniques are described in Section 5.6.

### 5.3.4 The Forward-Backward Algorithm

The Viterbi algorithm computes the MAP assignment for the hidden states efficiently. For efficiently computing the marginal probability for a every state and position (see Figure 5.4c), the forward-backward algorithm is required.

Intuitively, the probability that a state sequence $y$ has state $z \in Y$ at position $t$, that is the probability that $y_t = z$ is the product of the probabilities that the prefix $y[1:t]$ ends up at state $z$ and the probability that the suffix $y[t:T]$ originates at $z$.

The name forward-backward algorithm stems from the fact, that the algorithm essentially consists of one pass of the forward algorithm, which computes prefix probabilities, and another pass of the forward algorithm starting at the end of the sentence and moving towards the beginning which computes suffix probabilities. Finally, the forward and suffix probabilities are combined to give the marginal probability of all paths where the state at position $t$ is $z$. These passes are called the forward and backward pass.

Formally, the suffix probabilities computed by the backward pass are defined by equation (5.12).

Since a backward pass of the forward algorithm carries the same complexity as the forward pass, we can see that the complexity of the forward-backward algorithm is the same as the complexity of the forward algorithm, however, there is a constant factor of two compared to the forward algorithm.

$$b_{t,z} = \begin{cases} \left( \sum_{z' \in Y} t_z(z') \cdot b_{t+1,z'} \right) \cdot e_z(x_{t+1}) & , 1 < t < T \\ t_z(f) & , t = T+1,\ z = f. \end{cases} \tag{5.12}$$

### 5.3.5 Sparse Forward-Backward Algorithms

FIXME (Pal et al., 2006).

[5] Sequential decoding, an approximate inference algorithm, which was used for decoding before the Viterbi algorithm was in common use (Forney, 2005) is very similar to beam search. Indeed, it could be said that Viterbi invented an exact inference algorithm, which is once more broken by beam search.

## 5.4 Estimation

HMMs can be trained in different ways depending on the quality of the available data, but also on the task at hand. The classical setting presented by Rabiner (1989) is nearly completely unsupervised: the HMM is trained exclusively from observations. Some supervision is nevertheless usually required to determine the number of hidden states[6]. Additionally priors on the emission and transitions distributions may be required to avoid undesirably even distributions (Cutting et al., 1992, Johnson, 2007).

The unsupervised training setting has two important and interrelated applications:

1. Modeling a complex stochastic process from limited data. Here the HMM can be contrasted to a Markov chain (Manning and Schütze, 1999, 318–320), where each emission can occur in a unique state leading to a higher degree of data sparsity and inability to model under-lying structure.

2. Uncovering structure in data, for example part-of-speech induction (Johnson, 2007).

The classical method for unsupervised Maximum likelihood estimation of HMMs is the *Baum-Welch algorithm* (Rabiner, 1989), which is an instance of the *expectation maximization algorithm* (EM) (Dempster et al., 1977) for HMMs.

In POS tagging and morphological disambiguation, the supervised training scenario is normally used. Supervised training consists of annotating a text corpus with POS labels and estimating the emission and transition probabilities from the annotated data.

Straight-forward counting is sufficient to get the ML estimates for the transition and emission distributions. For example, one can simply count how often a determiner is followed by a noun, an adjective or some other class. Similarly, one can count how many often a verb label emits “dog” and how often the noun label emits “dog”.

Even in large training corpora, “dog” might very well never receive a verb label[7]. Nevertheless, “dog” can be a verb, for example in the sentence “Fans may dog Muschamp, but one thing’s for certain: he did things the right way off the field.”. To avoid this kind of problems caused by data sparsity, both emission and transition counts need to be smoothed.

### 5.4.1 Counting for Supervised ML Estimation

When HMMs are used in linguistic labeling tasks, such as part-of-speech tagging, they are usually estimated in a supervised manner. Each label is thought to represent a hidden variable, and the HMM models the transitions from one label type to another and the emission of words from each label type.

Figure 5.6 shows one sentence from the Penn Treebank (Marcus et al., 1993). The sentence is labeled with POS tags which are taken to be the hidden states of an HMM. When estimating an HMM tagger for the corpus, transitions probabilities, for example $t_{\texttt{NNP,VBZ}}$, and emission probabilities, for example $e_{\texttt{NNP}}(\texttt{Dutch})$ can in principle be computed directly from the corpus. For example the transition probability $t_{\texttt{NNP,VBZ}}$ and the emission probability $e_{\texttt{NNP}}(\texttt{Dutch})$ in the Penn Treebank are simply:

$$t_{\texttt{NNP,VBZ}} = \frac{\text{Count of POS tag pair } \texttt{NNP VBZ} \text{ in the corpus}}{\text{Count of POS tag } \texttt{NNP} \text{ in the corpus}} = \frac{4294}{114053} \approx 0.04$$

[6] Although methods for determining the number of states from the data exist (**?**).

[7] There are ten occurrences of “dog” in the Penn Treebank and all of them are analyzed as nouns.

| | |
|---|---|
| Mr. | NNP |
| Vinken | NNP |
| is | VBZ |
| chairman | NN |
| of | IN |
| Elsevier | NNP |
| N.V. | NNP |
| , | , |
| the | DT |
| Dutch | NNP |
| publishing | VBG |
| group | NN |
| . | . |

Figure 5.6: foo

$$e_{\texttt{NNP}}(\texttt{Dutch}) = \frac{\text{Number of times } \texttt{Dutch} \text{ was tagged } \texttt{NNP} \text{ in the corpus}}{\text{Count of POS tag } \texttt{NNP} \text{ in the corpus}} = \frac{14}{114053} \approx 1.2 \cdot 10^{-4}$$

Simple computation of co-occurrences is insufficient because of data-sparsity. Words do not occur with all POS tags in the training corpus and all compbinations of POS tags are never observed. Sometimes this is not a problem. For example, “Dutch” could never be a preposition. We know that the probability that a preposition state emits “Dutch” is $0$. However, there are at least three analyses that are perfectly plausible: noun (the Dutch language), adjective (property of being from The Nederlands) and proper noun (for example in the restaurant name “The Dutch”).

Since “Dutch” occurs only 14 times in the Penn Treebank, it is not surprising that all of these analyses do not occur. Specifically, the noun analysis is missing. An HMM based on direct counts will therefore never analyze “Dutch” as a noun.

It is tempting to think that missing analyses are a minor problem because they only occur for relatively rare words such as “Dutch”. Unfortunately, a large portion of text is made up from rare words. The problem therefore has very real consequences.

The usual approach is to use a family of techniques called *smoothing*. In smoohing, zero counts and all other counts are modified slightly to counter-act aprsity.

Smoothing of emission proabilities and transition probabilities differ slightly. For transition probabilities it is common practice to use counts of both tag pairs and single tags to estimate tag probabilities either in a back-off scheme (**?**) or using interpolation (Brants, 2000). Many sophisticated interpolation schemes can be used for example Kneser-Ney (**?**).

Many systems such as the HMM tagger by Brants (2000) do not smooth emission probabilities for words seen in the training corpus. However, words *not* seen in the training corpus, or out-of-vocabulary (OOV) words still require special processing. The simplest method is to estimate combined statistics for all words occurring one time in the training corpus and use these statistics for OOV words (**?**). Lidstone smoothing is another similar approach (**?**). Another approach would be to build models to guess the analysis of OOV words using the longest suffix of the word shared with a word in the training data.

Brants (2000) employs a specialized emission model for OOV words, which combines both approaches. It assigns a probability $p(y|x)$ for any label $y \in \mathcal{Y}$ and an arbitrary word $x$ based on suffixes $s_i$ of the word different lengths. The subscript $i$ indicates suffix length.

The model uses relative frequencies $\hat{p}(y|s_i)$ of label $y$ given each suffix $s_i$ of $x$ that occurs in the training data. The frequencies for different suffix lengths are recursively combined into probability estimates $p(y|s_i)$ using successive interpolations

$$p(y|s_{i+1}) = \frac{\hat{p}(y|s_{i+1}) + \theta \cdot p(y|s_i)}{1+\theta}.$$

The base case $p(y|s_0)$, for the empty suffix $s_0$, is given by the overall frequency of label type $y$ in the training data, i.e. $p(y|s_0) = \hat{p}(y)$, and the interpolation coefficient $\theta$ is the variance of the frequencies of label types in the training data

$$\theta = \frac{1}{|\mathcal{Y}|-1} \sum_{y \in \mathcal{Y}} (\hat{p} - \hat{p}(y))^2.$$

Here $\hat{p}$ is the average frequency of a label type. Finally, $p(y|x) = p(y|s_I)$, where $s_I$ is the longest suffix of $x$ that occurs in the training data. However, a maximal suffix length is imposed to avoid over-fitting. Brants (2000) uses $10$ for English. Moreover, the training data for the emission model is restricted to include only "rare" words, that is words whose frequency does not exceed a given threshold. This is necessary, because the distribution labels for OOV words usually differs significantly from the overall label distribution in the training data.

Brants (2000) does not discuss the choice of $\theta$ in great length. It is, however, instructive to consider the effect of the magnitude of $\theta$ on the emission model. When the variance of label type frequencies, that is $\theta$, is great, shorter suffixes and the prior distribution of label types will weigh more than long suffixes. This is sensible as (1) a high $\theta$ implies that the distribution of words into label types is eschewed a priori and (2) long suffix statistics are sparse and thus prone to overfitting. When $\theta$ is low, the prior distribution of word classes is closer to the even distribution. Therefore, there is no choice but to trust longer suffixes more.

For morphologically complex languages, the smoothing scheme employed by Brants (2000) may be inferior to a longest suffix approach utilized by Silfverberg and Lindén (2011) and Lindén (2009). This may happen because productive compounding. For languages with writing systems that radically differ from English, such as Mandarin Chinese, suffix based methods work poorly. Other methods, such as basing the guess on all symbols in the word, may work better. Huang et al. (2007) smooth symbol emission probabilities using geometric mean.

### 5.4.2 The EM algorithm for Unsupervised ML Estimation

The Baum-Welch, or Expectation Maximization, algorithm for HMMs is an iterative hill-climbing algorithm, that can be used to find locally optimal parameters for an HMM given a number of unlabeled independent training examples which are drawn from the distribution that is being modeled by the HMM. Here is a short outline of the algorithm:

1. Random initialize the emission and transition parameters.

2. Use the forward-backward algorithm to compute posterior marginals over input positions.

3. Use the posterior marginals as *soft counts* to estimate new parameters.

4. Repeat steps 2 and 3 until the improvement of likelihood of the training data is below a threshold value.

In step 2, the algorithm computes the maximally likely state distribution for each position given the current parameters. In step 3, the state distributions for each position in the input data are used to infer the MAP parameters for the HMM. Therefore, the marginal probability of the training data has to increase on every iteration of steps 2 and 3, or possible remain the same, if the current parameters are optimal.

There are no guarantees that the optimum found by the EM algorithm is global. Therefore, several random restarts are used and parameters giving the best marginal probability for the training data are used.

A more formal treatment of the EM algorithm can be found in Bilmes (1997).

## 5.5 Model Order

The standard HMM presented above is called a *first order model* because the next hidden state is determined solely based on the current hidden state. This model is easy to estimate and resistant to over-fitting caused by data-sparsity, but it fails to capture some key properties of language. For example, in the Penn Treebank, the probability of seeing a second adverb `RB` following and adverb is approximately, 0.08. If the first order assumption were valid, the probability of seeing a third adverb following two adverbs should also be 8%, however it is lower, around 5%.

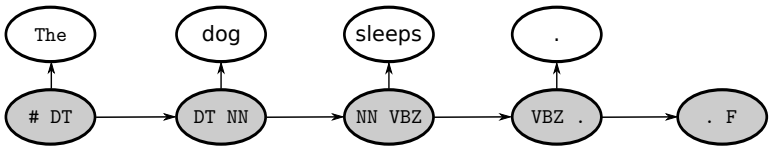



Figure 5.7: foo

The example with adverbs is poor at best, but it illustrates the kind of effect *second order* information can have. Second order HMMs are models where transitions are conditioned on two preceding hidden states. Equivalently, in POS tagging, the hidden states can be taken to be pairs of POS tags, e.g. `DT, NN`. In such a model transitions can only occur to a subset of the hidden state set. For example a transition from `DT, NN` to `NN, VBZ` is possible, but a transition to `JJ, NN` is impossible. Figure 5.7 illustrates a path with legal transitions.

Figure 5.7 implies that emissions in a second order model are conditioned on two labels like the transitions. However, many existing HMM based POS tagging systems such as Brants (2000) condition emissions only on one label, that is use $e_{t_i,t_{i-1}}(w_i) = p(w_i \mid t_i)$ instead of $e_{t_i,t_{i-1}}(w_i) = p(w_i \mid t_{i-1},\ t_i)$. The reason is probably data-sparsity. Therefore, these systems cannot be called HMMs in the strictest sense of the word. They are instead called trigram taggers.

Halácsy et al. (2007), show that it is possible to maintain the correct HMM formulation over-come the data sparseness problem and achieve gains over the more commonly used trigram tagger. However, they fail to describe the smoothing scheme used, which is crucial. This defect is partly remedied by the fact

that the system is open-source. One of the chief contributions of Silfverberg and Lindén (2011) was to investigate the effect of different ways of estimating the emission parameters in a generative trigram tagger paying attention to smoothing.

Increasing model order unfortunately leads to increased data sparsity, because the number of hidden states increases. Therefore, smoothing transition probabilities is even more important than in the first order case. Even using smoothing, third and higher order models tend to generalize to unseen data more poorly than lower order models because of over-fitting (**?**).

An alternative to increasing model order, is to use so called latent annotations (Huang et al., 2009) in an otherwise regular first order HMM. Conceptually, each label for example `NN` is split into a number of sub-states `NN1`, `NN2` and so on. Expectation maximization is used to train the model in a partly supervised fashion. Splitting labels, and indeed any increase in order, is probably works better for label sets with quite few labels. Otherwise, it will simply contribute data sparsity.

## 5.6 HMM taggers and Morphological Analyzers

The inventory of POS labels that are possible for a given word form tends to be small. For example the English "dog" can get two of the Penn Treebank POS tags singular noun `NN` and `VB` infinitive verb form. The remaining 43 POS tags can never label "dog". Consequently, in an HMM POS tagger, only the states corresponding to `VB` and `NN` should ever emit the word "dog".

A `tag dictionary` (Brants, 2000) can be used in combination with the Viterbi algorithm to limit the set of hidden states that could emit a word. The tag dictionary can be constructed from the training corpus. Additionally, an external lexical resource, such as a morphological analyzer, can be used. Such a lexical resource can help to compensate for missing statistics for OOV words. In the frequent setting, where most rare words have quite few analyses, this can have a substantial effect on tagging accuracy.

## 5.7 Enriching the emission and transition models

- Halácsy et al. (2007) and Silfverberg and Lindén (2011).

## 5.8 Problems

In the standard first order HMM an observation depends only on the current hidden state. If the hidden state is given, the observation cannot be influenced by the hidden states at other positions in the input or the other observations. This facilitates estimation and makes the system resistant to over-fitting, but at the same time it severly limits the set phenomena tht the model can capture.

An example from POS tagging the Penn Treebank illustrates this problem. The Penn Treebank has two labels for common nouns: `NN` for singular nouns and `NNS` for plural nouns.

- Local normalization.
- Inability to use word context.
- Label bias.

- The inability to use rich features, causes problems in domains other than POS tagging and in POS tagging for MR languages.
- Smoothing is difficult.
- Differences in performance between generative HMMs and discriminative approaches are even greater for morphologically complex languages and small training sets.
- OOV words may require different mechanisms depending on language again causing problems for MR lanuages.

### 5.8.1 Summary

A SUMMARY

# Chapter 6

# Finite-State Machines

This thesis deals primarily with machine learning but Silfverberg and Lindén (2011) presents a weighted finite-state implementation of Hidden Markov Models. Therefore, a quick overview of finite-state calculus is required.

## 6.1 Weighted Finite-State Automata

Automata can be seen as a formalization of the concept of algorithm. They represent a restricted type of algorithm in the sense that they can only operate on symbol strings and they only operation they perform is to accept or reject a string. Although, this might sound quite restrictive, it turns out that most computational problems can be formalized as such *decision problems* involving only acceptance or rejection of symbol strings.

Every automaton is associated with a *formal language* which is a (possible infinite) set of finite strings from the set of all strings of some finite alphabet. The automaton solves the decision problem of this language, i.e. accepts exactly those strings that belong to the language. *Weighted formal languages* are an extension to the concept of formal language, where each string should be assigned a weight. If the weights can be interpreted as probabilities, a weighted formal language over an alphabet $\Sigma$ can be seen as a probability distribution over the set of strings of the alphabet. However, this is not always possible because all weights cannot be interpreted as probabilities.

Several well know classes of algorithms exist. The most famous ones are Turing machines which, in a sense, subsume all existing automata **?**. In this thesis I have, however, utilized another class of automata, Finite-state machines. They are more restricted than Turing machines or another well know class, stack automata, because they utilize only a finite amount of memory. All real world implementations of automata of course utilize only a finite amount of memory.

The restriction on memory limits the set of problems that finite-state machines can solve. However, at the same time it allows for a rich algebra which allows one to combine finite-state machines to produce new finite-state machines.

The machine in Figure 6.1 accepts sequences of Penn Treebank labels which correspond to singular noun phrases that can have an adjective attribute (JJ) with an optional adverb (RB) expressing degree.

Typically finite-state machines are represented as state transition graphs. An example is given in Figure

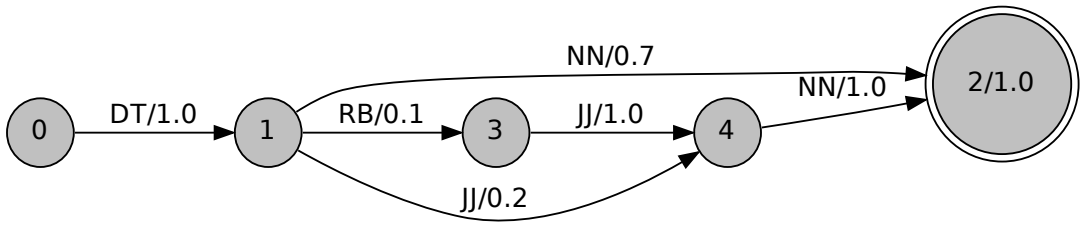



Figure 6.1: A finite-state machine accepting a subset of the singular noun phrases in Penn Treebank.

6.1. The machine has a set of numbered *states* (0, 1, 2, 3 and 4) and *transitions* from one state to another. The transitions are labeled using symbols from a finite alphabet (e.g. NN) and weights from a *weight semiring*, when the machine is weighted. The weight semiring in this example is the *probability semiring* Allauzen et al. (2007) where weights are probabilities that can be added and multiplied in the usual fashion.

Operation starts in the designated *start state* (0 in Figure 6.1) and it has to end in a *final state* (2 in Figure 6.1 marked with a double ring). A string is accepted, if and only if there is a sequence of transitions leading from the start state to a final state where the symbols in the transition labels spell out the input string and the product of the weights along the path is non-zero. For example the machine in Figure **??** accepts the string "DT NN" with weight 0.7 but rejects "DT JJ" because the string inds when the machine is in state 4 but that is not a finite state.

There may be several or no *accepting paths* for a given string. If there are several paths for some string, the machine is called *ambiguous*. More generally, a machine is called *non-deterministic* if some state has several out-going transitions with the same label. Trivially, ambiguous machines are non-deterministic. In the case of ambiguous machines, the weight of a string is the sum of the weights of all of its accepting paths or zero if there are no accepting paths.

**Weighted formal languages** Formally, weighted languages are mappings $M : \Sigma^* \to \mathbb{K}$ from the set of arbitrary strings $\Sigma^*$ of some finite alphabet $\Sigma$ into some *weight semiring* $(\mathbb{K}, \oplus, \otimes, \mathbb{0}, \mathbb{1})$ where $\mathbb{K}$ is a set of weights, $\oplus$ and $\otimes$ are addition and product operators for weights and $\mathbb{0} \in \mathbb{K}$ and $\mathbb{1} \in \mathbb{K}$ are the additive and multiplicative identity.

**Weight semirings** As mentioned above, the weight semiring in Figure 6.1 is the probability semiring, where weights belong to the set of non-negative reals $[0, \infty)$ and addition and product are given by the regular real addition and product operations. Even though probabilities reside in $[0, 1]$, the addition of probabilities can result in quantities that are larger than $1$. Because finite-state algebra does include operations that add probabilities, the weight set needs to include all non-negative reals.

The general weight semiring $(\mathbb{K}, \oplus, \otimes, \mathbb{0}, \mathbb{1})$ is an abstraction of the probability semiring. The set $\mathbb{K}$ is an arbitrary set but the operations $\oplus \to \mathbb{K} \times \mathbb{K} \to \mathbb{K}$ and $\oplus \to \mathbb{K} \times \mathbb{K} \to \mathbb{K}$ need to satify the following requirements Allauzen et al. (2007)

1. $(\mathbb{K}, \oplus, \mathbb{0})$ is a commutative and associative monoid.

2. $(\mathbb{K}, \otimes, \mathbb{1})$ is an associative monoid.

3. $\otimes$ distributes with respect to $\oplus$.

4. $\mathbb{0}$ is the annihilator of $\otimes$.

If $\oplus$ is a group operation, the semiring is in fact a ring. Many useful weight semirings are, however, not rings. Often the semiring $(\mathbb{K}, \oplus, \otimes, \mathbb{0}, \mathbb{1})$ is denoted simply as $\mathbb{K}$. Paralleling the regular sum notation $\Sigma_{i \in I} x_i$ and product notation $\prod_{i \in I} x_i$, I use the notations $\bigoplus_{i \in I} x_i$ and $\bigotimes_{i \in I} x_i$, where $I$ is a denumerable set.[1] Specifically $\oplus_{i \in \emptyset} x_i = \mathbb{0}$ and $\otimes_{i \in \emptyset} x_i = \mathbb{1}$.

Weights in the probability semiring and the addition and product operations have an intuitive interpretation but from a practical point of view the probability semiring is sub optimal. The biggest drawback is that repeated multiplication of probabilities gives rise to very small quantities and under-flow becomes a problem. Therefore, the so called *logarithmic semiring* is more commonly used. It can be derived by applying a logarithmic transformation $x \mapsto -\log(x)$ to the weights and operations in the probability semiring.

In the logarithmic semiring, numerical under-flow is not a problem but the addition operation given by $x \oplus y = -\log(\exp(-x) + \exp(-y))$ is resource intensive. Therefore, another semiring, the *tropical semiring*, is often used. The addition operation in the tropical semiring is given by $x \oplus y = \min(x, y)$. Computationally, this operation is light. A theoretical motivation is given by the fact that $\min$ preserves the magnitude of the sum although not its exact value. In practice, this is often sufficient **?**. All machines in this thesis use tropical weights.

**Weighted finite-state automata** Formally, a weighted finite-state automaton of weight semiring $\mathbb{K}$ is a structure $M = (\Sigma, Q, q_0, \rho, E)$ where

1. $\Sigma$ is a finite symbol set (also called an alphabet).

2. $Q$ is a finite set of states.

3. $q_0 \in Q$ is the unique start state.

4. $\rho : Q \to \mathbb{K}$ is the final weight map.

5. $T \subset Q \times (\Sigma \cup \{\epsilon\}) \times Q \times \mathbb{K}$ is a finite set of transitions.

The final weight map $\rho$ associates each state $q \in Q$ with a final weight. The final states of $M$ are $\{q \in Q \,|\rho(q) \neq \mathbb{0}\}$.

Each transition $x \in T$ consists of a source state $\mathrm{s}(x)$, an input symbol $\mathrm{i}(x)$, a target state $\mathrm{t}(x)$ and a weight $\mathrm{w}(x)$. The input symbol may be $\epsilon$ which denotes the empty symbol. For the single outgoing transition $x$ in state 4 in Figure 6.1, the source state $\mathrm{s}(x) = 4$, the input symbol $\mathrm{i}(x) =$ "NN", the target state $\mathrm{t}(x) = 2$ and the weight $\mathrm{w}(x) = 1.0$.

A sequence of transitions $x_1, ..., x_n \in T$ is a *path*, if $\mathrm{s}(x_1) = q_0$ and $\mathrm{t}(x_{k-1}) = \mathrm{s}(x_k)$ for all $k$. As a special case, the empty sequence is also a path. The weight of path $p = (x_1, ..., x_n)$ is $\mathrm{w}_M(p) = (\prod_{i=1}^{n} \mathrm{w}(x_i)) \otimes \rho(x_n)$ and the weight of the empty sequence is $\rho(q_0)$. A path $p$ is called successful when $\mathrm{w}_M(p) \neq \mathbb{0}$.

[1] Infinite sums and products are not defined in all semi rings, for example the probability semiring. In this case, it is often possible to augment the semirings with an infinity element $\infty$. This problem does not often cause problems in practice and will not be examined further.

| Operation | Symbol | Definition |
|---|---|---|
| Union | $M_1 \oplus M_2$ | $\mathrm{w}_{M_1 \oplus M_2}(s) = \mathrm{w}_{M_1}(s) \oplus \mathrm{w}_{M_2}(s)$ |
| Concatenation | $M_1 \otimes M_2$ | $\mathrm{w}_{M_1 \otimes M_2}(s) = \bigoplus_{s_1 s_2 = s} \mathrm{w}_{M_1}(s_1) \otimes \mathrm{w}_{M_2}(s_2)$ |
| Power | $M^n$ | $\mathrm{w}_{M^n}(s) = \bigoplus_{s_1 \ldots s_n = s} \mathrm{w}_M(s_1) \otimes \ldots \otimes \mathrm{w}_M(s_n)$ |
| Closure | $\bigoplus_{n=0}^{\infty} M^n$ | |
| Intersection | $M_1 \cap M_2$ | $\mathrm{w}_{M_1 \cap M_2}(s) = \mathrm{w}_{M_1}(s) \otimes \mathrm{w}_{M_2}(s)$ |

Table 6.1: A selection of operators from the finite-state algebra.

Each path $p = (x_1, ..., x_n)$ is associated with a unique, possibly empty, string $s \in \Sigma^*$ such that there is a subsequence $j_i, ..., j_m$ of $1, ..., n$ for which $i(x_{j_1}), ..., i(x_{j_m}) = s$ and $i(x_l) = \epsilon$ whenever $l \notin \{j_1, ..., j_m\}$. If the path $p$ is associated with the string $s$, it is called a *path of* $s$.

The set of paths of a string $s$ is denoted $P_s$ and the weight assigned to $s$ by the automaton $M$ is $\mathrm{w}_M(s) = \bigoplus_{p \in P_s} \mathrm{w}_M(p)$. When $P_s = \emptyset$, $\mathrm{w}_M(s) = \mathbb{0}$. The string $s$ belongs to the weighted language $L(M)$ accepted by $M$ if $L(M)(s) = \mathrm{w}_M(s) \neq \mathbb{0}$.

## 6.2 Finite-State Algebra

Finite-state machines use only a finite fixed amount of memory. Therefore, they cannot solve all computational problems. There is, for example, no finite-state machine which accepts only strings of prime number length. This can be proved using the pumping lemma of regular language (Sipser, 1996) which are the languages whose decision problems finite-state automata can solve.

Although the computational power of finite-state machines is limited, they are closed under a number of very useful operations which correspond to set theoretical operations of the languages recognized by the machines. The collection of these operations is called the *finite-state algebra*.

Table 6.1 gives an overview of a number of well known finite-state operations.

## 6.3 Finite-State Transducers

Language processing frequently requires translation of one signal such as speech or text into another signal, for example text in another language in the case of machine translation or annotated text in the case of part of speech tagging. These do not seem like the kinds of processing tasks that finite-state machines can solve because, as we saw above, finite-state machines solve decision problems.

Weighted Finite-state transducers are an extension of weighted finite-state automata. Whereas finite-state automata simply accept or reject a symbol sequence with a given weight, finite-state transducers simultaneously output another symbol sequence.

## 6.4 Weighted Finite-State Machines

- Weight semirings.
- Weighted Intersecting Composition

# Chapter 7

# Conditional Random Fields

## 7.1 Discriminative modeling

As seen in Chapter 5, the HMM POS tagger can be viewed as a state machine which alternates between sampling observations, that is words, from a state specific observation distributions, and sampling successor states, that is the morphological labels, from state specific transition distributions. Each emission and each successor state is conditioned *solely* on the current state. These independence assumptions are harsh. For example the Finnish cannot be adequately modeled, because the model does not include direct information about neighboring words in a sentence.

Although information about for example word collocations and orthography is quite useful in morphological labeling, it is often difficult to incorporate more elaborate contextual information in a generative model. As Sutton and McCallum (2012) note, there are two principal methods of doing this are improving the emissions model, which may be intractable because the model needs to account for complex dependencies between words in a sentence and their orthographic features, and replacing the usual emission model with for example a Naive Bayes' model.

In a domain closely related to morphological labeling, namely biomedical entity extraction,Ruokolainen and Silfverberg (2013) show that the Naive Bayes approach fails. In fact, adding richer context modeling such as adjacent words, worsens the performance of the modeling. One reason for this may be that overlapping information sources tend to cause the Naive Bayes model to give overly confident probability estimates (Sutton and McCallum, 2012). Combining them in a structured manner can therefore be problematic.

In contrast to generative sequence models, discriminative sequence models such as Maximum Entropy Markov Models (Ratnaparkhi, 1998) and Conditional Random Fields (Lafferty et al., 2001) can incorporate overlapping sources of information. They model the conditional distribution of label sequences $p(y \mid x)$ directly instead of modeling the joint distribution $p(x,\ y)$. Therefore, they do not need to model the distribution of sentences at all.

Discriminative models assign probabilities $p(y \mid x)$ for label sequences $y$ and word sequences $x$ by extracting local features from the input sentence and label sequence. Examples of local features include $x_t$ *is "dog" and* $y_t$ *is "NN"* and $y_{t-1}$ *is "DT" and* $y_t$ *is "NN"*. Each feature is associated with a parameter value and the parameter values are combined to give the conditional likelihood of the entire label sequence. Naturally, the label sequence which maximizes the conditional likelihood given sentence $x$ is the label

sequence returned by the discriminative POS tagger.

In generative models, emissions and transitions are independent. Both are determined exclusively based on the current label. Contrastingly, in discriminative models, there are no emissions or transitions. Instead, it is customary to speak about unstructured features relating exclusively to the input sentence, and structured features, which incorporate information about the label sequence. Simplifying a bit, discriminative models make no independence assumptions among features relating to a single position in the sentence. This allows for improved fit to training data but parameter estimation becomes more complex as we shall soon see. Moreover, discriminative models are more prone to over-fitting. This is of course the famous bias-variance trade-off (Geman et al., 1992).

## 7.2 Maximum Entropy Modeling

### 7.2.1 Example

## 7.3 Basics

I will now describe a CRF POS tagger from a practical point-of-view. The tagging procedure encompasses two stages: feature extraction and inference using an exact or approximate inference algorithm. Whereas inference in CRFs is very similar to inference in HMMs, we did not discuss feature extraction in association to HMMs. This is because HMM taggers use a restricted set of features (the current word and preceding labels).

| | | | | |
|---|---|---|---|---|
| $y$ | DT | NN | VBZ | . |
| $x$ | The | dog | eats | . |

Features are true logical propositions, which connect aspects of the input sentence with labels or parts of the label sequence. Given sentence $x$ and label sequence $y$ of length $n$, we extract features at every position $t$ in the sentence. For example at position $2$ in sentence $x$, we could extract *The current word $x_t$ is "dog" and the label is "NN"* and *The previous label is "DT" and the current label is "NN"*. We could, however, not extract the same feature *The current word is "dog" and the label is "NN"* at position $1$, because this proposition is false when $t = 1$ (the word at position 1 is "The" and the label is "VBZ").

Features are conjunctions of two parts: a feature template, for example *The current word is "dog"* and a label *the label is "NN"*. The set of features recognized by a CRF POS tagger contains all conjunctions $f\&y$ of feature templates $f$ present in the training data and labels $y$. For example, the tagger would know *The current word is "dog" and the label is "DT"* although it is unlikely that this feature would ever be observed in actual training data.

Ratnaparkhi (1996) introduced a rather rudimentary feature set and variations of this feature set are commonly used in the literature (for example Collins (2002) and Lafferty et al. (2001)). Let $W$ be the set of word forms in the training data. Additionally let $P$ and $S$ be the sets of prefixes and suffixes of maximal length $4$ of all words $w \in W$. Then, the Ratnaparkhi feature set contains the unstructured feature templates in Table 7.1 and the structured feature templates in Table 7.2.

These feature templates are then combined with all labels occurring in the training set. It is instructive to try to estimate the number of features when using a realistic training set of size around a million words.

| Feature template | Example |
|---|---|
| The current word is $w$ | The current word is “dog” |
| The current word has prefix $p$ | The current word has prefix “d-” |
| The current word has suffix $s$ | The current word has suffix “-og” |
| The current word contains a digit | |
| The current word contains a hyphen | |
| The current word contains a upper case letter | |
| The previous word is $w$ | The previous word is “The”. |
| The next word is $w$ | The next word is “eats”. |
| The word before the previous word is $w$ | |
| The word after the next word is $w$ | |

Table 7.1: foo

| Feature template | Example |
|---|---|
| The label of the previous word is $y$ | The label of the previous word is “NN”. |
| The label of the previous two words are $y'$ and $y$ | The labels of the two previous words are “DT” and “NN”. |

Table 7.2: foo

The number of features is be $O(\max(|Y|^2,\ |W|) \cdot |Y|)$. For small label sets and large training data, the bulk of the feature set tends to consist of unstructured features. However, for large label sets in the order of $1,000$ labels, there will be a significant number of structured features (one billion in this case). This necessitates either dropping second order structured features or using sparse feature representations. All structured features simply cannot be represented in memory. We will see techniques to circumvent these problems. Especially the averaged perceptron is essential.

It is common to represent the CRF using linear algebra. Each position $t$ in the sentence is represented as a vector $\phi_t$ whose dimensions correspond to the entire space of possible features. The selection of features is finite because it is limited by the training data. There are only finitely many word forms, suffixes, morphological labels and so on in the training data. The elements of each vector $\phi_t$ represent activations of features. In the present work all elements are either $0$ or $1$ mirroring false and true truth values, but other activations in $\mathbb{R}$ can also be used, if the truth values of the feature propositions exist on a non-binary scale.

In order to represent sentence positions as vectors, we need an injective index function $I$ which maps features onto consecutive integers starting at 1. For each feature $f$, $I(f)$ will be an element in $\phi_t$. In a concrete implementations, the index function $I$ could be implemented as a hash function.

Given a sentence $x$ and label sequence $y$, we can extract the set of features $F_t(x)$ for each position $t$ in $x$. Let $\phi_t \in \mathbb{R}^N$ be a vector defined by

$$\phi_t(i) = 1, \ \text{ if } i \leq N \text{ and } I(f) = i \text{ for some } f \in F_t$$

all other entries in $\phi_t$ are $0$.

Given a parameter vector $\omega \in \mathbb{R}^N$, the probability $p(y|x)$ is

$$p(y|x) \propto \prod_{t=1}^{T} \exp(\omega^\top \phi_t)$$

Specifically, the same parameter vector $\omega$ is shared by all sentence positions and the probability $p(y|x)$ is a log linear combination of parameter values in $\omega$.

Lafferty et al. (2001)

## 7.4 Logistic Regression

The simplest Conditional Random Field is the *Logistic Regression Model* (LRM). It is an unstructured probabilistic discriminative model. In this section, I will present a formal treatment of the LRM because it aids in understanding more general CRFs.

### 7.4.1 The Model

Regular linear regression models a *real valued quantity* $y$ based on independent variables $x_1$, ..., $x_n$. In contrast the LRM is a regression model which models *the probability* that an observation $x$ belongs to a class $y$ in a finite class set $Y$. For example, the logistic classifier can be used to model the probability of a tumor belonging to the class MALIGNANT or BENIGN. The probability is based on quantifiable information about the tumor such as its size, shape and the degrees of expression of different genes in the tumor cells. These quantifiable information sources are the *feature templates* of the logistic classifier and combined with class labels they make up the features of the model.

The material at hand deals with linguistic data where most information sources are binary, for example whether a word ends in suffix "-s" and whether a word is preceded by the word "an". In other domains such as medical diagnostics, more general features can be used. These can be real valued numerical measurements such as the diameter of a tumor. This treatment of logistic classifiers will focus on the binary valued case. When using binary features, we can equate the example $x$ with the set of feature templates $F_x \subset F$ that it *activates*, that is *Tumor diameter* $\geq$ *5 cm*, *Preceded by "an"* and so on. Examples that activate the exactly same feature templates will be indistinguishable from the point of view of the Logistic Regression model.

The logistic classifier associates each combination of a feature template and class with a unique feature and a corresponding real valued parameter. Intuitively, the logistic classifier models correlations of feature templates and classes by changing the parameter values of the associated features. For example, it might associate the feature template *Tumor diameter* $\geq$ *5 cm* more strongly with the class MALIGNANT than the class BENIGN if large tumors are cancerous more often than smaller ones. This could be reflected in the parameter values of the model that correspond to the features $f =$ *Tumor diameter* $\geq$ *5 cm and class is MALIGNANT* and $f' =$ *Tumor diameter* $\geq$ *5 cm and class is BENIGN* so that the parameter value for $f$ is greater than the parameter value for $f'$. In general parameter values, however, also depend on other features and feature correlations in the model. Therefore we can say that the parameter value of, $f$ will be guaranteed to be greater than the parameter value of $f'$ when $f$ is the sole feature template and the model

accurately reflects the original distribution of class labels among examples. In the general case, where there are several feature templates, this might fail to hold.

Formalizing the notation used in Section 7.3, let $F$ be a finite set of feature templates and $Y$ a finite set of classes. Each combination of feature template $f \in F$ and class $y \in Y$ corresponds to a unique feature. Therefore, the model will have $|F \times Y|$ features in total. Let $\theta$ be a real valued parameter vector in $\mathbb{R}^{|F \times Y|}$ and let I be a 1-to-1 index function which maps each combination of feature template and class onto the indexes of $\theta$, that is $1 \leq \mathrm{I}(f, y) \leq |F \times Y|$.

For each example $x$, let $F_x$ be the set of feature templates that $x$ activates and let $y \in Y$ be a class. Then the feature vector associated with $x$ and $y$ is $\phi(x, y) = \{0, 1\}^{|F \times Y|}$ defined by

$$\phi(x, y)[i] = \begin{cases} 1 & \text{iff } i = \mathrm{I}(f, y) \text{ for some } f \in F_x, \\ 0 & \text{otherwise.} \end{cases}$$

Now the conditional probability $p(y \mid x)$ defining the Logistic classifier is given by Equation (7.1). The equation defines a probability distribution over the set of classes $Y$ because each quantity $p(y \mid x; \theta)$ is a positive real and the quantities sum to 1.

$$p(y \mid x; \theta) = \frac{\exp(\theta^\top \phi(x, y))}{\sum_{z \in Y} \exp(\theta^\top \phi(x, z))} \tag{7.1}$$

Often a special bias term is used in Equation 7.1. It is

The Logistic Regression Model is log-linear as demonstrated by Equation 7.2, which represents the model using a cost function.

$$-\log p(y \mid x; \theta) = log(\mathrm{Z}(x; \theta)) - \theta^\top F_y(x), \text{ where } Z(x; \theta) = \sum_{z \in Y} \exp(\theta^\top F_z(x)) \tag{7.2}$$

Given labeled training data $\mathcal{D} = \{(x_1,\ y_1),\ ...,\ (x_n,\ y_n)\}$, there exist several options for estimating the parameters $\theta$. The most commonly used is the maximum likelihood, or equivalently minimum cost, estimation. The minimum cost estimate for the parameters $\theta$ using $\mathcal{D}$ is given by equation (7.3), where $\mathrm{Z}(\mathcal{D}; \theta) = \sum_{(x,\ y) \in \mathcal{D}} \mathrm{Z}(x; \theta)$ is the partition function of the entire data set $\mathcal{D}$.

$$\theta = \arg\min_{\theta'} \Big( \log(\mathrm{Z}(\mathcal{D}; \theta)) - \sum_{(x,\ y) \in \mathcal{D}} {\theta'}^\top F_y(x) \Big) \tag{7.3}$$

The probability $p(y \mid x; \theta)$ has exponential form, which means that the probability is proportional to a product of factors of the form $e^{ap}$, where $a$ is an activation (0 or 1) and $p$ is a parameter. This has three significant consequences:

1. The function $\theta \mapsto p(y \mid x; \theta)$ is smooth,
2. it is convex,
3. there exists a *unique* $\theta$ maximizing the likelihood of the training data $\mathcal{D}$, and
4. the model $p(y \mid x; \theta)$ is maximally unbiased.

Smoothness follows from the fact that each factor $a \mapsto e^{ap}$ is smooth and products and sums of smooth functions are smooth. Convexity of the likelihood follows by a straightforward application of the Hölder inequality . Property 3 is a consequence of properties 1 and 2 and Property 4 follows from the discussion in Section 7.2.

The log-linear form of the logistic classifier is motivated by the concept of maximum entropy, which was introduced in Subsection 7.2.1.

Although the maximization in Equation 7.1 cannot be solved for exactly in general, the convexity and smoothness of $p(y \mid x; \theta)$ mean that efficient numerical methods can be used for approximating the maximum to an arbitrary precision.

## 7.5 The Logistic Regression Model as a Classifier

Inference for a Logistic Regression Model means finding the probability of each class label $y \in Y$ given example $x$. The full computation of the probability is, however, not needed when the model is used as a classifier. For simply finding the class $y_{max}$ which maximizes the conditional likelihood in equation 7.4 given fixed parameters $\theta$ it is sufficient to maximize the numerator of $p(y \mid x; \theta)$.

$$y_{max} = \arg\max_{y \in Y} p(y \mid x; \theta) = \arg\max_{y \in Y} \frac{\exp(\theta^\top \phi(x, y))}{\mathrm{Z}(x; \theta)} = \arg\max_{y \in Y} \exp(\theta^\top \phi(x, y)) \tag{7.4}$$

To avoid underflow when using finite precision real numbers (such as floating-point numbers), the maximization is usually rephrased as the minimization of a cost-function in Equation 7.5

$$y_{max} = \arg\min_{y \in Y} \theta^\top \phi(x, y) \tag{7.5}$$

From a practical implementation perspective, the minimization in Equation 7.5 boils down to computing one inner product $\theta^\top \phi(x, y)$ for each label $y \in Y$ and finding the minimum. Using a suitable sparse approach each of the inner products can be computed in $\mathrm{O}(|F_x|)$ time, where $F_x$ is the set of feature templates activated by example $x$. Therefore, the worst-case complexity of classification is dependent on the size of the label set $Y$ and the number of feature templates $f \in F$, that is the complexity is $\mathrm{O}(|Y||F|)$.

## 7.6 Estimation

As seen in Section **??**, the Logistic Regression Model is smooth, that is the likelihood $p(y_1 \mid x_1; \theta) ... p(y_n \mid x_n; \theta)$ of a labeled training data set $\mathcal{D} = \{(x_1, y_1), ..., (x_n, y_n)\}$ is a smooth function of the parameter vector $\theta$. This allows formulation of the parameter estimation task for the Logistic Regression Model as a optimization task whose solution can be approximated using numerical techniques.

## 7.7 CRF – A Structured Logistic Classifier

## 7.8 Note on Terminology

- The term perceptron tagger is commonly found in the litterature, e.g. Collins (2002).
- The model is called a CRF.
- The estimator can be a ML, Perceptron, pseudo likelihood, pseudo perceptron...

## 7.9 Inference

- Inference using Viterbi.

## 7.10 Estimation

- Iterative process: label data, adjust parameters and repeat.
- Use SGD or L-BFGS (Vishwanathan et al., 2006) for ML estimation.
- Use averaged perceptron (Collins, 2002).
- Dev data for adjusting hyper parameters: number of iterations and regularization hyper-parameters, model order.
- Problems with exact estimation.
- Layered CRF Mueller et al. (2013), Weiss and Taskar (2010) and Charniak and Johnson (2005).

## 7.11 Approximate Estimation

- Beam search.
- Violation fixing.
- Label guessing.

## 7.12 CRF taggers and Morphological Analyzers

## 7.13 Enriching the Structured Model

- Utilizing sub-label structure.

# Chapter 8

# Lemmatization

## 8.1 Introduction

## 8.2 Data-Driven Lemmatization

- Classifier based: Grzegorz Chrupala and van Genabith (2008).
- Finite-state based: Lindén (2009).
- Combination: Hulden et al. (2014).

## 8.3 Combining Morphological Analyzers and Data-Driven Lemmatization

# Chapter 9

# Conclusions

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# Contributions

# Articles