Bayesian Ensembles of Crowds and Deep Learners for Sequence Tagging

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Abstract

Current methods for sequence tagging, a core task in NLP, are data hungry. Crowdsourcing is a relatively cheap way to obtain labeled data, but the annotators are unreliable. To address this, we develop a modular Bayesian method for aggregating sequence labels from multiple annotators and evaluate different models of annotator reliability. Our approach integrates black-box sequence taggers as components in the aggregation model to improve the quality of predictions. We evaluate our model on crowdsourced data for named entity recognition and information extraction tasks, showing that our sequential annotator model outperforms previous methods. We publish our code to encourage adaptation and reuse.

1 Introduction

The high demand for labeled training data in current NLP methods, particularly deep learning, is widely recognized (Zoph et al., 2016; Rastogi et al., 2016; Gormley et al., 2014). A common NLP task that has benefited from deep learning is *sequence tagging*, which involves classifying sequences of tokens for tasks such as named entity recognition, part-of-speech tagging, or information extraction. Neural network sequence taggers are typically trained on tens of thousands of documents (Ma and Hovy, 2016; Lample et al., 2016), which presents a challenge when facing new domains or tasks, where obtaining labels is often time-consuming or costly.

Labeled data can be obtained cheaply by crowdsourcing, in which large numbers of untrained workers annotate documents instead of more expensive experts. For sequence tagging, this results in multiple sequences of unreliable labels for each document. Probabilistic methods for aggregating these labels have been shown to be more accurate than simple heuristics such as majority voting (Raykar et al., 2010; Sheshadri and Lease, 2013; Rodrigues et al., 2013; Hovy et al., 2013). However, work on sequence tagging is limited and existing methods cannot model dependencies between the annotators' labels and hence miss error patterns such as a tendency to label overly long spans (Rodrigues et al., 2014; Nguyen et al., 2017). In this paper, we remedy this by proposing a sequential annotator model and applying it to tasks that follow a *beginning, inside, outside* (*BIO*) scheme, in which the first token in a span of type 'x' is labeled 'B-x', subsequent tokens are labeled 'I-x', and tokens outside spans are labeled 'O'.

When learning from noisy or small datasets, commonly-used methods based on maximum likelihood estimation may produce over-confident predictions (Xiong et al., 2011; Srivastava et al., 2014). In contrast, Bayesian inference accounts for model uncertainty when making predictions, and enables hyperparameter tuning in unsupervised scenarios through Bayesian model selection (Bishop, 2006). Unlike alternative methods that optimize the values for model parameters, Bayesian inference integrates over all possible values of a parameter, weighted by a prior distribution that captures background knowledge. The resulting posterior probabilities improve downstream decision making as they include the probability of errors due to a lack of knowledge. For example, during active learning, posterior probabilities assist with selecting the most informative data points (Settles, 2010). We therefore develop a Bayesian sequence combination method, building on prior work that has demonstrated the advantages of Bayesian inference for aggregating unreliable classifications (Kim and Ghahramani, 2012; Simpson et al., 2013; Felt et al., 2016; Paun et al., 2018).

Aggregated label quality can be improved by

modeling the text features as well as the annotators (Simpson et al., 2015; Felt et al., 2016). For complex tasks such as sequence tagging, we may wish to exploit existing state-of-the-art models, such as neural networks that do not account for model uncertainty. In this paper, we show how to integrate existing black box methods into the aggregation model to construct ensembles of deep learners and human annotators. Our method learns the reliability of each black box method and avoids the need to aggregate crowdsourced data using a separate pre-processing step before training a sequence tagger.

This paper provides the following contributions:

- We propose *Bayesian sequence combination (BSC)*, a method for aggregating sequence labels from multiple annotators that models sequential dependencies between tags
- A technique for wrapping existing black-box sequence taggers into the aggregation model to improve the quality of aggregated labels
- Theoretical and empirical comparisons of annotator models for sequence tagging, including the novel *seq* model of sequential annotations

The following sections discuss related work, annotator models for sequence tagging, our BSC model, and our variational inference approach that enables us to integrate existing sequence taggers. Then, we evaluate a range of Bayesian and non-Bayesian aggregation methods with simulated annotators and two crowdsourced NLP datasets, showing that our sequential model consistently outperforms the previous state-of-the-art, and benefits from the inclusion of automated sequence taggers. We make all of our code freely available[1]

1.1 Related Work

Sheshadri and Lease (2013) benchmarked several aggregation models for non-sequential classifications, obtaining the most consistent performance from that of Raykar et al. (2010), who model the reliability of individual annotators using probabilistic confusion matrices, as proposed by Dawid and Skene (1979). Simpson et al. (2013) showed that a Bayesian variant of of Dawid and Skene (1979)'s model, independent Bayesian classifier combination (*IBCC*) (Kim and Ghahramani, 2012) can outperform maximum likelihood approaches and simple heuristics when combining crowds of image annotators. To reduce the number of parameters in multi-class problems, Hovy et al. (2013) proposed *MACE*, and showed that it performed better under a Bayesian treatment on NLP tasks. Paun et al. (2018) further illustrated the advantages of Bayesian models of annotator ability on NLP classification tasks with different levels of annotation sparsity and noise. We expand this work by detailing the relationships between several annotator models and extending them to sequential classification. Here we focus on the core annotator representation, rather than extensions for clustering annotators (Venanzi et al., 2014; Moreno et al., 2015), modeling their dynamics (Simpson et al., 2013), adapting to task difficulty (Whitehill et al., 2009; Bachrach et al., 2012), or time spent (Venanzi et al., 2016).

To accout for disagreement between annotators when training a sequence tagger, Plank et al. (2014) modify the loss function of the learner. However, typical cross entropy loss naturally accommodates probabilities of labels as well as discrete labels (Bekker and Goldberger, 2016). A contrasting approach is *CRF-MA* (Rodrigues et al., 2014), a CRF-based model that assumes only one annotator is correct for any given label. Recently, Nguyen et al. (2017) proposed a hidden Markov model (HMM) approach that outperformed CRF-MA, called *HMM-crowd*. Both CRF-MA and HMM-crowd use simpler annotator models than Dawid and Skene (1979) that do not capture the effect of sequential dependencies on annotator reliability. Neither CRF-MA nor HMM-crowd use a fully Bayesian approach. In this paper, we develop a sequential annotator model and a fully Bayesian method for aggregating sequence labels.

While HMM-crowd uses only a simple conditional independence model of text features, Nguyen et al. (2017) and Rodrigues and Pereira (2018) also train neural network sequence taggers directly on crowdsourced data by adding a layer to handle worker reliability. However, the proposed approaches did not outperform either CRF-MA (Rodrigues and Pereira, 2018) or HMM-crowd (Nguyen et al., 2017). A similar approach by Albarqouni et al. (2016) integrates a CNN classifier for image annotation into an aggregation method based on expectation maximization (EM) (Dempster et al., 1977). Yang et

[1] http://github.com/******

al. (2018) adapt a Bayesian neural network so that it can be trained concurrently with an annotator model, also using EM. In contrast to previous work, we do not require neural networks to be adapted, nor assume that their predictions are reliable when aggregating annotations. Instead, we propose to learn the reliability of existing sequence taggers, allowing untrusted, off-the-shelf taggers to enhance the performance of the aggregation method.

2 Modeling Sequential Annotators

When combining multiple annotators with varying skill levels, we can improve performance by modeling their individual reliability. Here, we describe several existing models that do not consider dependencies between annotations in a sequence, then provide an extension that captures sequential dependencies. Each of the approaches presented employs a different function, A, to model the likelihood of the annotator choosing the label c_τ given the true label, t_τ, for token τ.

Accuracy model (acc): simply models the annotator's accuracy, π, as follows:

$$A = p(c_\tau = i | t_\tau = j, \pi) = \begin{Bmatrix} \pi & \text{where } i = j \\ \frac{1-\pi}{J-1} & \text{otherwise} \end{Bmatrix}, \tag{1}$$

where c_τ is the label given by the annotator for token τ, t_τ is its true label and J is the number of classes. This is the basis of several previous methods (Donmez et al., 2010; Rodrigues et al., 2013). It assumes reliability is constant, which means that when one class label is far more common than others, a spammer who always selects the most common label will nonetheless have a high π.

MACE (Hovy et al., 2013): assumes constant accuracy, π, but when an annotator is incorrect, they label according to a spamming distribution, $\boldsymbol{\xi}$, that is independent of the true label, t_τ.

$$\begin{aligned} A &= p(c_\tau = i | t_\tau = j, \pi, \boldsymbol{\xi}) \\ &= \begin{Bmatrix} \pi + (1-\pi)\xi_j & \text{where } i = j \\ (1-\pi)\xi_j & \text{otherwise} \end{Bmatrix}. \end{aligned} \tag{2}$$

This addresses the case where spammers choose the most common label when the classes are imbalanced. While MACE can capture spamming patterns, it does not explicitly model different rates of errors per class. This could be an issue for sequence tagging using the BIO encoding, for example, if an annotator frequently labels longer spans than the true spans by starting the spans early. In this case, they may more frequently mis-label the 'B' tokens than the 'I' or 'O' tokens, which cannot be modeled by MACE.

Confusion vector (CV): this approach learns a separate accuracy for each class label (Nguyen et al., 2017) using parameter vector, $\boldsymbol{\pi}$, of size J:

$$A = p(c_\tau = i | t_\tau = j, \boldsymbol{\pi}) = \begin{Bmatrix} \pi_j & \text{where } i = j \\ \frac{1-\pi_j}{J-1} & \text{otherwise} \end{Bmatrix}. \tag{3}$$

This model does not capture spamming patterns where one of the incorrect labels has a much higher likelihood than the others.

Confusion matrix (CM) (Dawid and Skene, 1979): this model can be seen as an expansion of the confusion vector so that $\boldsymbol{\pi}$ becomes a $J \times J$ matrix with values given by:

$$A = p(c_\tau = i | t_\tau = j, \boldsymbol{\pi}) = \pi_{j,i}. \tag{4}$$

This requires a larger number of parameters, J^2, compared to the $J + 1$ parameters of MACE or J parameters of the confusion vector. CM can model spammers who frequently chose one label regardless of the ground truth, as well as annotators with different error rates for each type of 'B-x', 'I-x' and 'O' label. For example, if an annotator is better at detecting type 'x' spans than type 'y', or if they frequently mis-label the start of a span as 'O' when the true label is 'B-x', but are otherwise accurate. However, the confusion matrix ignores dependencies between annotations in a sequence, such as the fact that an 'I' cannot immediately follow an 'O'.

Sequential Confusion Matrix (seq): we introduce a new extension to the confusion matrix to model the dependency of each label in a sequence on its predecessor, giving the following likelihood:

$$A = p(c_\tau = i | c_{\tau-1} = \iota, t_\tau = j, \boldsymbol{\pi}) = \pi_{j,\iota,i}, \tag{5}$$

where $\boldsymbol{\pi}$ is now three-dimensional with size $J \times J \times J$. In the case of disallowed transitions, e.g. from $c_{\tau-1}$ ='O' to c_τ ='I', the value $\pi_{j,c_{\tau-1},c_\tau} = 0$, $\forall j$ is fixed *a priori*. The sequential model can capture phenomena such as a tendency toward overly long sequences, by learning that $\pi_{O,O,O} > \pi_{O,I,O}$, or a tendency to split spans by inserting 'B' in place of 'I' by increasing the value of $\pi_{I,I,B}$ without affecting $\pi_{I,B,B}$ and $\pi_{I,O,B}$.

The annotator models we presented, which include the most widespread models for NLP annotation tasks, can therefore be seen as extensions of one another. The next section shows how these models can be used as part of a model for aggregating sequential annotations. The experiments in Section 5 test whether the more expressive seq annotator model, which has more parameters to learn, is beneficial in a realistic setting.

3 A Model for Bayesian Sequence Combination

The generative story for our approach, *Bayesian sequence combination (BSC)*, is as follows. We assume a transition matrix, $\boldsymbol{T}$, where each entry is $T_{j,\iota} = p(t_\tau = \iota | t_{\tau-1} = j)$. We draw each row of the transition matrix, $T_j \sim \text{Dir}(\boldsymbol{\gamma}_j)$, where Dir is the Dirichlet distribution. For each document, n, in a set of N documents, we draw a sequence of class labels, $\boldsymbol{t}_n = [t_{n,1}, ..., t_{n,L_n}]$, of length L_n, from a categorical distribution: $t_{n,\tau} \sim \text{Cat}(\boldsymbol{T}_{t_{n,\tau-1}})$. The set of all labels for all documents is referred to as $\boldsymbol{t} = \{\boldsymbol{t}_1, ..., \boldsymbol{t}_N\}$.

For each of K annotators, we choose one of the annotator models defined in Section 2. The number of parameters depends on the choice of model: for *acc*, only one parameter, $\pi^{(k)}$, is drawn for annotator k; for *MACE*, we draw a single value $\pi^{(k)}$ and a vector $\xi^{(k)}$ of length J, while for *CV* we draw J independent values of $\pi_j^{(k)}$, and for *CM* we draw a vector $\boldsymbol{\pi}_j^{(k)}$ of size J for each true label value $j \in \{1, ..., J\}$; in the case of *seq*, we draw vectors $\boldsymbol{\pi}_{j,\iota}^{(k)}$ for each true label value for each previous label value, ι. All parameters of these annotator models are probabilities, so are drawn from Dirichlet priors. We refer to the set of hyperparameters for k's annotator model as $\boldsymbol{\alpha}^{(k)}$. Given its parameters, the annotator model defines a likelihood function, $A^{(k)}(t_{n,\tau}, \boldsymbol{c}_{n,\tau}, \boldsymbol{c}_{n,\tau-1})$, where $\boldsymbol{c}_{n,\tau}$ is the τth label of document n. The argument $\boldsymbol{c}_{n,\tau-1}$ is only required if $A^{(k)}$ is an instance of *seq* and is ignored by the other annotator models. We draw annotator k's label for each token τ in each document n according to:

$$c_{n,\tau}^{(k)} \sim \text{Cat}([A^{(k)}(t_{n,\tau}, 1, \boldsymbol{c}_{n,\tau-1}^{(k)}), ..., A^{(k)}(t_{n,\tau}, J, \boldsymbol{c}_{n,\tau-1}^{(k)})]). \quad (6)$$

The annotators are assumed to be conditionally independent of one another given the true labels, $\boldsymbol{t}$, which means that their errors are assumed to be uncorrelated. This is a strong assumption when considering that the annotators have to make their decisions based on the same input data. However, in practice, dependencies do not usually cause the most probable label to change (Zhang, 2004), hence the performance of classifier combination methods is only slightly degraded, while avoiding the complexity of modeling dependencies between annotators (Kim and Ghahramani, 2012).

Black-box Sequence Taggers: As an extension to our model, we can integrate S automated methods as additional noisy annotators. In comparison to human annotators, sequence taggers can quickly label large numbers of documents, providing a cheap source of additional annotations across the whole dataset. We model each sequence tagger, s, using an annotator model, $B^{(s)}$, of one of the types described in Section 2 (analogous to $A^{(k)}$ for a human annotator), with hyperparameters $\boldsymbol{\beta}^{(s)}$. Each sequence tagger generates a sequence of labels, $\boldsymbol{d}_n^{(s)}$, for each document n (analogous to $\boldsymbol{c}_n^{(k)}$ produced by human annotators) according to:

$$d_{n,\tau}^{(s)} \sim \text{Cat}([B^{(s)}(\boldsymbol{t}_{n,\tau}, 1, d_{n,\tau-1}^{(s)}), ..., B^{(s)}(\boldsymbol{t}_{n,\tau}, J, d_{n,\tau-1}^{(s)})]). \quad (7)$$

In the generative model, we draw a sequence of text tokens, $\boldsymbol{x}_n$, from a likelihood, $p\left(\boldsymbol{x}_n | \boldsymbol{d}_n^{(s)}, \boldsymbol{\theta}^{(s)}\right)$, given internal parameters, $\boldsymbol{\theta}^{(s)}$, and label sequence, $\boldsymbol{d}_n^{(s)}$. This likelihood is defined by the black-box sequence tagger. If the sequence tagger is Bayesian, its parameters, $\boldsymbol{\theta}^{(s)}$, may also be drawn from an unknown prior distribution. However, since we are treating the tagger as a black box, we do not need to know these internal details. In the next section, we explain how we can avoid computing this likelihood explicitly during inference, and instead use only the sequence tagger's existing training and prediction functions to learn $\boldsymbol{\theta}^{(s)}$ in parallel with the parameters of the BSC model. Like the human annotators, each sequence tagger is assumed to produce labels that are conditionally independent of the other sequence taggers given $\boldsymbol{t}$.

Joint distribution: the complete model can be

represented by the joint distribution, given by:

$$p(\boldsymbol{t}, \boldsymbol{A}, \boldsymbol{B}, \boldsymbol{T}, \boldsymbol{\theta}, \boldsymbol{c}, \boldsymbol{d}, \boldsymbol{x}|\boldsymbol{\alpha}, \boldsymbol{\beta}, \boldsymbol{\gamma}) \tag{8}$$
$$= \prod_{k=1}^{K} \left\{ p(A^{(k)}|\boldsymbol{\alpha}^{(k)}) \prod_{n=1}^{N} p(\boldsymbol{c}_n^{(k)}|A^{(k)}, \boldsymbol{t}) \right\}$$
$$\prod_{j=1}^{J} p(\boldsymbol{T}_j|\boldsymbol{\gamma}_j) \prod_{n=1}^{N} \prod_{\tau=1}^{L_n} p(\boldsymbol{t}_n|\boldsymbol{T}_{t_{n,\tau-1}}) \prod_{s=1}^{S} \Big\{ p(\boldsymbol{\theta}^{(s)})$$
$$p(B^{(s)}|\boldsymbol{\beta}^{(s)}) \prod_{n=1}^{N} \Big\{ p(\boldsymbol{x}|\boldsymbol{d}^{(s)}, \boldsymbol{\theta}^{(s)}) p(\boldsymbol{d}^{(s)}|B^{(s)}, \boldsymbol{t}) \Big\} \Big\},$$

where each term is defined by the distributions of the generative model described in this section.

4 Inference using Variational Bayes

Given a set of annotations, $\boldsymbol{c} = \{\boldsymbol{c}^{(1)}, .., \boldsymbol{c}^{(K)}\}$, from K annotators, our aim is to obtain a posterior distribution over sequence labels, $\boldsymbol{t}$. To do this, we employ *variational Bayes* (*VB*) (Attias, 2000). In comparison to other Bayesian approaches such as Markov chain Monte Carlo (MCMC), VB is often faster, readily allows incremental learning, and provides easier ways to determine convergence (Bishop, 2006). Unlike maximum likelihood methods such as standard expectation maximization (EM), VB considers prior distributions and accounts for parameter uncertainty in a Bayesian manner. The trade-off is that VB requires us to approximate the posterior distribution. Here, we apply the *mean field* assumption to assume a variational approximation that factorizes between subsets of parameters or latent variables, so that each subset, z, has a *variational factor*, $q(z)$:

$$p(\boldsymbol{t}, \boldsymbol{A}, \boldsymbol{B}, \boldsymbol{T}, \boldsymbol{\theta}|\boldsymbol{c}, \boldsymbol{x}, \boldsymbol{\alpha}, \boldsymbol{\beta}, \boldsymbol{\gamma}) \approx \prod_{k=1}^{K} q(A^{(k)})$$
$$\prod_{j=1}^{J} q(\boldsymbol{T}_j) \prod_{n=1}^{N} q(\boldsymbol{t}_n) \prod_{s=1}^{S} \Big\{ q(B^{(s)}) q(\boldsymbol{\theta}^{(s)}) \Big\}. \tag{9}$$

The labels produced by the sequence taggers, $\boldsymbol{d}$, can be marginalized analytically so do not require a separate factor. Each variational factor has the form $\ln q(z) = \mathbb{E}[\ln p(z|\boldsymbol{c}, \neg z)]$, where $\neg z$ contains all the latent variables except z. We perform approximate inference by using coordinate ascent to update each variational factor, $q(z)$, in turn, taking expectations with respect to the current estimates of the other variational factors. Each iteration reduces the KL-divergence between the true and approximate posteriors of Equation 9, and hence optimizes a lower bound on the log marginal likelihood, also called the evidence lower bound or ELBO (Bishop, 2006; Attias, 2000). The complete VB algorithm is described in Algorithm 1, which makes use of the update equations for the log variational factors given below.

Input: Annotations, $\boldsymbol{c}$
Randomly initialize $\mathbb{E} \ln A^{(k)}, \forall k$, $\mathbb{E} \ln B^{(s)}, \forall s$, $\mathbb{E} \ln \boldsymbol{T}_j, \forall j$ and $\hat{d}_{n,\tau}^{(s)}(i), \forall s, \forall n, \forall \tau, \forall i$.
while not_converged$(r_{n,\tau,j}, \forall n, \forall \tau, \forall j)$ **do**
  Update $r_{j,n,\tau}$, $s_{t_{j,n,\tau-1}, t_{\iota,n,\tau}}$, $\forall j, \forall \tau, \forall i, \forall \iota$, using forward-backward algorithm
  Retrain all sequence taggers using $\tilde{\boldsymbol{d}}^{(s)}$ as training labels for tagger s
  Use sequence taggers to predict $\hat{d}_{n,\tau}^{(s)}(i)$, $\forall s, \forall n, \forall \tau, \forall i$
  Update $\ln q(A^{(k)})$ and $\mathbb{E} \ln A^{(k)}, \forall k$
  Update $\ln q(B^{(s)})$ and $\mathbb{E} \ln B^{(s)}, \forall s$
  Update $\ln q(\boldsymbol{T}_j)$ and $\mathbb{E} \ln T_{j,\iota}, \forall j, \forall \iota$
end
Output: Label posteriors, $r_{n,\tau,j}, \forall n, \forall \tau, \forall j$, most probable sequence of labels, $\hat{\boldsymbol{t}}_n, \forall n$ using Viterbi algorithm

Algorithm 1: The VB algorithm for BSC.

The prior distributions chosen for our generative model are conjugate to the distributions over the latent variables and model parameters, meaning that each $q(z)$ is the same type of distribution as the corresponding prior distribution defined in Section 3. The parameters of each variational distribution can be computed in terms of expectations over the other subsets of variables. For the true labels, $\boldsymbol{t}$, the variational factor is:

$$\ln q(\boldsymbol{t}_n) = \sum_{n=1}^{N} \sum_{\tau=1}^{L_n} \sum_{s=1}^{S} \mathbb{E} \ln B^{(s)} \Big(t_{n,\tau}, d_{n,\tau}^{(s)}, d_{n,\tau-1}^{(s)} \Big)$$
$$+ \sum_{n=1}^{N} \sum_{\tau=1}^{L_n} \sum_{k=1}^{K} \mathbb{E} \ln A^{(k)} \left(t_{n,\tau}, c_{n,\tau}^{(k)}, c_{n,\tau-1}^{(k)} \right)$$
$$+ \mathbb{E} \ln T_{t_{n,\tau-1}, t_{n,\tau}} + \text{const.} \tag{10}$$

From this factor, we compute the posterior probability of each true token label, $r_{n,\tau,j} = \mathbb{E}[p(t_{n,\tau} = j|\boldsymbol{c})]$, and of each label transition, $s_{n,\tau,j,\iota} = \mathbb{E}[p(t_{n,\tau-1} = j, t_{n,\tau} = \iota|\boldsymbol{c})]$, using the forward-backward algorithm (Ghahramani, 2001), which

consists of two passes. The *forward pass* for each document, n, starts from $\tau = 1$ and computes:

$$\ln r^{-}_{n,\tau,j} = \ln \sum_{\iota=1}^{J} \left\{ r^{-}_{n,\tau-1,\iota} \mathrm{e}^{\mathbb{E}\ln T_{\iota,j}} \right\} + ll_{n,\tau}(j),$$

$$ll_{n,\tau}(j) = \sum_{k=1}^{K} \mathbb{E}\ln A^{(k)}\left(j, c^{(k)}_{n,\tau}, c^{(k)}_{n,\tau-1}\right) + \sum_{s=1}^{S} \sum_{i=1}^{J}\sum_{\iota=1}^{J} \mathbb{E}\ln B^{(s)}(j,i,\iota)\, \hat{d}^{(s)}_{n,\tau}(i)\hat{d}^{(s)}_{n,\tau-1}(\iota), \quad (11)$$

where $\hat{d}^{(s)}_{n,\tau}(i)$ is defined below in Equation 20, and $r^{-}_{n,0,\iota} = 1$ where $\iota =$'O' and 0 otherwise. The *backwards pass* starts from $\tau = L_n$ and scrolls backwards, computing:

$$\ln \lambda_{n,L_n,j} = 0, \qquad \ln \lambda_{n,\tau,j} = \ln \sum_{\iota=1}^{J} \exp\big\{ \ln \lambda_{i,\tau+1,\iota} + \mathbb{E}\ln T_{j,\iota} + ll_{n,\tau+1}(\iota)\big\}. \quad (12)$$

By applying Bayes' rule, we arrive at $r_{n,\tau,j}$ and $s_{n,\tau,j,\iota}$:

$$r_{n,\tau,j} = \frac{r^{-}_{n,\tau,j}\lambda_{n,\tau,j}}{\sum_{j'=1}^{J} r^{-}_{n,\tau,j'}\lambda_{n,\tau,j'}} \quad (13)$$

$$s_{n,\tau,j,\iota} = \frac{\tilde{s}_{n,\tau,j,\iota}}{\sum_{j'=1}^{J}\sum_{\iota'=1}^{J} \tilde{s}_{n,\tau,j',\iota'}} \quad (14)$$

$$\tilde{s}_{n,\tau,j,\iota} = r^{-}_{n,\tau-1,j}\lambda_{n,\tau,\iota}\exp\{\mathbb{E}\ln T_{j,\iota} + ll_{n,\tau}(\iota)\}.$$

Each row of the transition matrix has the factor:

$$\ln q(\boldsymbol{T}_j) = \ln \mathrm{Dir}\left([N_{j,\iota} + \gamma_{j,\iota}, \forall \iota \in \{1,..,J\}]\right), \quad (15)$$

where $N_{j,\iota} = \sum_{n=1}^{N}\sum_{\tau=1}^{L_n} s_{n,\tau,j,\iota}$ is the expected number of times that label ι follows label j. The forward-backward algorithm requires expectations of $\ln \boldsymbol{T}$ that can be computed using standard equations for a Dirichlet distribution:

$$\mathbb{E}\ln T_{j,\iota} = \Psi(N_{j,\iota} + \gamma_{j,\iota}) - \Psi\left(\sum_{\iota=1}^{J}(N_{j,\iota} + \gamma_{j,\iota})\right), \quad (16)$$

where Ψ is the digamma function.

The variational factor for each annotator model is a distribution over its parameters, which differs between models. For *seq*, the variational factor is:

$$\ln q\left(A^{(k)}\right) = \sum_{j=1}^{J}\sum_{l=1}^{J} \mathrm{Dir}\left(\left[\boldsymbol{N}^{(k)}_{j,l,m} \forall m \in \{1,..,J\}\right]\right)$$

$$N^{(k)}_{j,l,m} = \alpha^{(k)}_{j,l,m} + \sum_{n=1}^{N}\sum_{\tau=1}^{L_n} r_{n,\tau,j}\delta_{l,c^{(k)}_{n,\tau-1}}\delta_{m,c^{(k)}_{n,\tau}}, \quad (17)$$

where δ is the Kronecker delta. For *CM*, *MACE*, *CV* and *acc*, the factors follow a similar pattern of summing pseudo-counts of correct and incorrect answers. The forward-backward passes also require the following expectation terms for *seq*, which are standard equations for Dirichlet distributions and can be simplified for the other annotator models:

$$\mathbb{E}\ln A^{(k)}(j,l,m) = \Psi\left(N^{(k)}_{j,l,m}\right) - \Psi\left(\sum_{m'=1}^{J}\left(N^{(k)}_{j,l,m'}\right)\right). \quad (18)$$

The variational factor, $q(B^{(s)})$, for each sequence tagger's annotator model has the same form as $q(A^{(k)})$, substituting $\delta_{l,c^{(k)}_{n,\tau-1}}$ for $\hat{d}^{(s)}_{n,\tau}(i)$, as defined in below in Equation 20.

Black-box sequence taggers: the parameters of tagger s have the following variational factor:

$$\ln q\left(\boldsymbol{\theta}^{(s)}\right) = \ln p\left(\boldsymbol{x}|\boldsymbol{\theta}^{(s)}, \tilde{\boldsymbol{d}}^{(s)}\right) + \ln p\left(\boldsymbol{\theta}^{(s)}\right) + \mathrm{const},$$

$$\tilde{d}_{n,\tau} = \mathbb{E}\left[p(d^{(s)}_{n,\tau} = i|B^{(s)}, t_{n,\tau})\right] = \sum_{j=1}^{J}\sum_{\iota=1}^{J} r_{n,\tau,j}\tilde{d}_{n,\tau-1}\mathbb{E}B^{(s)}(j,i,\iota). \quad (19)$$

The expectations, $\tilde{\boldsymbol{d}}^{(s)}_n$, fill the role of training labels, allowing us to use the training function of the black-box sequence taggers to update the variational factor, $q\left(\theta^{(s)}\right)$. Many black-box sequence taggers, including most neural networks, use maximum likelihood (ML) to find optimal point values, $\hat{\boldsymbol{\theta}}^{(s)}$, rather than their posterior distribution. If we integrate such sequence taggers, our complete inference procedure becomes a hybrid between VB and ML expectation maximization (EM) (see Bishop (2006)). The sequence tagger may also require training using discrete labels, in which case we introduce a further ML step and approximate $\tilde{\boldsymbol{d}}^{(s)}_n$ by the most probable values at each token.

The update equations for other factors require expectations of $\boldsymbol{d}_n$ with respect to $\boldsymbol{\theta}^{(s)}$, or their ML approximation:

$$\hat{d}^{(s)}_{n,\tau}(i) = \mathbb{E}\left[p(d^{(s)}_{n,\tau} = i|\boldsymbol{x}_n, \boldsymbol{\theta}^{(s)})\right] \approx p\left(d^{(s)}_{n,\tau} = i|\boldsymbol{x}_n, \hat{\boldsymbol{\theta}}^{(s)}\right) \quad (20)$$

These values are the predictions obtained from the black-box sequence tagger given tokens $\boldsymbol{x}$.

Therefore, our method requires only training and prediction functions to integrate a sequence tagger, while its annotator model, $B^{(s)}$, accounts for the sequence tagger's reliability. This means we can treat sequence taggers as black boxes, even if their predictions are noisy or over-confident. Pre-trained taggers can also be used, for example, to make use of taggers that were trained on different domains with more annotated data.

4.1 Predicting the Sequence Labels

The approximate posterior probabilities of the true labels, $r_{j,n,\tau}$, provide confidence estimates for the labels. However, it is often useful to compute the most probable sequence of labels, $\hat{\boldsymbol{t}}_n$, using the Viterbi algorithm (Viterbi, 1967). To apply the algorithm, we use the converged variational factors to compute $\mathbb{E}[\boldsymbol{T}]$, $\mathbb{E}[A^{(k)}], \forall k$, $\mathbb{E}[B^{(s)}], \forall s$ and $\hat{d}^{(s)}_{n,\tau}(i), \forall s, \forall n, \forall \tau, \forall i$. The most probable sequence is particularly useful because, unlike $r_{j,n,\tau}$, the sequence will be consistent with any transition constraints imposed by the priors on the transition matrix $\boldsymbol{T}$, such as preventing 'O'→'I' transitions by assigning them zero probability. We can also make predictions for unlabeled documents in a similar manner, simply omitting the human annotations, $\boldsymbol{c}$, and relying only on the predictions of the black-box sequence taggers, $\hat{\boldsymbol{d}}^{(s)}$.

4.2 Modular Implementation of Variational Inference

The variational inference method described in Section 4 is naturally suited to a modular implementation. We divide the BSC model, as defined in Section 3 and Equation 8, into three modules: (a) the true label model, which defines the distribution over sequences of labels, $q(\boldsymbol{t}_n)$; (b) the annotator model, which may be one of those described in Section 2 and implements $q(A^{(k)})$ and $q(B^{(s)})$; and (c) black-box sequence taggers, which are existing implementations that provide training and prediction functions to predict true labels given text tokens, $\boldsymbol{x}$. The true label model exposes methods to compute $r_{n,\tau,j}$ and $s_{n,\tau,j,\iota}$, $\forall n, \forall \tau, \forall j, \forall \iota$, while the annotator models provide methods to initialize and update $q(A^{(k)})$ and $q(B^{(s)})$, and compute expectations according to Equation 18. By allowing individual functions to be replaced without rewriting the inference method, the modular implementation makes it easier to adapt the model to different types of annotations, and to test each component part. For example, new annotator models could, in future, be introduced to aggregate continuous-valued ratings or pairwise preferences.

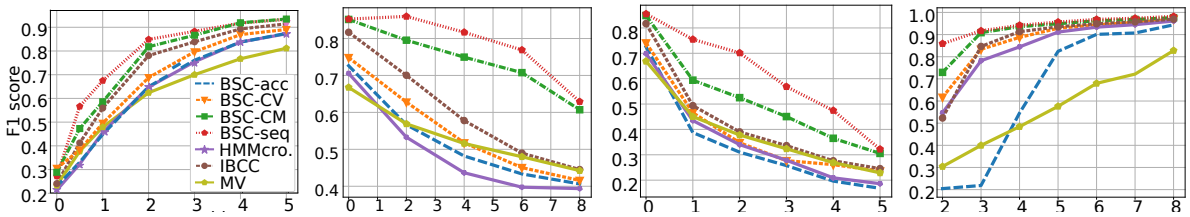
5 Experiments

We evaluate Bayesian sequence combination (BSC) with each of the annotator models described in Section 3 to assess whether the sequential annotator model, *seq*, improves the quality of the inferred sequence tags. The first experiment uses simulated annotators to investigate the effects of different types of error on aggregation methods. We then introduce two NLP datasets to test performance in passive and active learning scenarios, analyze errors, and visualize the learned annotator models. The experiments also assess whether including including sequence taggers into the probabilistic model improves the aggregated sequence tags as well as the sequence taggers' predictions on test data.

5.1 Evaluated Methods

As well-established non-sequential baselines, we include token-level majority voting (*MV*), *MACE* (Hovy et al., 2013), Dawid-Skene (*DS*) (Dawid and Skene, 1979) and independent Bayesian classifier combination (*IBCC*) (Kim and Ghahramani, 2012), a Bayesian treatment of Dawid-Skene. We also test the sequential *HMM-crowd* method (Nguyen et al., 2017), which uses a combination of maximum *a posteriori* (or smoothed maximum likelihood) estimates for the confusion vector (CV) annotator model and variational inference for an integrated hidden Markov model (HMM). MACE and IBCC are variants of BSC-MACE and BSC-CM, respectively, with non-sequential true label models. HMM-Crowd and DS use non-Bayesian inference steps and can be compared with their Bayesian variants, BSC-CV and IBCC, respectively.

BSC is tested with each of the different annotator models described in Section 2 and two black box sequence taggers. As the default for all annotator models, we integrate a simple black-box classifier that treats all text features as conditionally independent of each other and of the sequence of labels. To determine the effect of each component of the model we also test BSC-CM and BSC-seq without a text model (*notext*), and with the transition matrix, $\boldsymbol{T}$, replaced by simple independent class probabilities (labeled $\backslash\boldsymbol{T}$). We also test the



(a) Annotator accuracy bias (b) Short span bias (c) Missed span bias (d) Good workers out of 10

Figure 1: F1 scores with simulated annotators. Each plot shows the effect of varying one characteristic.

Data -set	Sentences with crowd total	dev	test	without crowd dev	test	Tokens /sent.	Annotators total	/doc	Span type	Gold spans	Span length mean	std.
NER	6056	2800	3256	216	231	13	47	4.9	PER	6282	1.19	0.49
									LOC	6482	1.73	0.57
									ORG	5789	1.55	0.92
									MISC	3059	1.44	0.80
PICO	9480	191	191	191	191	150	312	6.0	pop.	700	7.74	7.38

Table 1: Numbers of sentences, annotators, and spans for datasets used in our experiments. Sentences with crowd all have crowdsourced labels. Only dev and test sentences have gold sequence labels.

integration of BSC-seq with the BiLSTM-LSTM-CRF of Lample et al. (2016) as a black-box sequence tagger, labeled *BSC-seq+LSTM*. This ensemble is compared against the same LSTM-based method trained on the output predictions of HMM-crowd and BSC-seq (labeled →LSTM). We use the implementation of Lample et al. (2016), which must be trained on discrete labels and outputs discrete predictions rather than probabilities. We follow the authors' recommendations for hyperparameters except for the optimizer, for which we use Adam to improve the convergence rate as recommended by Reimers and Gurevych (2017).

5.2 Simulated Annotators

Simulated data allows us to test the effect of one type of error in the crowdsourced data, while keeping other characteristics of the data constant. We generate crowds of 10 annotators for four experiments, which test the effect of varying (a) average annotator accuracy, (b) short span bias, i.e. the probability of not including the last tokens in a span, (c) missed span bias, i.e. the probability of missing a span entirely, and (d) the ratio of good to uninformative annotators in the crowd. We simulate annotators using the generative model of BSC-seq, drawing annotator labeling probabilities from Dirichlet distributions. By default, Dirichlet parameters corresponding to incorrect answers are 1, those for correct answers are 2.5, and disallowed transitions (O→I) are close to 0. We then change the parameters of these Dirichlet distributions to obtain the variations described above. We repeat each experiment 25 times, in each case generating 25 documents of 100 tokens each.

Figure 1 shows the F1-scores for our tested methods. Where annotator accuracy is high, majority voting is less accurate than methods that model individual annotator behavior, although the difference decreases as we introduce more errors. Among the BSC variants, performance increases with the complexity of the annotator model, from BSC-acc to BSC-seq, suggesting that the richer seq model can be successfully learned on a small dataset. There are some benefits for the Bayesian approaches, IBCC and BSC-CV, over the similar models, DS and HMM-crowd, respectively, in handling all four types of annotator error.

5.3 Crowdsourced Datasets

We use two datasets containing both crowdsourced and gold sequential annotations. The CoNLL 2003 named-entity recognition dataset (Tjong Kim Sang and De Meulder, 2003), *NER*, contains gold labels for four named entity categories (PER, LOC, ORG, MISC), with crowdsourced labels provided by (Rodrigues et al., 2014). *PICO* (Nguyen et al., 2017), consists of medical paper abstracts that have been annotated by a crowd to indicate text spans that identify

	NER				Hyperparams.			PICO				Hyperparams.		
	Prec.	Rec.	F1	CEE	γ_0	ϵ_0	α_0	Prec.	Rec.	F1	CEE	γ_0	ϵ_0	α_0
Best worker	76.4	60.1	67.3	17.1				64.8	53.2	58.5	17.0			
Worst worker	55.7	26.5	35.9	31.9				50.7	52.9	51.7	41.0			
MV	79.9	55.3	65.4	6.24				82.5	52.8	64.3	2.55			
MACE	74.4	66.0	70.0	1.01	.1	.1	0	25.4	84.1	39.0	58.2	.1	.1	0
DS	79.0	70.4	74.4	2.80				71.3	66.3	68.7	0.44			
IBCC	79.0	70.4	74.4	**0.49**	.1	1	.1	72.1	66.0	68.9	**0.27**	.1	10	10
HMM-crowd	80.5	69.4	74.6	1.04	0	.1	0	76.5	66.2	71.0	0.79	0	.1	0
HMM-crowd→LSTM	81.8	69.5	75.2	12.2	0	.1	0	76.5	66.5	71.2	13.0	0	.1	0
BSC-acc	**83.4**	54.3	65.7	0.96	10	.1	10	**89.4**	45.2	60.0	1.59	.1	.1	10
BSC-MACE	67.9	74.1	70.9	0.89	10	10	1	46.7	84.4	60.1	1.98	.1	100	.1
BSC-CV	81.4	64.7	72.1	0.89	10	1	1	74.9	67.2	71.1	0.84	.1	1	.1
BSC-CM	79.9	72.2	75.8	1.46	.1	100	.1	60.1	78.8	68.2	1.49	.1	100	1
BSC-seq	80.3	74.8	77.4	0.65	.1	1	1	72.9	77.6	75.1	1.10	100	1	1
BSC-CM-notext	74.7	69.7	72.1	1.48	.1	1	.1	62.7	74.8	68.2	1.32	100	100	.1
BSC-CM\$\boldsymbol{T}$	80.0	73.0	76.3	0.99	.1	100	.1	65.8	66.7	66.2	0.28	.1	100	.1
BSC-seq-notext	81.0	69.8	75.0	0.52	.1	1	1	81.2	59.2	68.5	0.73	.1	.1	.1
BSC-seq\$\boldsymbol{T}$	60.5	42.3	49.8	0.93	.1	1	1	51.2	70.4	59.8	1.04	.1	.1	1
BSC-seq→LSTM	80.2	75.3	77.7	11.0	.1	1	1	75.7	75.4	75.5	25.5	100	1	1
BSC-seq+LSTM	82.3	**75.9**	**78.9**	0.59	.1	1	1	78.7	**78.6**	**78.7**	1.15	100	1	1

Table 2: Aggregating crowdsourced labels: estimating true labels for documents labeled by the crowd.

the population enrolled in a clinical trial. Further information about the datasets is shown in Table 5. Note that NER spans are typically much shorter than those in PICO.

Evaluation metrics: For NER we use the CoNLL 2003 F1-score, which considers only exact span matches to be correct. For PICO, we use the relaxed F1-measure (Nguyen et al., 2017), which counts the matching fractions of spans when computing precision and recall. Since the spans in PICO are longer than those of NER, partial matches may still contain much of the required information. We also compute the cross entropy error (*CEE*) at the level of tokens to compare the probability estimates produced by aggregation methods, which are useful for decision-making tasks such as active learning.

5.4 Aggregating Crowdsourced Labels

In this task, we use the aggregation methods to combine multiple crowdsourced labels and predict the true labels for the same documents. For both datasets, we provide all the crowdsourced labels as input to the aggregation method. In both cases, we split the gold-labeled documents into 50% validation and test sets. For NER, we use the split given by Nguyen et al. (2017), while for PICO, the split was not available so our results are not directly comparable to theirs.

We tune the hyperparameters using a validation set. To limit the number of hyperparameters to tune, we optimize only three values for BSC. Hyperparameters of the transition matrix, $\boldsymbol{\gamma}_j$, are set to the same value, γ_0, except for disallowed transitions, (O→I, transitions between types, e.g. I-PER→I-ORG), which are set to 0.1. For the annotator models (both $\boldsymbol{A}$ and $\boldsymbol{B}$), all values are set to α_0, except for disallowed transitions, which are set to 0.1, then ϵ_0 is added to hyperparameters corresponding to correct annotations (e.g. diagonal entries in a confusion matrix). We use ϵ_0 to encode the prior assumption that annotators are more likely to have an accuracy greater than random. This avoids the non-identifiability problem, in which the class labels become switched around. We use validation set F1-scores to choose values from $[0.1, 1, 10, 100]$, training on a small subset of 250 documents for NER and 500 documents for PICO. For the integrated BSC-seq+LSTM, we found better validation set performance for both our datasets if the LSTM is first excluded while the other parameters converge before training the LSTM. This likely reduces over-fitting resulting from the maximum likelihood step used to inte-

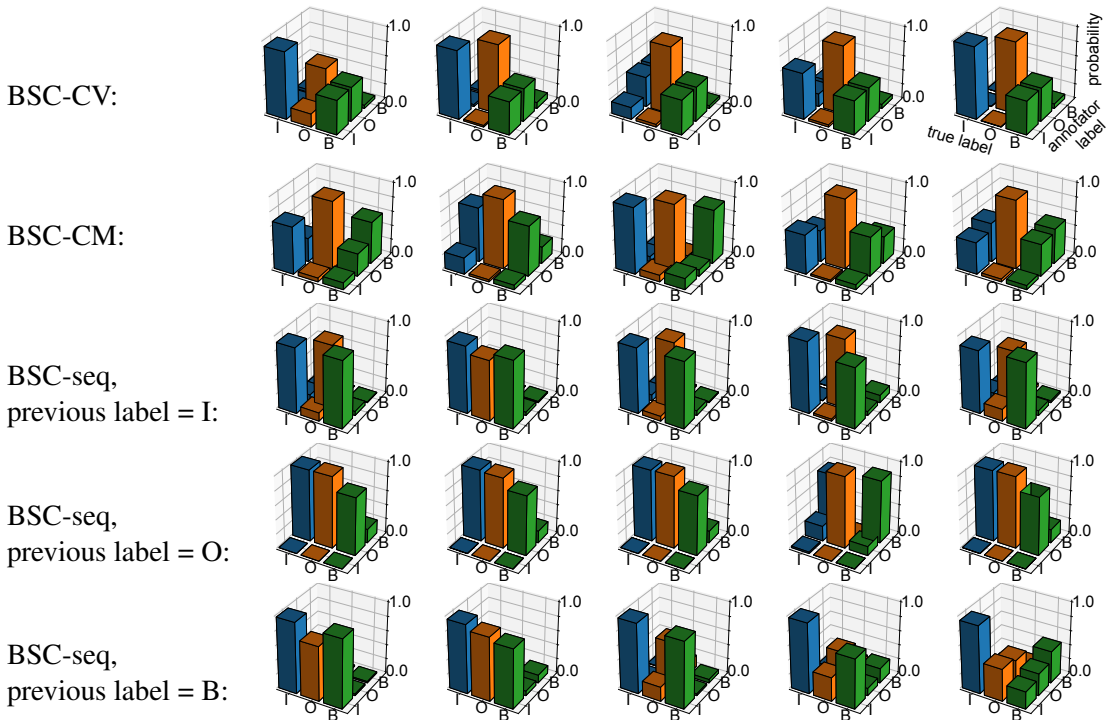


Figure 2: Clusters of confusion matrix representations from each BSC-*** annotator model trained on PICO.

grate the LSTM as a black-box sequence tagger.

The results of the aggregation task are shown in Table 2. Although DS and IBCC do not consider sequence information nor the text itself, they both perform well on both datasets, with IBCC reaching better cross entropy error than DS due to its Bayesian treatment. The improvement of DS over the results given by Nguyen et al. (2017) may be due to implementation differences. Neither MACE, BSC-acc nor BSC-MACE perform strongly, with F1-scores sometimes falling below MV. The acc and MACE annotator models may be a poor match for the sequence labeling task if annotator competence varies greatly depending on the true class label.

BSC-seq outperforms the other approaches, although without the text model (BSC-seq-notext) or the transition matrix (BSC-seq$\backslash \boldsymbol{T}$), its performance decreases. However, for BSC-CM, the results are less clear: BSC-CM-notext differs from IBCC only in the inclusion of the transition matrix, $\boldsymbol{T}$, yet IBCC outperforms BSC-CM-notext. This suggests that the combination of these elements is important: the seq annotator model is effective in combination with the transition matrix and simple text model. Integrating an LSTM improves performance further in both datasets, and outperforms an LSTM trained on the output of HMM-crowd or BSC-seq.

We categorize the errors made by key methods and list the counts for each category in Table 3. All machine learning methods shown reduce the number of spans that were completely missed by majority voting. BSC-seq+LSTM increases the number of exact span matches on NER, but reduces this number substantially on PICO while increasing the number of partial matches and false positives (where no true span was present). This is due to a larger number of split spans, where a 'B' token is inserted incorrectly inside a span. Therefore, while BSC-seq outperforms the alternatives in terms of F1-score and missing spans, further work may be required to improve the distinction between 'B' and 'I' tokens.

To determine whether BSC-seq learns distinctive confusion matrices depending on the previous labels, we plot the learned annotator models for PICO as probabilistic confusion matrices in Figure 2. As the dataset contains a large number of annotators, we clustered the confusion matrices inferred by each model into five groups by applying K-means to their posterior expected values. In all clusters, BSC-CV learns different accuracies for B, I and O (the diagonal entries). These differ-

Method	Dataset	exact match	type wrong only	partial match	missing span	false +ve	late start	early start	late finish	early finish	fused spans	split span
MV	NER	4307	304	228	1773	100	96	10	15	85	17	26
HMM-crowd	NER	4519	361	256	924	182	101	15	26	97	28	22
BSC-CV	NER	4431	275	243	1245	177	100	17	23	89	29	16
BSC-CM	NER	4534	387	258	734	269	111	23	37	86	39	12
BSC-seq+LSTM	NER	4581	351	261	564	195	93	42	33	85	39	17
MV	PICO	168	0	32	185	48	9	11	1	0	3	9
HMM-crowd	PICO	190	0	47	124	81	13	21	0	0	5	8
BSC-CV	PICO	196	0	46	117	81	10	25	0	0	11	0
BSC-CM	PICO	203	0	54	77	192	18	15	8	0	4	18
BSC-seq+LSTM	PICO	81	0	421	75	216	20	6	232	3	24	393

Table 3: Counts of different types of span errors.

ences may explain its improvement over BSC-acc. BSC-CM differs from BSC-CV in that the first, fourth and fifth clusters have off-diagonal values with different heights for the same true label value. The second cluster for BSC-CM encodes likely spammers who usually choose 'O' regardless of the ground truth. The confusion matrices for BSC-seq are very different depending on the worker's previous annotation. Each column in the figure shows the confusion matrices corresponding to the same cluster of annotators. The first column, for example, shows annotators with a tendency toward I→I or O→O transitions, while the following clusters indicate very different labeling behavior. The model therefore appears able to learn distinct confusion matrices for different workers given previous labels, which supports the use of sequential annotator models.

5.5 Active Learning

Active learning iteratively selects informative data points to be labeled so that a model can be trained using less labeled data. Posterior probabilities output by Bayesian methods account for uncertainty in the model parameters, hence can be used to choose data points that most rapidly reduce that uncertainty. We hypothesize that BSC will learn more quickly than non-sequential methods in an active learning scenario. We simulate active learning using *uncertainty sampling* (Settles, 2010), as described in Algorithm 2. The LSTM implementation provided by Lample et al. (2016) outputs discrete label predictions, so to allow direct comparison of BSC against a neural sequence tagger, we modify the network to output probabilities for

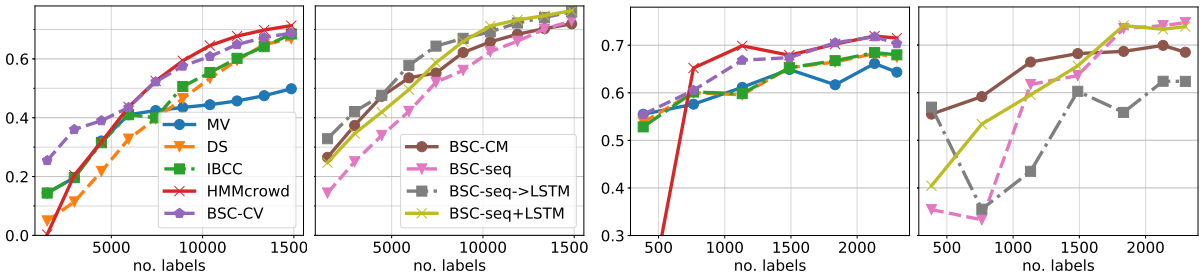
Input: A random $initial_set$ of training labels, the same for all methods.

Set training set $\boldsymbol{c} = initial_set$
while *training set size* < max_no_labels **do**
  Train model on $\boldsymbol{c}$
  Predict sequence labels for all documents
  Compute the mean entropy of the sequence labels of each document: $-\frac{1}{L_n}\sum_{\tau=1}^{L_n}\sum_{j=1}^{J} p(t_{n,\tau} = j|\boldsymbol{c}) \ln p(t_{n,\tau} = j|\boldsymbol{c})$
  Select $batch_size$ documents with highest mean entropy, add their annotations to $\boldsymbol{c}$
end

Algorithm 2: Active learning simulation for each method using uncertainty sampling.

the active learning simulation. For MV, probabilities are estimated by fractions of votes.

Figure 3 plots the mean F1 scores over ten repeats of the active learning simulation. IBCC learns more rapidly than DS on NER due to its Bayesian approach, which may also explain the stronger performance of BSC-CV compared to the similar HMM-crowd model, although this does not hold for the PICO dataset. BSC variants outperform non-sequential IBCC. BSC-CM and BSC-CV are strongest on PICO with small numbers of labels, but are later overtaken by BSC-seq, which may require more data to learn its more complex model. On NER, BSC-CM continues to outperform the more complex BSC-seq, but the integrated LSTM clearly improves BSC-seq+LSTM. BSC-seq→LSTM performs strongly



(a) NER (b) PICO

Figure 3: F1-scores for active learning simulations using uncertainty sampling.

	NER				PICO			
	Prec.	Recall	F1	CEE	Prec.	Recall	F1	CEE
HMM-crowd→LSTM	**78.7**	59.0	67.5	15.9	**75.6**	61.6	67.9	13.5
BSC-seq→LSTM	74.3	**62.8**	**68.1**	15.65	82.3	**66.4**	**73.5**	19.6
BSC-seq+LSTM	72.3	64.2	68.0	**0.6**	**87.4**	57.9	69.7	**0.9**
LSTM trained on gold labels	77.6	75.3	76.5	11.10	too few training labels			

Table 4: Prediction performance on test datasets with training on crowdsourced labels.

on NER but poorly on PICO, where fewer labels were provided, while BSC-seq+LSTM appears more robust to this problem.

5.6 Prediction with Crowd-Trained LSTMs

In previous work (Nguyen et al., 2017), HMM-crowd→LSTM produced better predictions for documents not labeled by the crowd, compared with training an LSTM directly on crowdsourced data, or training on labels obtained from non-sequential aggregation methods. We evaluate whether the performance gains of BSC-seq→LSTM for aggregation also result in better predictions on unannotated documents. We also test whether BSC-seq+LSTM can provide meaningful confidence estimates when the sequence tagger it integrates produces only discrete labels. For NER, we evaluate on the CoNLL English test set (Tjong Kim Sang and De Meulder, 2003).

The results in Table 4 show that for F1-scores, BSC-seq→LSTM outperforms the previous state-of-the-art, HMM-crowd→LSTM. BSC-seq+LSTM produces a low cross entropy error, indicating that the probabilities it outputs are a good reflection of confidence and are likely to be more suitable to downstream decision-making tasks than the raw outputs from the LSTM sequence tagger.

6 Discussion and Conclusions

We proposed BSC-Seq, a Bayesian approach to aggregating sequence labels, which models the effect of label sequences on annotator reliability. Our results reinforce previous work that has demonstrated the benefits of modeling annotator reliability when aggregating noisy data, such as crowdsourced labels. We showed that sequential models outperform non-sequential baselines and that BSC-seq improves the state-of-the-art over HMM-crowd. Its performance depends on the combination of sequential annotator model, label transition matrix, and text model. We further improved the quality of aggregated labels, by integrating existing sequence taggers into our variational inference approach as black-box training and prediction functions. This technique performed well with larger amounts of labeled data, but may benefit from the use of pre-trained neural sequence taggers when the dataset is very small. Future work will evaluate integrating sequence taggers built on Bayesian deep learning, which may improve active learning. We will also investigate how to set priors for the reliability of black-box methods by testing them on other training sets of similar size.

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