A Bayesian Approach for Sequence Tagging with Crowds

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Abstract

Current methods for sequence tagging, a core task in NLP, are data hungry, which motivates the use of crowdsourcing as a cheap way to obtain labelled data. However, annotators are often unreliable and current aggregation methods cannot capture common types of span annotation error. To address this, we propose a Bayesian method for aggregating sequence tags that reduces errors by modelling sequential dependencies between the annotations as well as the ground-truth labels. By taking a Bayesian approach, we account for uncertainty in the model due to both annotator errors and the lack of data for modelling annotators who complete few tasks. We evaluate our model on crowdsourced data for named entity recognition, information extraction and argument mining, showing that our sequential model outperforms the previous state-of-the-art, and that Bayesian approaches outperform non-Bayesian alternatives. We also find that our approach can reduce crowdsourcing costs through more effective active learning, as it better captures uncertainty in the sequence labels when there are few annotations.

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). We make all of our code freely available[1]

This paper introduces *Bayesian sequence combination (BSC)*, the first Bayesian method for aggregating sequence labels from multiple annotators. As a component of BSC, we also introduce the *sequential confusion matrix (seq)*, a probabilistic model of annotator noise and bias, which goes beyond previous work by modelling sequential dependencies between annotators' labels. Further contributions include a theoretical comparison of the probabilistic models of annotator noise and bias, and an empirical evaluation on three sequence labelling tasks, in which *BSC* with *seq* consistently outperform the previous state of the art.

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.

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:

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

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,

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

$\boldsymbol{\xi}$, that is independent of the true label, t_τ.

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

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:

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

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:

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

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:

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

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 $c_\tau =$'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 choice of annotator model for a particular annotator depends on the developer's understanding of the annotation task: if the annotations have sequential dependencies, this suggests the *seq* model; for non-sequential classifications *CM* may be effective with small ($\leq$ 5) numbers of classes; *MACE* may be more suitable if there are more classes. However, there is also a trade-off between the expressiveness of the model and the number of parameters that must be learned. Simpler models with fewer parameters, such as *acc*, which may be effective if there are only small numbers of annotations from each annotator. Our experiments in Section 5 investigate this trade-off on NLP tasks involving sequential annotation. The next section shows how these models can be used as part of a model for aggregating sequential annotations.

3 A Generative 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, $T_j \sim \mathrm{Dir}(\boldsymbol{\gamma}_j)$, 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: $t_{n,\tau} \sim \mathrm{Cat}(\boldsymbol{T}_{t_{n,\tau-1}})$. The set of all labels for all documents is referred to as $\boldsymbol{t} = \{\boldsymbol{t}_1, ..., \boldsymbol{t}_N\}$.

In the generative model, we assume one of the annotator models described in Section 2 for each of K annotators. The number of parameters depends on the choice of annotator 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:

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

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).

Joint distribution: the complete model can be represented by the joint distribution, given by:

$$p(\boldsymbol{t}, \boldsymbol{A}, \boldsymbol{B}, \boldsymbol{T}, \boldsymbol{\theta}, \boldsymbol{c}, \boldsymbol{d}, \boldsymbol{x} | \boldsymbol{\alpha}, \boldsymbol{\beta}, \boldsymbol{\gamma}) \quad (7)$$

$$= \prod_{k=1}^{K} \left\{ p(A^{(k)} | \boldsymbol{\alpha}^{(k)}) \prod_{n=1}^{N} p(\boldsymbol{c}_n^{(k)} | A^{(k)}, \boldsymbol{t}) \right\}$$

$$\prod_{j=1}^{J} p(\boldsymbol{T}_j | \boldsymbol{\gamma}_j) \prod_{n=1}^{N} \prod_{\tau=1}^{L_n} p(\boldsymbol{t}_n | \boldsymbol{T}_{t_{n,\tau-1}}) \quad (8)$$

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*, $q(z)$:

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

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.

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:

$$\ln q(\boldsymbol{t}_n) = \sum_{n=1}^{N} \sum_{\tau=1}^{L_n} \sum_{k=1}^{K} \mathbb{E} \ln A^{(k)} \left(t_{n,\tau}, c_{n,\tau}^{(k)}, c_{n,\tau-1}^{(k)} \right) + \mathbb{E} \ln T_{t_{n,\tau-1}, t_{n,\tau}} + \mathrm{const}. \quad (10)$$

Input: Annotations, $\boldsymbol{c}$

Randomly initialize $\mathbb{E}\ln A^{(k)}, \forall k, \mathbb{E}\ln \boldsymbol{T}_j, \forall j$

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

  Update $\ln q(A^{(k)})$ and $\mathbb{E}\ln A^{(k)}, \forall k$, given current $\boldsymbol{c}$, $r_{j,n,\tau}$

  Update $\ln q(\boldsymbol{T}_j)$ and $\mathbb{E}\ln T_{j,\iota}, \forall j, \forall \iota$, given current $s_{t_{j,n,\tau-1},t_{\iota,n,\tau}}$

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.

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). Please see supplementary material for the detailed update equations.

Each row of the transition matrix has the factor:

$$\ln q(\boldsymbol{T}_j) = \ln \mathrm{Dir}\left([N_{j,\iota} + \gamma_{j,\iota}, \forall \iota \in \{1,..,J\}]\right), \quad (11)$$

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:

$$\mathbb{E}\ln T_{j,\iota} = \Psi(N_{j,\iota} + \gamma_{j,\iota}) - \Psi\left(\sum_{\iota=1}^{J}(N_{j,\iota} + \gamma_{j,\iota})\right), \quad (12)$$

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:

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

$$N_{j,l,m}^{(k)} = \alpha_{j,l,m}^{(k)} + \sum_{n=1}^{N}\sum_{\tau=1}^{L_n} r_{n,\tau,j}\delta_{l,c_{n,\tau-1}^{(k)}}\delta_{m,c_{n,\tau}^{(k)}}, \quad (13)$$

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:

$$\mathbb{E}\ln A^{(k)}(j,l,m) = \Psi\left(N_{j,l,m}^{(k)}\right) - \Psi\left(\sum_{m'=1}^{J}\left(N_{j,l,m'}^{(k)}\right)\right). \quad (14)$$

data -set	#sentences or docs total	dev	test	#annotators total	/doc	#gold spans	span length
NER	6,056	2,800	3,256	47	4.9	21,612	1.51
PICO	9,480	191	191	312	6.0	700	7.74
ARG	8,000	60	100	105	5	73	17.52

Table 1: Dataset statistics. Span lengths are means.

4.1 Most Likely 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 $\mathbb{E}[\boldsymbol{T}]$ and $\mathbb{E}[A^{(k)}], \forall k$. 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.

5 Experiments

Datasets. We compare BSC to alternative methods on three NLP datasets containing both crowdsourced and gold sequential annotations: *NER*, the CoNLL 2003 named-entity recognition dataset (Tjong Kim Sang and De Meulder, 2003), which 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 the population enrolled in a clinical trial. *ARG* (Trautmann et al., 2019) contains a mixture of argumentative and non-argumentative sentences, in which the task is to mark the spans that contain pro or con arguments for a given topic. Dataset statistics are shown in Table 1. The datasets differ in typical span length, with argument components in ARG

	NER				PICO				ARG			
	Prec.	Rec.	F1	CEE	Prec.	Rec.	F1	CEE	Prec.	Rec.	F1	CEE
Best worker	76.4	60.1	67.3	17.1	64.8	53.2	58.5	17.0	62.7	57.5	60.0	44.20
Worst worker	55.7	26.5	35.9	31.9	50.7	52.9	51.7	41.0	25.5	19.2	21.9	70.33
MV	79.9	55.3	65.4	6.24	82.5	52.8	64.3	2.55	40.0	31.5	34.8	14.03
MACE	74.4	66.0	70.0	1.01	25.4	84.1	39.0	58.2	31.2	32.9	32.0	2.62
DS	79.0	70.4	74.4	2.80	71.3	66.3	68.7	0.44	45.6	49.3	47.4	0.97
IBCC	79.0	70.4	74.4	**0.49**	72.1	66.0	68.9	**0.27**	44.9	47.9	46.4	**0.85**
HMM-crowd	80.1	69.2	74.2	1.00	75.9	66.7	71.0	0.99	43.5	37.0	40.0	3.38
BSC-acc	**83.4**	54.3	65.7	0.96	**89.4**	45.2	60.0	1.59	36.9	32.9	34.8	6.47
BSC-MACE	67.9	74.1	70.9	0.89	46.7	**84.4**	60.1	1.98	55.7	53.4	54.5	2.80
BSC-CV	83.0	64.6	72.6	0.93	74.9	67.2	71.1	0.84	37.9	34.2	36.0	4.73
BSC-CM	79.9	72.2	75.8	1.46	60.1	78.8	68.2	1.49	**56.0**	57.5	56.8	3.76
BSC-seq	80.3	**74.8**	**77.4**	0.65	72.9	77.6	**75.1**	1.10	54.4	**67.1**	**60.1**	3.26
BSC-CM-notext	74.7	69.7	72.1	1.48	62.7	74.8	68.2	1.32	55.1	58.9	57.0	2.75
BSC-CM$\backslash\boldsymbol{T}$	80.0	73.0	76.3	0.99	65.8	66.7	66.2	0.28	52.9	49.3	51.1	1.69
BSC-seq-notext	81.3	71.9	76.3	0.52	81.2	59.2	68.5	0.73	36.9	52.0	43.2	5.64
BSC-seq$\backslash\boldsymbol{T}$	64.2	44.4	52.5	0.77	51.2	70.4	59.8	1.04	0.11	0.05	0.07	6.38

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

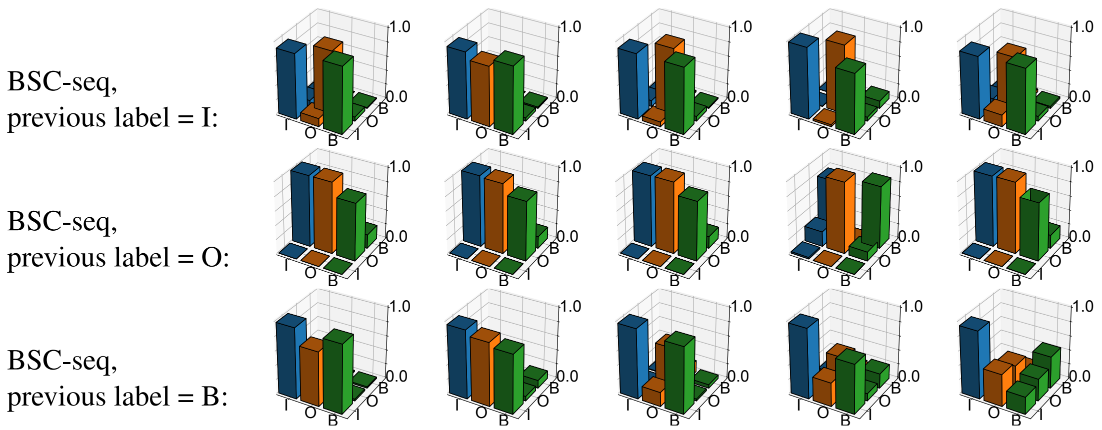

Figure 1: Clusters of confusion matrix representations from each BSC-*** annotator model trained on PICO.

the longest, while named entities in NER spans are often only one token long.

The gold-labeled documents were split into validation and test sets. For NER, we use the split given by Nguyen et al. (2017), while for PICO and ARG, we make random splits since there were not splits available from previous work. This means that the figures we obtain for PICO are not directly comparable to (2017).

Evaluation metrics. For NER and ARG we use the CoNLL 2003 F1-score, which considers only exact span matches to be correct. Incomplete named entities are typically not useful, and for ARG, it is desirable to identify complete argumentative units that make sense on their own. For medical trial populations, partial matches still contain much of the information, so for PICO we use a relaxed F1-score, as in Nguyen et al. (2017), which counts the matching fractions of spans when computing precision and recall.

We also compute the cross entropy error (*CEE*, also known as log-loss). While this is a token-level rather than span-level metric, it evaluates the quality of the probability estimates produced by aggregation methods, which are useful for tasks such as active learning.

Evaluated Methods. Bayesian sequence combination (BSC) is designed to be combined with different annotator models, so we evaluate it in combination with all of the annotator models described in Section 3. 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), which uses the *CM* annotator model, and independent Bayesian classifier combination (*IBCC*) (Kim and Ghahramani, 2012), which is a Bayesian treatment of Dawid-Skene. We also compare against the state-of-the-art 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). HMM-Crowd and DS use non-Bayesian inference steps and can be compared with their Bayesian variants, BSC-CV and IBCC, respectively.

Besides the annotator models, BSC model also makes use of text features and a transition matrix, $\boldsymbol{T}$, over true labels. We test the effect of these components by running BSC-CM and BSC-seq with no text features (*notext*), and without the transition matrix, which is replaced by simple independent class probabilities (labeled $\backslash\boldsymbol{T}$).

We tune the hyperparameters using the validation sets. 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 $1e-6$; 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 $1e-6$, 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 350 documents for PICO.

Aggregation Task. This task is to combine multiple crowdsourced labels and predict the true labels. The results 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.

redo the BSC-seq line for NER – the number of splits looks wrong 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. Note that BSC completely removes all “invalid” spans (O-¿I transitions) due to the sequential model and setting the priors hyperparameters to zero for those transitions. BSC-seq has much lower “length error”, which is the mean difference in number of tokens between the predicted and gold spans. It also reduces the number of missing spans, although in NER and ARG that comes at the cost of producing more false positives (predicting spans where there are none). From this, we can see that BSC-seq

Visualising Annotator Models. 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 1. 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, then plotted the means for each cluster. In all clusters, BSC-CV learns different accuracies for B, I and O (the diagonal entries). These differences 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

Method	Dataset	exact match	wrong type	partial match	missing span	false +ve	late start	early start	late finish	early finish	fused spans	splits	inv-alid	length error
MV	NER	2869	304	196	1775	100	96	10	15	85	17	26	81	0.04
IBCC	NER	3742	386	187	829	345	107	27	43	77	47	29	74	0.12
HMM-crowd	NER	3650	334	115	1045	210	109	22	33	89	37	23	0	0.03
BSC-CV	NER	3381	284	80	1399	121	94	17	18	90	22	8	0	0.00
BSC-CM	NER	3856	362	63	863	315	124	25	63	77	53	13	0	0.14
BSC-seq	NER	3995	353	110	686	357	84	29	25	88	28	26	0	0.09
MV	PICO	144	0	60	145	48	9	11	1	0	3	9	40	1.26
IBCC	PICO	193	0	53	103	100	14	10	0	2	3	10	19	0.45
HMM-crowd	PICO	189	0	54	106	84	13	21	0	0	5	8	0	1.99
BSC-CV	PICO	156	0	76	117	81	10	25	0	0	11	0	0	2.15
BSC-CM	PICO	216	0	50	83	157	10	19	0	0	4	17	0	2.42
BSC-seq	PICO	168	0	86	95	67	17	19	5	0	4	9	0	0.61
MV	ARG	17	0	26	14	4	9	1	0	2	0	0	9	5.27
IBCC	ARG	27	1	21	8	9	7	2	0	1	0	3	9	3.43
HMM-Crowd	ARG	20	0	23	14	4	7	2	0	2	0	0	4	4.87
BSC-CV	ARG	18	0	25	14	4	12	2	0	2	0	0	0	5.37
BSC-CM	ARG	35	1	12	9	9	7	2	0	1	1	0	0	2.11
BSC-Seq	ARG	39	3	12	3	20	6	4	0	0	1	0	0	0.46

Table 3: Counts of different types of span errors.

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.

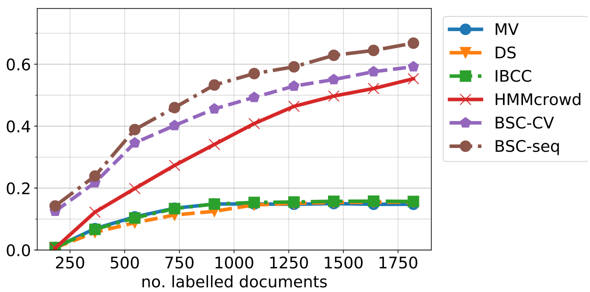

Figure 2: F1-scores for active learning simulations on NER using an uncertainty sampling strategy that selects the least-confident sequences.

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 rapidly reduce uncertainty. We hypothesize that BSC will learn more quickly than non-sequential methods in an active learning scenario. While various active learning methods could be applied here, in this paper we wish to demonstrate only that BSC may serve as a good foundation for active learning, and defer a deeper investigation of active learning techniques to future work. We therefore simulate active learning using the *least confidence* strategy (Settles and Craven, 2008), as described in Algorithm 2. Figure 2 plots the mean

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 $\boldsymbol{c}$

  For all documents, compute $LC = 1 - p(\boldsymbol{t}^*|\boldsymbol{c})$, where $\boldsymbol{t}^*$ is the probability of the most likely sequence of labels for that document.

  Obtain annotations for the $batch\_size$ documents with the highest values of LC (least confidence), and add them to $\boldsymbol{c}$

end

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

F1 scores over ten repeats of the active learning simulation on the NER dataset (some methods are omitted for clarity). When the number of iterations is very small, neighter IBCC nor DS are able to outperform majority vote, and only produce a very small benefit as the number of labels grows. This highlights the need for a sequential model such as BSC or HMM-crowd for effective active learning. IBCC learns slightly quicker than DS, while BSC-CV clearly outperforms HMM-crowd: we believe this difference is due to the Bayesian treatment of IBCC and BSC, which means they are better able to estimate confidence than DS and HMM-crowd, which use maximum likelihood inference. BSC-seq produces the best overall performance, and the gap grows as the number of labels increases, since more data is required to learn the more complex model.

6 Conclusions

We proposed BSC, a novel Bayesian approach to aggregating sequence labels that can be combined with several different models of annotator noise and bias. To model the effect of dependencies between labels on annotator noise and bias, we introduced the *seq* annotor model. Our results demonstrated the benefits of BSC over established non-sequential methods, such as MACE, Dawid and Skene (DS), and IBCC. We also showed the advantages of a Bayesian approach for active learning, and that the combination of *BSC* with *seq* annotator model improves the state-of-the-art over HMM-crowd on three NLP tasks with different types of span annotations. In future work, we plan to adapt active learning methods for easy deployment on crowdsourcing platforms, and for investigate techniques for automatically selecting good hyperparameters without recourse to a development set, which is often unavailable at the start of a crowdsourcing process.

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A Update Equations for the Forward-Backward Algorithm

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

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

$$ll_{n,\tau}(j) = \sum_{k=1}^{K} \mathbb{E} \ln A^{(k)} \left(j, c^{(k)}_{n,\tau}, c^{(k)}_{n,\tau-1} \right) \quad (15)$$

where $r^{-}_{n,0,\iota} = 1$ where $\iota =$'O' and 0 otherwise. The *backwards pass* starts from $\tau = L_n$ and scrolls backwards, computing:

$$\ln \lambda_{n,L_n,j} = 0, \qquad \ln \lambda_{n,\tau,j} = \ln \sum_{\iota=1}^{J} \exp \big\{ \ln \lambda_{i,\tau+1,\iota} + \mathbb{E} \ln T_{j,\iota} + ll_{n,\tau+1}(\iota) \big\}. \tag{16}$$

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

$$r_{n,\tau,j} = \frac{r^{-}_{n,\tau,j} \lambda_{n,\tau,j}}{\sum_{j'=1}^{J} r^{-}_{n,\tau,j'} \lambda_{n,\tau,j'}} \tag{17}$$

$$s_{n,\tau,j,\iota} = \frac{\tilde{s}_{n,\tau,j,\iota}}{\sum_{j'=1}^{J} \sum_{\iota'=1}^{J} \tilde{s}_{n,\tau,j',\iota'}} \tag{18}$$

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