# Improving Estimates of Transitions from Satellite Data: A Hidden Markov Model Approach*

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**Abstract**

Satellite-based image classification facilitates low-cost measurement of the Earth's surface composition. However, misclassified imagery can lead to misleading conclusions about transition processes. We propose a correction for transition rate estimates based on the econometric measurement error literature to extract the signal (truth) from its noisy measurement (satellite-based classifications). No ground-truth data is required in the implementation. Our proposed correction produces consistent estimates of transition rates, confirmed by longitudinal validation data, while transition rates without

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correction are severely biased. Using our approach, we show how eliminating deforestation in Brazil's Atlantic forest region through 2040 could save $100 billion in CO2 emissions.

**Keywords**: Measurement Error, Remote-Sensing Data, Land Cover, Hidden Markov Model

**JEL Codes**: C13, Q15, R14

# 1 Introduction

In recent years, publicly available satellite-based data combined with increasingly sophisticated machine learning algorithms have provided unprecedented access to regional and global estimates of Earth's surface composition. Remote sensing data provide relatively low-cost information that is difficult to obtain by other means, with high spatial resolution and wide geographic and temporal coverage. Not surprisingly, they are increasingly used across a number of fields, including economics, geography, biology, ecology, and political science, and in setting policy.[1]

However, image classification techniques, which are used to convert the spectral signature of a pixel into an interpretable category, can lead to non-negligible misclassifications and bias areal estimates (Czaplewski, 1992; Jain, 2020). These classification errors can also affect estimates of the transition processes of outcomes of interest – our focus in this paper. Intuitively, errors in classifications can make transition rates appear excessively high. For example, much of the apparent land cover change in satellite-based data may be the result of misclassification (Abercrombie and Friedl, 2016). When remotely sensed rates of land cover change are used as inputs by decision makers (e.g., regulation in Brazilian Amazonia is based on remotely sensed deforestation rates;

[1]See Donaldson and Storeygard (2016) for an overview of applications of remotely sensed data in economics. Geographers, biologists, and ecologists have also explored remote-sensing data to investigate land cover and degradation, terrestrial and marine ecosystems, sea level, biodiversity, and carbon emissions and carbon sequestration (Foley et al., 2005; Geller et al., 2017).

see Assunção et al., 2019) biases in transition rates can undermine efficient policy design and enforcement. Similarly, Fowlie et al. (2019) show how errors in satellite-based measures of pollution can lead to misleading information about pollution trends in different geographic areas, leading to over-regulation in "clean" areas and under-regulation in "dirty" areas.

To mitigate these concerns, researchers typically impose a set of heuristic and ad hoc adjustments to stabilize classifications across years. Yet, Friedl et al. (2010) provide strong evidence that typical heuristic adjustments do not eliminate excessive rates of land cover change. An alternative solution is to correct classification errors using validation data that can be treated as ground truth (Czaplewski, 1992). However, extensive validation data are expensive to obtain and extremely scarce in practice (Goldblatt et al., 2016), and even when validation data exists, there may be few observations available, which limits the accuracy of the estimates.

In this paper, we propose a different approach. We present a hidden Markov model (HMM) that corrects for misclassification bias. A HMM is the combination of an unobserved Markov process with observations that depend only on the contemporaneous hidden state (McLachlan and Peel, 2000). For instance, when studying land use change, the ground truth land use is the hidden state and classifications based on remote sensing imagery are the observations.[2] The idea here is to extract the signal (truth) from its noisy measurement (satellite-based classifications). The framework assumes that researchers either have access to panel data (with at least three time periods) of satellite-based classifications, or that they can generate such classifications themselves using remotely sensed data.

Based on Hu's seminal work on non-classical measurement error (summarized in Hu (2017, 2020)), we show how the HMM assumptions allow us to uniquely recover both the true transition probabilities *and* the misclassification probabilities from the observed data. The required assumptions (fully discussed below in Section 4) are not very restrictive in practice and some of them are testable. We discuss two different estimators for the hidden Markov model: a minimum distance (MD) estimator, that builds directly from the constructive identification results; and a maximum

[2]We use "land use" and "land cover" interchangeably in this paper.

likelihood (ML) estimator, which is implemented using the expectation-maximization (EM) algorithm (Dempster et al., 1977; van Handel, 2008). Given estimated transition probabilities, we can construct the most likely trajectory of the states for each pixel in the data.

From the perspective of implementation, there are at least two attractive features to the HMM approach. First, we do not require ground-truth data to implement the correction. Second, the HMM estimator can be implemented using classified data and not raw remote sensing data. These features allow for a division of labor between remote sensing specialists, who can classify the raw data, and applied researchers, who can implement the correction in their application.

We investigate the performance of our strategy in two different settings: (i) a land use change study based on rich longitudinal ground-truth validation data, and (ii) an empirical application focused on the Brazilian Atlantic Forest, one of the world's most threatened biodiversity hotspots.[3] In the first setting, we conduct a validation exercise using ground-truth longitudinal data for the state of Mato Grosso, Brazil, from 2006 to 2010 – a major center of agricultural production with rapid land use change within Brazil's Legal Amazon, a bio-administrative unit covering the Brazilian Amazon biome. The panel data provide a unique opportunity to test the performance of the HMM correction because they allow us to observe true transition rates (typical validation data are composed of a single or repeated cross-sections). Our HMM-based corrections estimate transition rates accurately; in contrast, transition rates computed without correction for misclassification are 3 to 9 times higher than observed in the ground truth data. We also improve the overall accuracy of the original classifications by finding the most likely sequence of land uses for each pixel in the data based on the HMM estimates.

Our second empirical application of the HMM correction concerns the social benefits from eliminating deforestation in Brazil's Atlantic Forest. The Atlantic Forest biome is located in the

[3]We also carry out an extensive Monte Carlo study, presented in the Online Appendix. There, we find that the HMM method estimates transition probabilities and misclassification probabilities accurately, and we document important trade-offs between the two estimators: while the MD estimator is substantially faster, the ML estimator performs better in terms of mean-square errors.

most developed region of the country and is the most degraded Brazilian biome, containing only roughly 30% of its original forest cover. This highly biodiverse area has been the target of various initiatives aimed at slowing deforestation and the resulting CO2 emissions, and it was included in Brazil's National Determined Contribution to the Paris Climate Agreement. Applying the HMM correction to a rich remotely sensed database of Brazilian land cover, we obtain an estimate of 2.78 million tons of carbon currently present in the forest (equivalent to roughly $774 billion in social value). Using the raw data without correction, we obtain an estimate of just 2.39 million tons of carbon (equivalent to roughly $666 billion). The significantly lower estimated value based on the raw data is a consequence of predicting excessive land use transitions, which leads to lower predicted ages of the forest, and therefore lower carbon stocks (younger trees store less carbon). Simulating forward to 2040 using the HMM estimates, we predict that eliminating all deforestation from the Atlantic Forest would prevent approximately $100 billion value in carbon emissions. Beyond the current application (and in contexts other than deforestation), the approach we develop can help evaluate accurately the effectiveness, and optimality, of relevant environmental policies.

**Related Literature.** To the best of our knowledge, the closest papers to ours are by Abercrombie and Friedl (2016), Sandler and Rashford (2018), and Alix-Garcia and Millimet (2021). Like us, Abercrombie and Friedl (2016) consider an HMM-based correction to errors in classifications. They implement the HMM forward-backward algorithm (see van Handel, 2008, Chapter 3) to determine the most likely land cover for each pixel in a given year. In contrast to their work, we link the HMM procedure to formal identification results based on a set of explicit assumptions, bringing transparency to the contexts in which the correction is most appropriate and highlighting which assumptions can be tested in the data directly. Most crucially, we allow for the estimation of time-varying transition probabilities, which is essential in many applied studies, e.g. when estimating how (and explaining why) deforestation processes may change over time.

Sandler and Rashford (2018) and Alix-Garcia and Millimet (2021) focus on accurately modeling land use as a discrete choice problem. Both papers extend (in different directions) the maximum

likelihood estimator with misclassified choices proposed by Hausman et al. (1998), and show that their estimators perform well in practice, while standard models (e.g., probit) result in estimated coefficients that are too close to zero, resembling an attenuation bias problem.[4] We focus instead on estimating accurately the land use variable and the transition probabilities – our contributions are therefore highly complementary.

This paper is organized as follows: Section 2 discusses the sources and consequences of misclassifications in remote sensing data. Section 3 formalizes the misclassification problem. Section 4 presents the HMM, the formal identification results, and two estimation methods. Section 5 describes the validation exercise using ground-truth data. Section 6 presents our empirical application focused on the Brazilian Atlantic Forest, and Section 7 concludes.[5]

[4]Sandler and Rashford (2018) extend Hausman et al. (1998) to cover multinomial choice models, apply it to satellite-based agricultural land cover data in the US, and find that biofuel policies can have impacts on land use that are orders of magnitude larger than when misclassifications are ignored (in some cases, corrected effects are 350% larger than the uncorrected effects). Alix-Garcia and Millimet (2021) extend Hausman et al. (1998) to allow for misclassification rates that depend on covariates and incorporate the scobit family of binary choice models, which introduces an additional shape parameter into the link function – nesting the logit model as a special case, and helping estimation when the outcome is of the rare-events type, as in the deforestation case. Applying their correction to a conservation cash-transfer program in Mexico, they find greater conservation impacts than when misclassifications are ignored.

[5]The Online Appendix presents (i) relevant mathematical derivations for the HMM correction; (ii) the measurement error in observed transition probabilities that is implied by the HMM model, and its consequences for regression analyses; (iii) the details of the EM and Viterbi algorithms; (iv) the Monte Carlo simulation studies; and (v) additional details on the carbon stock empirical application. Code for replicating the Monte Carlo simulations in R is available at https://github.com/atorch/hidden_markov_model.

# 2 Sources and Consequences of Misclassifications

**Sources of Misclassifications.** In general, classifications are performed following four steps in remote sensing projects: data acquisition, pre-processing, analysis, and evaluation. Each step is associated with different types of potential errors, as we discuss next (Lillesand et al., 2015).

First, data is *acquired* by satellites as raw imagery. At this stage, errors may occur due to the combination of the specific sensor characteristics of the satellite (including sensor noise and response), the angle of the satellite with respect to the sun and the earth's surface, and atmospheric conditions, including cloud cover and haze. Second, *pre-processing* operations are used to correct for these errors (geometric and radiometric corrections), but such corrections are imperfect and may introduce new errors. Third, researchers *analyze* the images by training a classification algorithm on the pre-processed data. Continuous efforts to develop better algorithms, together with increased computer power, may help reduce errors, but are unlikely to eliminate them completely. Finally, the output classifications, extrapolated to the "held-out" or "testing" data set, are compared to ground-truth data to evaluate and improve the accuracy of the classification. Here, ground-truth data sampling may lead to further discrepancies due to, e.g., location accuracy (i.e., ground points may not coincide exactly with the pre-processed pixels) and scale misalignment (i.e., the size of ground-truth areas may be different from the units mapped from the imagery).

In general, specialists often consider overall accuracies for land cover classifications (namely, the percentage of correct classifications) to be acceptable when they are greater than 85%, though this threshold may vary depending on the context (Xie et al., 2020).[6] Indeed, classification accuracies can be lower in practice, given the difficulties involved. For instance, the widely-used Cropland Data Layer (CDL), developed by the US Department of Agriculture, National Agricultural Statistics

[6]For continuous variables, such as pollution, a common measure of overall accuracy (though not the only one) is based on the $R^2$ obtained from regressing the remotely sensed-based variable on the true measurement (based on ground-level monitors). In practice, the $R^2$'s can vary in the 0.6–0.9 range; see, e.g., van Donkelaar et al. (2019) for a satellite-based measure of air quality in the US and Canada.

Service (USDA NASS), has an overall accuracy of roughly 90%, in Iowa in 2018; the Mapbiomas data, Collection 5.0, has an overall accuracy of approximately 91.2% for the Brazilian territory, and around 90% for the Atlantic Forest biome, over the years 1985–2018; and the GlobeLand30, a global scale land cover mapping with 30 meters resolution launched by China in 2010, has an overall accuracy of 80% in 2010.[7]

**Consequences of Misclassification.** Remotely sensed data can be used to document and investigate spatial and temporal trends, as well as in regression analyses and causal inference studies; misclassifications in satellite-based data can affect the results of any of these types of studies.

Transition rates themselves are frequently important objects of interest. In the context of deforestation and afforestation rates, misclassification tends to exaggerate the rate at which land is moving in and out of forest, especially when misclassification rates are large relative to the true transition rates (which are typically low given large conversions costs). Even if the net rate of forest cover is accurate, exaggerated gross flows can have misleading implications for carbon dynamics because forest biomass takes many decades to accumulate (yonger forests hold less carbon than older forests). The erroneous rates can therefore distort the effectiveness, and optimality, of environmental policies in practice. The same reasoning applies to understanding the consequences

[7]The CDL Cropland Data Layer has recall rates (i.e., the percentage of correct predictions given the true land use) of roughly 92% for corn and soy, a recall of roughly 49% for alfalfa, and of 41% for winter wheat, in Iowa in 2018; see `https://www.nass.usda.gov/Research_and_Science/Cropland/metadata/metadata_ia18.htm` for more detail. The overall accuracies of the Mapbiomas data presented above are based on the most aggregated land cover classifications; for the more disaggregated classifications, the accuracies drop slightly to 87% for the national territory, and to 86% for the Atlantic Forest. The recall rate in Brazil (Atlantic Forest) is around 96% (91%) for forest and roughly 79% (84%) for pasture; see `https://mapbiomas.org/en/accuracy-analysis`. For the GlobeLand300, overall accuracies can drop to less than 65% depending on the classifier used; see Chen et al. (2015).

for biodiversity, as they also depend asymmetrically on the estimated rate of habitat destruction and recovery. Estimating transition rates accurately is important more generally, beyond the land cover example; e.g., they are critical inputs for climate change models, which require well-documented evolution of polar ice coverage, sea levels, wildfires, wind patterns, relative humidity, and surface temperature, among other factors (all of which can be measured remotely based on satellite information, given the low spatial coverage of ground monitors); transitions are also important to study investment decisions in, say, housing innovations as in Marx et al. (2019).

In terms of regression analyses and causal inference, we note that measurement error in transition rates is not necessarily classical and can therefore lead to biases in linear and nonlinear models, and when transition rate is either the dependent or the independent variable.[8] In Online Appendix B, we explain formally how measurement error in transition rates leads to biases in linear, logit, and nested logit regression models when the transition rates are the dependent variable. We also show via simulation, in Online Appendix D.5, how this measurement error in a dependent variable leads to biased estimates of a policy designed to reduce deforestation. Researchers using remote sensing data in regression analyses should therefore be cautious when using remotely sensed transition rates. The HMM framework we outline below can help provide unbiased parameter estimates for many of these scenarios.

# 3 Framework

In this section, we illustrate how misclassification of remote sensing data can affect estimates of transition probabilities. Our running example is the land use classification problem, but results

[8]Our point is different from Hausman et al. (1998) in that we consider continuously measured outcomes (transition rates) rather than binary outcomes. In general, biases are a concern not only with remotely sensed transition rates, but any remotely-sensed variables, such as fire incidents affecting health outcomes (Rangel and Vogl, 2019) and weather shocks impacting civil conflicts (Harari and Ferrara, 2018).

can be applied to other classification problems using longitudinal remote-sensing data, such as pollution, fire incidents, and nighttime lights.

Let $S_{it} \in \mathcal{S}$ denote the ground truth land use at location $i$ at time $t$. In applications, a location is usually a pixel or a spatial point. The set of possible values that $S_{it}$ can take is $\mathcal{S} = \{s_1, ..., s_K\}$, $K < \infty$. We do not restrict the number of elements in $\mathcal{S}$, so the land cover categories may be specific and numerous, or they may be very broad such as forest and non-forest. Extensions to continuously distributed measurements, such as pollution or nighttime light, are possible, at the cost of more burdensome notation and additional technical details.[9] The true land use $S_{it}$ is not observed unless ground-truth data is collected for $i$ at $t$.

Suppose there exists an observable noisy measurement of $S_{it}$ denoted by $Y_{it} \in \mathcal{Y} = \{y_1, ..., y_K\}$. We assume the sets $\mathcal{Y}$ and $\mathcal{S}$ are equal, but we maintain the distinction in the notation for clarity. In typical applications, $Y_{it}$ is the output of a classification algorithm that relies on machine learning techniques to predict $S_{it}$ given a vector of (pre-processed) remote-sensing variables, $R_{it}$. For example, $R_{it}$ may be a vector including some vegetation index, and the reflectance patterns of different wavelengths (infrared, red, blue, etc.) for pixel $i$ at time period $t$. We can take $Y_{it} = f(R_{it})$, for some function $f$ that depends on the data used and the classification algorithm.

We assume the researcher has access to a longitudinal data of land use classifications $\{Y_{it} : i = 1, ..., N; t = 1, ..., T\}$, obtained from remote-sensing data analysis (performed by the researcher herself or by others). In practice, it is common to have a large set of spatial points $N$ and a small number of time periods $T$. Under standard regularity conditions, longitudinal data on $Y_{it}$ can be used to estimate the transition probabilities $\Pr[Y_{it+1}|Y_{it}]$, as well as the marginal distribution $\Pr[Y_{it}]$, with high accuracy. We can therefore treat these probabilities as known by the researcher

[9]For variables taking value on the real line, one needs to work in Hilbert spaces, with their corresponding operators (see, e.g., Hu and Schennach, 2008), instead of in Euclidean spaces with transformation matrices, as we do here. In empirical work, one may want to discretize continuously distributed variables in the data before applying our correction – we leave the investigation of optimal discretization for future research.

for identification purposes. Importantly, while not explicit in the notation, we consider the analysis conditional on some set of observable covariates. For instance, the data may come from different subregions of a larger region of interest; the analysis can then be performed separately for (i.e., conditioned on) each subregion.[10] Furthermore, we allow the transition probabilities and marginal distributions to vary by year, so the $t$ subscripts on $Y_{it}$ and $S_{it}$ should be understood to index the distribution the random variable is drawn from as well as the year of the observation.

For pixel $i$ at time period $t$, the probability of observing land use prediction $Y_{it} = y$ is given by

$$\Pr\left[Y_{it} = y\right] = \sum_{s \in \mathcal{S}} \Pr\left[Y_{it} = y | S_{it} = s\right] \Pr\left[S_{it} = s\right],$$

where $\Pr\left[Y_{it} = y | S_{it} = s\right]$ is the probability of observing land use $y$ when the ground truth land use is $s$; this is known as the misclassification probability when $y \neq s$. As mentioned previously, errors in classifications may be the combined result of the specific characteristics of the satellite, together with the pre-processing and classification operations (Lillesand et al., 2015).

In matrix notation, the equation above becomes

$$\mathbf{P}_{Y_t} = \Upsilon \mathbf{P}_{S_t}, \tag{1}$$

where $\mathbf{P}_{Y_t}$ is a $K \times 1$ vector with elements $\Pr\left[Y_{it} = y_k\right]$, $k = 1, ..., K$; the $K \times 1$ vector $\mathbf{P}_{S_t}$ has elements $\Pr\left[S_{it} = s_k\right]$; and $\Upsilon$ is a $K \times K$ matrix with $\Pr\left[Y_{it} = y_l | S_{it} = s_k\right]$, for $l, k = 1, ..., K$. We follow the literature and refer to the elements of $\Upsilon$ as misclassification probabilities, even though it includes the probabilities of correct classifications on the diagonal (also known as the "recall rate"), while the misclassification probabilities are the off-diagonal terms. For now, we consider the case where $\Upsilon$ is time-invariant, but the results can be extended to misclassifications that may change over time (discussed in Remark 1 below).

[10] Incorporating continuously distributed covariates, such as slope and altitude, is more cumbersome, but feasible. One can apply standard kernel smoothing techniques, or parameterize the transition probability functions.

While the vector $\mathbf{P}_{Y_t}$ can be estimated consistently using frequency estimators, it is not possible to recover the true land use distribution $\mathbf{P}_{S_t}$ without additional information. Further, there is no guarantee that the observed (estimated) transition $\Pr[Y_{it+1}|Y_{it}]$ is close to the true transitions $\Pr[S_{it+1}|S_{it}]$.[11]

# 4 Correction Based on the Hidden Markov Model

We now turn to our proposed solution. Here, we state Hu's (2017) conditions and results using our notation, and we discuss their plausibility and restrictiveness within the context of our satellite-based classification problem.[12]

For each point $i$, we assume the stochastic process $\{Y_{it}, S_{it} : t = 1, 2, ...\}$ follows a hidden Markov process. Specifically, we assume the ground truth land cover $\{S_{it}\}$ follows a first-order Markovian stochastic process with transition probabilities $\Pr[S_{it+1}|S_{it}]$, while $Y_{it+1}$ is independent of past values $\{Y_{it-h}, S_{it-h}\}$, $h \geq 0$, conditional on $S_{it+1}$. This conditional independence assumption means that, if we know the true land use $S_{it+1}$, past variables $(Y_{it}, S_{it})$ do not contain any additional information about the noisy land-use classification $Y_{it+1}$. This is a common assumption in the measurement error literature (Bound et al., 2001; Schennach, 2021). Formally,

$$\begin{aligned} & \Pr\left[Y_{it+1}, S_{it+1} | \{Y_{it-h}, S_{it-h}\}_{h\geq 0}\right] \\ = \; & \Pr\left[Y_{it+1}|S_{it+1}, \{Y_{it-h}, S_{it-h}\}_{h\geq 0}\right] \times \Pr\left[S_{it+1} | \{Y_{it-h}, S_{it-h}\}_{h\geq 0}\right] \\ = \; & \Pr[Y_{it+1}|S_{it+1}] \times \Pr[S_{it+1}|S_{it}] . \end{aligned} \tag{2}$$

[11] In principle, ground-truth data can be used to estimate $\Upsilon$, which would allow us to recover the true land use shares $\mathbf{P}_{S_t} = \Upsilon^{-1}\mathbf{P}_{Y_t}$, provided that $\Upsilon$ is invertible (Czaplewski, 1992). However, this approach suffers from the limitations discussed in the Introduction and does not recover true transition probabilities.

[12] The results are based on Section 2 of Hu (2017). See also Hu (2008) for his seminal contribution, with a more complete discussion and proofs, and Hu (2020) for a recent overview of econometric methods and applications to models with latent variables and measurement error.

The HMM assumption is motivated by the fact that land use predictions $Y_{it}$ are typically a function only of contemporaneous remote sensing data, $R_{it}$. If the process $\{R_{it}, S_{it}\}$ satisfies the HMM assumptions, then so must $\{f(R_{it}), S_{it}\}$ for any function $f$.[13] (Note that the observed process $\{Y_{it}\}$ does *not* necessarily follow a first-order Markov process.)

There are plausible situations in which equation (2) may be violated. One possibility occurs when misclassification probabilities are serially correlated; i.e., lagged values of $(Y_{it}, S_{it})$ may be useful in predicting current $Y_{it}$ given current land use $S_{it}$. This may happen, for example, when researchers use past values of remote sensing data $R_{it}$ to classify current land use $Y_{it}$. Another possibility is when true transitions may also depend on classified land uses, i.e., $\Pr[S_{it+1}|S_{it}, Y_{it}]$ – possible, e.g., when policymakers take actions based on the observed states.[14] Clearly, the appropriate application of the HMM depends on the context.

Equation (2) limits the potential datasets for which an HMM correction is appropriate. In some publicly available land cover datasets, such as Mapbiomas, ad hoc corrections have already been applied based on the time series of classifications, as mentioned in the Introduction. In such cases, it might not be reasonable to assume that misclassification probabilities do not depend on lagged

[13] To see why, note that for any random variable $Z$, if $R_{it} \perp\!\!\!\perp Z|S_{it}$ (in words, if $R_{it}$ is conditionally independent of $Z$ given $S_{it}$), it follows that $f(R_{it}) \perp\!\!\!\perp Z|S_{it}$ for any function $f$. In typical applications, the remotely-sensed data $R_{it}$ are complicated high-dimensional objects. In theory, we could fit an HMM using the process $\{R_{it}, S_{it}\}$. We opted for not doing so because the misclassification probabilities $\Pr[Y_{it}|S_{it}]$ can be represented by a $K \times K$ matrix, which is a much simpler object than a continuous distribution over high-dimensional sensor data. Finally, note that in typical annual classifications, one can make use of within-year time-series variation in remote-sensing data to classify annual land uses; for such cases, we extend our notation allowing the vector $R_{it}$ to incorporate within-year remote sensor covariates.

[14] While we do not investigate the full extent of these possibilities here, we note that identification is possible for some of these cases, involving a more complex Markov process for $(Y_{it}, S_{it})$ and a more demanding set of identifying assumptions, exploring the ideas in Section 2.5 of Hu (2017).

variables. However, even when such ad hoc correction has been applied, it may be possible to obtain the raw data – we did this for our empirical application.

**Useful Identities.** Given the HMM setting, there are a series of identities that are helpful to obtain the identification results. For any two random variables $X, W$, define the $K \times K$ matrix $\mathbf{M}_{X,W}$ with elements given by the joint distribution $\Pr[X = s_l, W = s_k]$, with $s_l, s_k \in \mathcal{S}$ and $l, k = 1, ..., K$. Similarly, for any given $y_{t+1} \in \mathcal{Y}$, define the matrix $\mathbf{M}_{y_{t+1},X,W}$, with elements $\Pr[Y_{it+1} = y_{t+1}, X = y_l, W = y_k]$, as well as the diagonal matrix $\mathbf{D}_{y_{t+1}|X}$, with diagonal entries $\Pr[Y_{it+1} = y_{t+1}|X = s_k]$.[15]

From the joint distribution of $(Y_{it}, Y_{it-1})$ we obtain

$$\mathbf{M}_{Y_t,Y_{t-1}} = \Upsilon \mathbf{M}_{S_t,Y_{t-1}}. \tag{3}$$

Similarly, from the joint distribution of $(Y_{it+1}, Y_{it})$ we get

$$\mathbf{M}_{Y_{t+1},Y_t} = \Upsilon \mathbf{M}_{S_{t+1},S_t} \Upsilon^\intercal, \tag{4}$$

where the superscript $^\intercal$ denotes transpose. And, from the joint distribution of $(Y_{it+1}, Y_{it}, Y_{it-1})$, we have for a given $Y_{it+1} = y_{t+1} \in \mathcal{Y}$,

$$\mathbf{M}_{y_{t+1},Y_t,Y_{t-1}} = \Upsilon \mathbf{D}_{y_{t+1}|S_t} \mathbf{M}_{S_t,Y_{t-1}}. \tag{5}$$

Identification and estimation of the HMM is based on (3)–(5). See Online Appendix A for a derivation of these equations.

[15] As we allow the distribution of $Y_{it}$ to vary by year, note that the time subscripts on $y_{t+1} \in \mathcal{Y}$ serve to define the distribution used for $Y_{it+1}$.

## 4.1 Identification of the Hidden Markov Model

Next, we outline the conditions needed to identify the Markov transition process $\Pr[S_{it+1}|S_{it}]$, the marginal distribution $\Pr[S_{it}]$ (including the initial distribution), and the misclassification probabilities $\Upsilon$ using at least three periods of data on $Y_{it}$.

The first two conditions were discussed above and we state them here for completeness.

**Condition 1.** *The joint process* $\{Y_{it}, S_{it}\}$ *follows a hidden first-order Markov process, satisfying equation* (2).

**Condition 2.** $Y_{it}$ *and* $S_{it}$ *have the same support, i.e.,* $\mathcal{Y} = \mathcal{S}$.[16]

Next, we impose a mild restriction on observed classifications $Y_{it}$:

**Condition 3.** *The matrix* $\mathbf{M}_{Y_t,Y_{t-1}}$ *has full rank, i.e.,* $\text{rank}\left(\mathbf{M}_{Y_t,Y_{t-1}}\right) = K$.

This condition is testable. If the land use classifications $Y_{it}$ are sufficiently persistent, $\mathbf{M}_{Y_t,Y_{t-1}}$ may be strictly diagonally dominant (note that for persistent processes, diagonal elements of this matrix will be larger than off-diagonal elements), and therefore full rank. This is plausible in land use applications because converting land is typically costly, which induces persistence in the data. Importantly, this condition implies that both matrices $\Upsilon$ and $\mathbf{M}_{S_t,Y_{t-1}}$ are invertible too (a fact that we use below); see equation (3). As a word of caution, note that, in practice, the larger the set of land uses considered (i.e., the larger the $K$), the less likely $\mathbf{M}_{Y_t,Y_{t-1}}$ will have full rank. That is because with more types of land uses in a given data (some of which could be rare), the higher the

[16] It is possible to extend the identification results to when the support of $Y_{it}$ has more points than the support of $S_{it}$; i.e., when $card(\mathcal{Y}) \geq card(\mathcal{S})$. To see how, note that we can first combine some values in the support of $\mathcal{Y}$ to obtain a transformed $\widetilde{Y}_{it}$ with support $\widetilde{\mathcal{Y}} = \mathcal{S}$, then apply the identifying assumptions to the process $(\widetilde{Y}_{it}, S_{it})$ and identify the parameters of the transformed process, and then "undo" the transformation and recover the entire process for the original $(Y_{it}, S_{it})$ – see Corollary 2.4.1 in Hu (2017). Though feasible, we do not exploit this possibility as Condition 2 seems reasonable for most applications.

chances that some of them will not be observed in a time period, leading to a zero column (or row) in $\mathbf{M}_{Y_t,Y_{t-1}}$. Therefore, researchers using the HMM approach need to be careful when selecting the set of land uses in practice.

Combining (3) and (5), we get

$$\mathbf{M}_{y_{t+1},Y_t,Y_{t-1}}\mathbf{M}^{-1}_{Y_t,Y_{t-1}} = \mathbf{\Upsilon}\,\mathbf{D}_{y_{t+1}|S_t}\,\mathbf{\Upsilon}^{-1}. \tag{6}$$

This is an eigenvalue-eigenvector decomposition of a matrix constructed entirely from the data, i.e., from $\mathbf{M}_{y_{t+1},Y_t,Y_{t-1}}\mathbf{M}^{-1}_{Y_t,Y_{t-1}}$. The columns of $\mathbf{\Upsilon}$ are the eigenvectors. Because each column of $\mathbf{\Upsilon}$ must sum to one, the scale of the eigenvectors is fixed. The diagonal elements of $\mathbf{D}_{y_{t+1}|S_t}$ are the eigenvalues. The next two assumptions guarantee a unique eigenvalue-eigenvector decomposition. The uniqueness of the decomposition means we can uniquely recover the misclassification probabilities $\mathbf{\Upsilon}$ and the diagonal matrix $\mathbf{D}_{y_{t+1}|S_t}$ from the joint distribution of the observed classifications $(Y_{it+1}, Y_{it}, Y_{it-1})$.

**Condition 4.** $\Pr[Y_{it+1} = y|S_{it} = s] \neq \Pr[Y_{it+1} = y|S_{it} = s']$ *for at least one* $y \in \mathcal{Y}$ *whenever* $s \neq s'$, *and* $s, s' \in \mathcal{S}$.

Condition 4 assumes the eigenvalues are all distinct. This is testable: we only need to perform the eigenvalue-eigenvector decomposition of $\mathbf{M}_{y_{t+1},Y_t,Y_{t-1}}\mathbf{M}^{-1}_{Y_t,Y_{t-1}}$ and check it.[17]

To interpret this condition, consider an example in which there are three land uses: forest, pasture, and crops. Take the observed $y$ as forest. Suppose it is very likely to observe a forest classification tomorrow (i.e. $Y_{it+1}$ = forest) when today's true land use is forest; moreover, suppose it is very unlikely that we would observe forest tomorrow when today's land use is pasture, and even less likely to see forest tomorrow when today's land use is crops (i.e., pasture and crops are

[17]Condition 4 corresponds to Assumption 3 in Hu (2017). We take the function $\omega(y)$ defined in his assumption to be the Dirac function.

both persistent, but pasture is abandoned more often than cropland). In this case,

$$\Pr\left[Y_{it+1} = y | S_{it} = \text{forest}\right] > \Pr\left[Y_{it+1} = y | S_{it} = \text{pasture}\right] > \Pr\left[Y_{it+1} = y | S_{it} = \text{crops}\right],$$

for $y = forest$, and so Condition 4 is satisfied here.

In case Condition 4 is violated for some $y$, we can use another land-use classification $y' \neq y$ for which the condition is valid. If we find no such $y$, then identification is not guaranteed. When Condition 4 holds for more than one value $y$, the model becomes overidentified.

Next we turn to the eigenvectors:

**Condition 5.** $\Pr\left[Y_{it} = s^* | S_{it} = s^*\right] > \Pr\left[Y_{it} = s | S_{it} = s^*\right]$ *for any* $s \neq s^*$, *and* $s, s^* \in \mathcal{S}$.

Condition 5 fixes the order of the eigenvectors. It implies $s^*$ is the mode of the distribution $\Pr\left[Y_{it} | S_{it} = s^*\right]$. In words, given that the true land use is $s^*$, the probability that the noisy measure $Y_{it}$ equals $s^*$ is greater than the probability that $Y_{it}$ equals any other land use $s \neq s^*$. This condition is satisfied when $\Upsilon$ is strictly diagonally dominant – this is reasonable as accurate land use classifiers (which is common in practice) should generate correct classifications well in excess of incorrect classifications. (Note however that this condition is less likely to be satisfied when $K$ is large: the greater the number of possible land uses, the less likely the correct classification $s^*$ will be the modal outcome.)[18]

Next, given identification of the misclassification probabilities $\Upsilon$ from the eigenvalue-eigenvector decomposition (6) under Conditions 1–5, we identify the joint distribution $\Pr\left[S_{it+1}, S_{it}\right]$ under the assumption that $\Upsilon$ is time-invariant. For completeness, we impose this condition explicitly (and discuss its relaxation in Remark 1 below):

**Condition 6.** $\Pr\left[Y_{it+1} | S_{it+1}\right] = \Pr\left[Y_{it} | S_{it}\right]$, *for all* $t$.

[18]Condition 5 corresponds to Assumption 4.2 in Hu (2017). Alternatively, one could instead assume the misclassification probabilities $\Pr\left[Y_{it} = y | S_{it} = s\right]$ are decreasing in $s$ for some $y$; this would correspond to Assumption 4.1 in Hu (2017) and it also pins down the ordering of the eigenvectors.

Given Condition 6 and equation (4), we obtain

$$\mathbf{M}_{S_{t+1},S_t} = \boldsymbol{\Upsilon}^{-1}\mathbf{M}_{Y_{t+1},Y_t}\left(\boldsymbol{\Upsilon}^{\intercal}\right)^{-1}, \tag{7}$$

which implies identification of $\mathbf{M}_{S_{t+1},S_t}$, and hence of both $\Pr[S_{it+1}|S_{it}]$ and $\Pr[S_{it}]$. The argument above leads to the following proposition:

**Proposition 1.** *(Theorem 1, Hu (2017)). Suppose Conditions 1–6 hold. Then, the joint distribution of the observed classifications* $(Y_{it+1}, Y_{it}, Y_{it-1})$ *uniquely identifies* $\Pr[Y_{it}|S_{it}]$, $\Pr[S_{it+1}|S_{it}]$, *and* $\Pr[S_{it}]$.

*Remark* 1. (Time-varying misclassifications.) It is plausible to consider misclassification probabilities that do not vary over time when there are no common shocks (due to, say, meteorological conditions) affecting atmospheric noise, nor technical difficulties requiring satellite maintainance that may affect the quality of the raw data, nor substantive technical changes to the pre-processing and classification operations generating $Y_{it}$ during the sampling period. However, when some of these conditions fail, misclassification probabilities may change over time – a possibility that we can accommodate in our framework.

Formally, denote the time-varying matrix by $\boldsymbol{\Upsilon}_t$. Equation (6) then becomes $\mathbf{M}_{y_{t+1},Y_t,Y_{t-1}}\mathbf{M}^{-1}_{Y_t,Y_{t-1}} = \boldsymbol{\Upsilon}_t\,\mathbf{D}_{y_{t+1}|S_t}\,\boldsymbol{\Upsilon}_t^{-1}$, which means that we still need just three time periods to identify the misclassification probabilities. We also need three time periods to identify the marginal distribution $\Pr[S_{it}]$ – see equation (1). However, equation (7) becomes $\mathbf{M}_{S_{t+1},S_t} = \boldsymbol{\Upsilon}^{-1}_{t+1}\mathbf{M}_{Y_{t+1},Y_t}\left(\boldsymbol{\Upsilon}_t^{\intercal}\right)^{-1}$, implying that we now need $T \geq 4$ periods of data to identify $\mathbf{M}_{S_{t+1},S_t}$ (we need $t+1$, $t$, and $t-1$ to identify $\boldsymbol{\Upsilon}_t$ and $t$, $t+1$, and $t+2$ to identify $\boldsymbol{\Upsilon}_{t+1}$). Clearly, $\boldsymbol{\Upsilon}_1$ and $\boldsymbol{\Upsilon}_T$ are not identified, and neither are the transition probabilities in the first and last time periods.

## 4.2 Estimators for the HMM Correction

We consider two estimators for the HMM correction: a minimum distance (MD) estimator and a maximum likelihood (ML) estimator. The estimators offer complementary advantages: we find the ML estimator is more precise while the MD estimator is computationally faster.

As mentioned previously, we assume the researcher has access to a panel data of classifications $\{Y_{it} : i = 1, ..., N; t = 1, ..., T\}$. Following Conley (1999), we allow $(Y_{it}, S_{it})$ to be a random field – i.e., we let an observation be a realization of a random process at a point in a Euclidean space. In the temporal dimension, we assume each point follows the hidden first-order Markov process discussed in the previous section; in the cross-sectional dimension, we assume weak dependence – that is, as the spatial distance between pixels increases, the outcomes $(Y_{it}, S_{it})$ and $(Y_{jt}, S_{jt})$, for $i \neq j$, become essentially independent.[19]

### 4.2.1 Minimum Distance Estimator

In principle, we can estimate the misclassification probabilities and the joint distribution of $S_{it}$ using a plug-in estimator based on equations (6)–(7). However, the eigenvalue-eigenvector decomposition may result in estimated probabilities that are negative or greater than one in some data sets. In our experience, this is more likely to happen when the sample size is small and the true parameters

[19]Specifically, we assume the sample consists of realizations of the random variables at a collection of locations inside a sample region. As in Conley (1999), we assume the sample region grows in area as the sample size increases to ensure that the vector indexing cross-sectional dependence is not superfluous. (That is in contrast to an "infill" asymptotics, in which case observations get increasingly dense in a fixed region, violating weak dependence.) We assume $(Y_{it}, S_{it})$ satisfies the mixing condition stated in Section 3.1.3 in Conley (1999) – see also his assumptions A1, A3, and B1–B3. These assumptions allow one to make use of Law of Large Numbers applied to weakly dependent data to obtain consistency of the estimators. Similarly, inference can be based on central limit theorems for stationary and mixing random fields on regular lattices, as developed, e.g., by Bolthausen (1982).

are close to one (e.g. transition probabilities of 0.99). For this reason, it is better to implement a constrained minimum distance estimator (as suggested by Hu, 2017, in his Section 2.6).

For convenience, we denote $\mathbf{M}_{S_{t+1},S_t} = \mathbf{M}_t$ for all $t$, and collect all matrices into $\mathbf{M} = \{\mathbf{M}_t : t = 1, ...T-1\}$, where $T \geq 3$. Define the following functions, for some $y \in \mathcal{Y}$,

$$\begin{aligned} g_{1yt}(\mathbf{M}, \mathbf{\Upsilon}) &= \left\| \mathbf{M}_{y_{t+2},Y_{t+1},Y_t} \mathbf{M}_{Y_{t+1},Y_t}^{-1} \mathbf{\Upsilon} - \mathbf{\Upsilon} \mathbf{D}_{y_{t+2}|S_{t+1}} \right\|, \\ g_{2t}(\mathbf{M}, \mathbf{\Upsilon}) &= \left\| \mathbf{M}_{Y_{t+1},Y_t} - \mathbf{\Upsilon} \mathbf{M}_t \mathbf{\Upsilon}^\intercal \right\|, \end{aligned} \tag{8}$$

where $\|\cdot\|$ is a matrix norm. Notice that $g_{1yt}$ is analogous to equation (6) with slight rearrangement, while $g_{2t}$ is analogous to equation (7). So, under the true joint distributions and misclassification probabilities, $\mathbf{M}$ and $\mathbf{\Upsilon}$, respectively, we have that $g_{1yt} = g_{2t} = 0$. (We omit $\mathbf{D}_{y_{t+2}|S_{t+1}}$ as an argument of $g_{1yt}$ because it is a function of $\mathbf{\Upsilon}$ and $\mathbf{M}_{S_{t+2},S_{t+1}}$.)

Let $g_1$ be a vector that stacks $g_{1yt}$ for all $t \in \{1, \ldots, T-2\}$, and let $g_2$ be a vector that stacks $g_{2t}$ for all $t \in \{1, \ldots, T-1\}$. Define the vector $g = (g_1^\intercal, g_2^\intercal)^\intercal$, and consider the population criterion function $Q(\mathbf{M}, \mathbf{\Upsilon}) = g(\mathbf{M}, \mathbf{\Upsilon})^\intercal \mathbf{W} g(\mathbf{M}, \mathbf{\Upsilon})$, where $\mathbf{W}$ is a symmetric positive-definite weighting matrix. By construction, $Q(\mathbf{M}, \mathbf{\Upsilon}) \geq 0$, and the true matrices $(\mathbf{M}, \mathbf{\Upsilon})$ are the unique solution to the following minimization problem:

$$\min_{\mathbf{M},\mathbf{\Upsilon}} \; g(\mathbf{M}, \mathbf{\Upsilon})^\intercal \; \mathbf{W} \, g(\mathbf{M}, \mathbf{\Upsilon}), \tag{9}$$

subject to each matrix entry being in $[0, 1]$ and probabilities summing up to one.

The minimum distance estimator is the sample analog of (9):

$$(\widehat{\mathbf{M}}, \widehat{\mathbf{\Upsilon}}) = \arg\min_{\mathbf{M},\mathbf{\Upsilon}} \; \widehat{g}(\mathbf{M}, \mathbf{\Upsilon})^\intercal \; \widehat{\mathbf{W}} \, \widehat{g}(\mathbf{M}, \mathbf{\Upsilon}), \tag{10}$$

subject to the same constraints as above, where $\widehat{g}$ is a vector with elements defined in the same way as in (8), but replacing $\mathbf{M}_{y_{t+1},Y_t,Y_{t-1}}$, $\mathbf{M}_{Y_t,Y_{t-1}}$, and $\mathbf{M}_{Y_{t+1},Y_t}$ by their respective frequency estimators $\widehat{\mathbf{M}}_{y_{t+1},Y_t,Y_{t-1}}$, $\widehat{\mathbf{M}}_{Y_t,Y_{t-1}}$, and $\widehat{\mathbf{M}}_{Y_{t+1},Y_t}$, and $\widehat{\mathbf{W}}$ is a data-dependent symmetric positive-definite weighting

matrix that converges in probability to $\mathbf{W}$.[20] This is a standard minimum distance estimator defined over a finite-dimensional parameter space: under i.i.d. data and standard regularity conditions, the estimator is consistent and asymptotically normal (Newey and McFadden, 1994). We expect that the same asymptotic properties can be established using arguments similar to Conley (1999). As usual, inference must be adjusted when parameters are at or near the boundary (Politis and Romano, 1994; Andrews, 1999, 2000).

In general, if we estimate a model with $K$ hidden states from $T$ years of data, we have to optimize over $K(1 + KT)$ parameters subject to $TK + 1$ equality constraints and boundary conditions for every parameter ensuring it is in [0,1]. For instance, when there are $K = 2$ states and $T = 3$ time periods, we have 7 parameters to estimate in total.[21]

### 4.2.2 Maximum Likelihood Estimator

Next, we consider a maximum likelihood estimator. Let $\Pr[Y_i]$ be the joint distribution of $Y_i = (Y_{i1}, ..., Y_{iT})$ for a given point $i$. The pseudo-log likelihood function is

$$L = \sum_{i=1}^{N} \ln \Pr[Y_i], \tag{11}$$

[20] When Condition 4 is satisfied for more than one value of $y \in \mathcal{Y}$, the vector $g_{1t}$ may be augmented accordingly. When that happens, or when $T \geq 4$, the model becomes overidentified. When the panel data is unbalanced (assuming that the data is missing-at-random), we only use the observations for which we have (i) two consecutive periods to estimate $\mathbf{M}_{Y_t,Y_{t-1}}$ and $\mathbf{M}_{Y_{t+1},Y_t}$, and (ii) three consecutive periods to estimate $\mathbf{M}_{y_{t+1},Y_t,Y_{t-1}}$.

[21] The total number of parameters in $T$ years, before accounting for constraints, is $K$ (corresponding to the initial distribution), plus $(T-1)K^2$ (corresponding to $(T-1)$ transition matrices), and $K^2$ (the misclassification matrix). The number of equality constraints is 1 (for the initial distribution), plus $(T-1)K$ (for the $T-1$ transition probability matrices), and $K$ (for the time-invariant misclassification probabilities).

where the likelihood function for observation $i$ integrates-out the hidden states:

$$\begin{aligned}\Pr[Y_i] &= \sum_{s_1 \in \mathcal{S}} \cdots \sum_{s_T \in \mathcal{S}} \Pr[S_{i1} = s_1] \Pr[Y_{i1} | S_{i1} = s_1] \\ &\times \prod_{t=2}^{T} \Pr[S_{it} = s_t | S_{it-1} = s_{t-1}] \Pr[Y_{it} | S_{it} = s_t] . \end{aligned} \tag{12}$$

The ML estimator chooses the initial distribution $\Pr[S_{i1}]$, the transition probabilities for $S_{it}$, and the misclassification probabilities that maximizes the function $L$. As is well-known, the ML estimator is consistent, asymptotically normal, and asymptotically efficient, under i.i.d. data and standard regularity conditions (Newey and McFadden, 1994). As before, we expect the asymptotic properties to extend to spatially weakly dependent data following the arguments developed by Conley (1999). Because maximizing $L$ directly is difficult in practice, we follow the literature and use the expectation-maximization (EM) algorithm (Dempster et al., 1977; van Handel, 2008) – see Online Appendix C for details.

While the ML estimator enforces Conditions 1 and 2 by construction (as well as Condition 6, when we assume misclassification probabilities are time-invariant), it does not impose Conditions 3–5 in the estimation routine. That is in contrast to the MD estimator, which imposes all identification conditions explicitly. Although feasible, imposing these conditions is not necessary in the ML estimation procedure because, when they hold in the data generating process (and so can be treated as regularity conditions), the ML estimator will converge in probability to the true transition and misclassification probabilities, which satisfy these conditions.

*Remark* 2. (Monte Carlo Simulations.) In Online Appendix D, we present our Monte Carlo study. Here, we highlight the main take-aways. First, we find that the HMM approach estimates transition probabilities and misclassification probabilities accurately, including cases where the transition probabilities are time-varying. Second, both MD and ML estimators outperform a standard frequency estimator that ignores misclassifications, which tends to overestimate transition rates when they are persistent. Third, we find important trade-offs between the two estimators. While the MD estimator is substantially faster, the ML estimator performs better in terms of mean-

square errors and is less likely to result in estimates of transition probabilities that are at the edge of the unit interval $[0, 1]$. Fourth, when using the (fast) MD estimator as the initial value for the (more accurate) ML estimator, the combined approach is about 10 times faster on average than the ML estimator alone with random initialization. ML initialized with the MD estimate also results in mean-square errors similar to the ML estimator, so this approach has much to recommend it. Fifth, when we allow misclassification probabilities to depend on past values of $(Y_{it}, S_{it})$, violating equation (2), our MD and ML estimators are biased (as expected), but they are substantially less biased than the frequency estimator ignoring errors in classifications. Finally, we find that when the ML estimates of transition rates are used as the dependent variable in a simple linear treatment effects regression analysis, one obtains unbiased estimates of the treatment effects. In contrast, using a frequency estimator leads to biased estimates of the impact of the treatment.

# 5 Validation Exercise Using Land Cover Data

We now investigate the performance of the HMM approach using unique validation data from the Brazilian Agricultural Research Corporation (Embrapa).[22] We outline the data, the implementation of our methodology, and the validation results.

## 5.1 Ground-Truth and Remote-Sensing Data

The ground-truth data contain information on land use at 409 spatial points observed annually from 2006 to 2010, in the state of Mato Grosso, Brazil. The state of Mato Grosso has attracted considerable interest from researchers and policy makers both because it is a major center of agricultural production within Brazil's Legal Amazon (a bio-administrative unit covering the Brazilian Amazon biome) and because of the rapid land use change there due to agricultural development. The field data were collected from private farms within 14 municipalities in the most intensely

[22] We are grateful to Alexandre Camargo Coutinho and Daniel De Castro Victoria, who generously shared their data with us.

cropped region of central Mato Grosso; see the study area and the sample points in Figure E1 of the Online Appendix.[23] The data is unprecedented in spatial and temporal coverage for the state – and arguably in general – and provide a unique opportunity to test the performance of the HMM correction in practice because they allow us to observe true land use transition probabilities and compare them to our estimates. Further, they also allow us to compare our HMM estimates of misclassification probabilities with a direct estimate of misclassifications $\Pr[Y_{it}|S_{it}]$.

Embrapa's land cover data include various land use categories, but the vast majority of points are either in crops or pasture. We therefore consider two land uses, $\mathcal{S} = \{\text{crops}, \text{pasture}\}$. A small number of points do not fit into either of these categories (e.g. points classified as natural vegetation); we drop these observations. Ultimately, we have 403 unique spatial points, each point observed for one to five years in 2006–2010 (resulting in an unbalanced panel).[24]

We merge the ground truth land use data with remote-sensing data. Specifically, we use measurements from the sixteen-day composite Terra MODIS 250m.[25] MODIS data provide measurements over time of five variables that we observe for each pixel $i$: the reflectance of (i) near infrared (NIR), (ii) middle infrared (MIR), (iii) red, and (iv) blue, as well as (v) the enhanced

[23]The data were collected via farmer or farm manager interviews. The cropping practices were recorded for each individual sites and integrated into a Geographic Information System (GIS) to be combined with the MODIS remote-sensing data (see more below). The area covered extends from the coordinate $(59^o25'14''W, 14^o2'39''S)$ [lower left] to the point $(54^o25'19''W, 11^o42'16''S)$ [upper right]. A total of 40 farmers or farm managers were interviewed as research participants. For more details, see Coutinho et al. (2011) and Brown et al. (2013).

[24]Of the 403 points, 63 are missing ground truth data in one or more years. Overall, we observe ground-truth land use for 93.5% of point-years. In the estimation procedure, we assume the missing data is missing at random.

[25]More precisely, the MOD13Q1 (Collection 5), with spatial resolution of 250 meters and 16-day composite interval, obtained from the United States Geological Survey's Land Processes Distributed Active Archive Center (LP DAAC). We used one MODIS tile (h12v10), which covers the entire field study area. This is consistent with the analysis in Brown et al. (2013).

vegetation index (EVI). Given that MODIS collects information for each pixel every sixteen days, each variable is recorded 23 times per year. In total, we have 115 MODIS covariates per year – these correspond to the vector of variables $R_{it}$ discussed previously in Section 3. We merge the MODIS data with the Embrapa ground-truth data considering the September-to-August harvest years for consistency. In this way, the 2006 ground-truth data, for instance, are merged with sensor data from September 2005 to August 2006.

## 5.2 Generating Land Use Classifications

After merging the ground truth and the MODIS datasets, we construct the satellite-based classifications, $\{Y_{it}\}$. To that end, we randomly split the panel data into two disjoint sets. The first ("training set") is used to train a machine learning classifier. We use a gradient-boosted ensemble of classification trees, commonly referred to as a GBM (Hastie et al., 2009, Chapter 10), to predict the land cover using the MODIS covariates.[26] With the second set of data ("test set"), we obtain the out-of-sample predictions $Y_{it} = f(R_{it})$ based on the GBM classifier. The out-of-sample predictions in the test set constitute our land use classification panel data, $\{Y_{it} : i = 1, ..., N, t = 1, ..., T\}$.

The training set contains 60 cross-sectional points (286 point-years) and the test set contains 343 points (1715 point-years).[27] We opt for a larger fraction of the Embrapa data set to be part of the test set in order to reflect the typical scenario faced by applied researchers using satellite-based data: they will typically have access to large panels of machine-learning-based classifications.

[26]The purpose of boosting is to apply "weak" classification algorithms sequentially to produce a "strong" classifier. The GBM uses a sequence of decision trees in which each individual tree tries to recover the loss (i.e., the difference between actual and predicted values) obtained by the previous ones in the sequence. The loss function is minimized using a gradient descent algorithm. To select the optimal number of trees, we follow standard practice and use cross-validation. See Chapter 10 of Hastie et al. (2009) for recommendations on tuning GBMs.

[27]Our results are similar when we select different sizes for the training set (e.g., 48 or 80 cross-sectional points).

## 5.3 Implementing the HMM Correction

We consider two hidden Markov model specifications: a restricted model with time-invariant transition probabilities, and another in which the transitions are allowed to vary over time. In both cases, we hold the misclassification probabilities to be the same over time. We estimate the HMM parameters using both the MD and the ML estimators.[28] The frequency estimator (ignoring misclassifications) is computed directly from the data, based on sample frequencies. Confidence intervals are calculated based on subsampling, as suggested by Politis and Romano (1994) and Andrews (1999, 2000) when parameters are at or near the boundary.[29]

## 5.4 Validation Results

The out-of-sample performance of our GBM classifications is shown in Table 1. This table presents the so-called "confusion matrix," which tabulates the test points according to their ground truth class and predicted class. It also allows us to estimate the misclassification probabilities $\Upsilon$ directly.

[Table 1 here]

The GBM's land use predictions are fairly accurate given the size of the training set and the difficulty of the classification problem. Overall, it correctly predicts land use for 92% of the test

[28] For the MD estimator, we use the identity matrix as the weighting matrix $\mathbf{W}$, and we use both $y_{t+1} = crops$ and $y_{t+1} = pasture$, as they both satisfy Condition 4.

[29] We implement 200 replications of a standard i.i.d. subsampling, resampling 250 spatial points over the sample time period. (We acknowledge, though, that this might not be completely accurate in the presence of spatial dependence.) The 95% confidence intervals are calculated as $[\widehat{\theta} - \delta_{0.025}, \widehat{\theta} + \delta_{0.975}]$, where $\widehat{\theta}$ denotes the parameter estimate, and $\delta_q$ is the quantile $q$ of the subsampling distribution. We do not implement bootstrap procedures because they are inconsistent when parameters are at or close to the boundary (Andrews, 2000). We treat the GBM parameters as fixed and subsample only on the test data, noting that researchers may not have access to the training data in practice.

points, which is in the range of acceptable accuracies (see Section 2). For crops, the fraction of correctly predicted (or the recall rate) is 92.6% (i.e., $\Pr[Y_{it} = \text{crops} \mid S_{it} = \text{crops}] = 0.926$), while the recall for pasture is 79.5% (i.e., $\Pr[Y_{it} = \text{pasture} \mid S_{it} = \text{pasture}] = 0.795$). This implies that $\Upsilon$ is diagonally dominant, as required for identification of the HMM approach (see Condition 5 in Section 4.1). This increases our confidence that the HMM is identified when applied to the Embrapa test data.[30]

Figure 1 shows the estimated results for the frequency estimator and the restricted HMM (i.e., imposing time-invariant transition probabilities). The ground-truth data indicate that the probability of switching from cropland to pasture in the following year equals 0.7%, while the probability of maintaining cropland is 99.3%. The ground-truth probability of switching from pasture to crops is 13.8%, and the probability of maintaining pasture land is 86.2%. So, both land uses are persistent over time, and cropland is more persistent than pasture.

[Figure 1 here]

The frequency estimator estimates transitions from crops to pasture as 6.2%, and transitions in the opposite direction, from pasture to crops, as 48.2%. These transitions are substantially biased: the first one is roughly 9 times higher than the truth, while the second is 3 times higher than the correct transition. In contrast, the HMM estimates for the transitions probabilities (using both MD and ML estimates) are approximately 1.2% for cropland to pasture and 6.5% from pasture to cropland, which are substantially closer to the true ground-truth transition probabilities than the frequency estimates. The confidence intervals in the figure indicate that these results hold even after accounting for sampling uncertainty. This is consistent with the Monte Carlo results discussed in the Online Appendix: the frequency estimator tends to overestimate switching rates when land use is persistent.

Figure 2 is analogous to Figure 1, but shows results for the *unrestricted* model, i.e. allowing for time-varying transition probabilities. The results are similar to the time-invariant case: the

[30] While not presented here, we find that the (testable) Conditions 3 and 4 are also satisfied in the data.

frequency estimator provides excessive land use changes, while the HMM corrections result in point estimates that are closer to the true transitions. That is the case even when true transitions are exactly zero, as in the first year of the data, 2006–2007. We also find some evidence that transition rates can vary over time (though not substantially in this data set).

[Figure 2 here]

Next, we turn to the HMM estimates of the misclassification probabilities; Figure 3 shows the results computed using MD and ML for both the restricted and unrestricted models. The point estimates are all reasonably close to the true misclassification probabilities obtained from the out-of-sample confusion matrix for the GBM predictions (see the last column in Table 1.) This is notable since the HMM is estimated using only panel data of observed classifications $\{Y_{it}\}$, with no information on true land uses $\{S_{it}\}$.

[Figure 3 here]

Finally, we generate the most likely sequence of land uses for each point in the test set based on the HMM maximum likelihood estimates (using the so-called "Viterbi" algorithm; see Online Appendix C) and reclassified the data points accordingly. Figure 4 shows that correcting classifications in this way increases the overall accuracy of the land use classifications to 96%, improving on our original classifier's accuracy of 92%.

[Figure 4 here]

# 6 Empirical Exercise: Carbon Stocks in the Atlantic Forest

We now investigate an application of the HMM approach by estimating the value of the carbon stocks in the Brazilian Atlantic Forest and how they might change over time if deforestation were curtailed. These carbon stocks represent part of the social costs of deforesting an area, and so quantifying them provides a crucial input to environmental policy analysis. Given that the carbon stock varies with the age of the forest, it is critical to obtain an accurate measure of the forest age,

which in turn can be estimated based on transition rates between forest and non-forest; the HMM approach allows the researcher to obtain accurate measurements of these important transition rates. We also use the HMM approach to compute the value of the carbon stock by 2040 if deforestation is completely eliminated between 2020 and 2040.

The Atlantic Forest is a region of approximately 1.4 million square kilometers, it occupies approximately 15% of the Brazilian territory (stretching from the northeastern to the southern regions), and it accounts for about 70% of the country's population and about 80% of the national gross domestic product. It has suffered centuries of exploitation and, as a result, it now contains only an estimated 30% of the original native forest cover (Rosa et al., 2021). It also hosts one of the world's most diverse and threatened tropical forest on the planet.[31] Given that the Atlantic Forest is a priority hot spot for biodiversity conservation, and is a tropical forest storing large amounts of carbon on the ground, it has been the focus of many conservation and restoration policy initiatives (Brancalion et al., 2016). Indeed, conserving this area is an important component of the country's National Determined Contribution to the Paris Climate Agreement.[32]

## 6.1 Data and Implementation

We use data from the Mapbiomas (Collection 5.0), an initiative that has produced annual land cover time series based on 30 meters resolution Landsat satellite data.[33] It covers the whole Brazilian territory from 1985 through the present and provides an unprecedented tool for understanding forest dynamics – consistent monitoring of forest dynamics in the Atlantic Forest was not possible until the creation of the MapBiomas project in 2015.

[31]The region harbors roughly 20,000 plant species, more than 1400 species of terrestrial vertebrates, and thousands of invertebrate species, many of which are endemic – and many of which are endangered (Laurance, 2009).

[32]For more details, see `http://www.mma.gov.br/images/arquivos/florestas/planaveg_plano_nacional_recuperacao_vegetacao_nativa.pdf`.

[33]Marcos Reis Rosa generously shared with us the MapBiomas data, for which we are extremely thankful.

The data for the Atlantic Forest includes a total 7.9 billion pixels observed from 1985 to 2020; Figure E2 in the Online Appendix presents a map with the data points. Mapbiomas considers several land cover classifications that are generated in each year using the random forest machine learning classification algorithm available in Google Earth Engine (Gorelick et al., 2017). We aggregate these land covers into three states: forest, deforested, and others.[34] In the notation of the paper, we treat these aggregated MapBiomas classifications for a given year and pixel as $Y_{it}$.

We split the biome into "tiles," each containing 1000 x 1000 pixels and covering an area of roughly 900 square kilometers. We exclude tiles where over 90% of the pixels are missing or over 50% of the land is water or sand. The HMM parameters are estimated separately for each tile; to ease computational burden, we randomly select 1% of the pixels within each of these tiles for estimation. (For the tiles where only two of the three aggregated classes are present in the observed data, we estimate a two state model.) Following our Monte Carlo study, we first estimate the HMM parameters using the (fast) MD estimator and then use these parameter estimates as starting values for the (more accurate) ML estimator. We exclude from the final results the tiles for which we obtain estimates for the misclassification probability matrix $\Upsilon$ that are not diagonally dominant, since that violates the assumptions underlying our procedure. In total, we run estimates for 1,174 tiles, roughly 75% of the Atlantic Forest. (For our counterfactual simulations, we assume that the forest age and transitions for this 75% is equal to the other 25%.)

[34] We combine savanna, grassland and forest from the raw data into a "forest" classification; we define the agriculture/pasture raw classifications as a "deforested" classification; and we combine wetlands, sand, rocky outcrop, and other non-forest classifications into an "other" classification. We allow for transitions between all of these states. We use Mapbiomas' random forest classifications generated year by year and that are prior to the application of the post-classification filters and map integration (after which the final classifications are obtained and that are publicly available online). Post-classification filters apply spatial and temporal filters. Map integration apply a set of specific hierarchical prevalence rules to solve for potential conflicting classifications. For details, see Souza et al. (2020).

To calculate the carbon stocks, we first compute the most likely land use path for each pixel, given the estimated HMM parameters for each tile. We do so in order to distinguish between older and newer forests. Specifically, we define the forest age as the number of years that the pixel has been classified as forest since the last time it was classified as deforested; for pixels that were never deforested, the age is greater than or equal to 32, which is the length of our panel data.[35] Then we make use of the cross-sectional carbon map developed by Englund et al. (2017) for the year 2017, and regress the carbon stock on the forest age and a forest indicator to generate an expected carbon stock for each pixel of a given forest age or non-forest.[36] We also translate the amount of the carbon stock into dollar values, using estimates of the social cost of carbon from the Interagency Working Group on Social Cost of Greenhouse Gases, United States Government (2021). We compare the estimated transition processes and carbon values described above with the corresponding results based on the raw classifications. For more details see Section E.2 of the Online Appendix.

Finally, for our counterfactual exercise, we treat the HMM-based classifications in 2020 as "truth" and simulate the Markov process forward from 2021 to 2040 under two scenarios. Our baseline scenario assumes that, within each tile, deforestation will remain constant at its 2020 level until 2040. Our "no-deforestation" scenario assumes that there will be no deforestation from 2020 to 2040.

## 6.2 Results

Figure 5 shows the evolution of the deforestation rate, the reforestation rate, and the fraction of land that is forested from 1986 to 2020, using the Mapbiomas raw data and the estimates from the HMM

[35]Using the paths implied by the HMM parameters, in 2017, 62% of the forested areas were at least 32 years old.

[36]This carbon map was specifically designed to provide accurate measures of above ground carbon for Brazil by combining information from other carbon maps and a detailed map of land use changes.

approach.[37] As expected, the raw data exhibits excessive transitions: the raw deforestation and reforestation rates are typically roughly three times the rates obtained under the HMM. The HMM correction therefore suggests that there should be less carbon emissions from deforestation but less carbon sequestration from regrowth than the raw data indicate. The substantial difference in the estimated rates is apparent despite the fact that the fractions of forested land are similar between the HMM and raw estimates, oscillating between 29% and 31.5% over time. (The HMM forest shares are around 0.5 percentage points above the raw data shares.)

[Figure 5 here]

These results illustrate that, even though uncorrected land use classifiers can generate reasonable estimates of the level of a given land cover in a given year, the corrected and uncorrected approaches will yield very different results for applications where land use transitions and/or the age distribution is important. In Online Appendix Figure E16, we show the difference in the age distribution of the forest between the raw data and the HMM-based classifcations. Consistent with Figure 5, we find that the raw data generate forests that are excessively young in light of the high deforestation and reforestation rates.

Next, we focus on the differences in the carbon stocks. Table 2, Panel A, presents the overall amount and value of the carbon stocks in 2020, the last year for which we have data. The HMM approach estimates approximately 2.8 billion tons of carbon on the ground, corresponding to a total social value of $774 billion (assuming a social cost of carbon of $76 per ton of CO2).[38] If instead we use the forest age implied from the raw data, we obtain an estimate of just 2.33 billion tons of carbon, which translates into $666 billion. Therefore, there is a $110 billion difference in the value of the carbon stock that results from the differences in the implied age distribution of the forest in

[37]For each year, we take the average over all of the tiles, weighting the deforestation rates by the share of land that is forest and the reforestation rate by the fraction of land that is not.

[38]The estimated social cost of carbon for 2020, based on the 2.5% discount rate, is $76 per ton of CO2, according to the Interagency Working Group on Social Cost of Greenhouse Gases, United States Government (2021).

the raw and HMM-based classifiers.

[Table 2 here]

Finally, we simulate forward up to 2040 the deforestation and reforestation processes under the baseline and the "no-deforestation" scenarios. Both scenarios are based on the corrected age distribution for 2020 derived from the HMM approach. Table 2, Panel B, shows the results. We find that eliminating all deforestation would preserve 270 million tons of carbon on the ground, which is equivalent to a social benefit of approximately $100 billion dollars.[39]

# 7 Conclusion

Remotely sensed data have proven useful in the study of a variety of important phenomena, including the pollution incidence, urbanization, land use change, and the evolution of biodiversity. In this paper, we show how econometric tools can be used to improve the measurement of remotely sensed transitions, such as rates of land use change. Relying on a set of assumptions that can be analyzed on a case-by-case basis, the method avoids the need for ground truth data. In the context of Brazilian land use change, we find the HMM correction performs well and makes an important difference in measured rates of land use change.

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[39]For 2040, we use the 2.5% discount rate of the Interagency Working Group estimate, corresponding to a social cost of carbon of $103 per ton of CO2.

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| | GBM Classification ($Y_{it}$) | | | *Fraction Correctly Predicted (Recall)* |
|---|---|---|---|---|
| Embrapa Data ($S_{it}$) | Crops | Pasture | **Total** | |
| Crops | 1409 | 112 | 1521 | 0.926 |
| Pasture | 15 | 58 | 73 | 0.795 |
| **Total** | 1424 | 170 | 1594 | |

**Table 1:** Confusion Matrix based on Embrapa Validation Data

| **Panel A: Carbon Stock and Social Value of Forest in 2020** | | |
|---|---|---|
| Measurement | Carbon Stock (billion tons) | Social Value (billion dollars) |
| HMM-Viterbi | 2.78 | 774.44 |
| Raw Data | 2.39 | 666.47 |
| **Panel B: Carbon Stock and Social Value in 2040** | | |
| Scenario | Carbon Stock (billion tons) | Social Value (billion dollars) |
| Baseline | 2.87 | 1085.17 |
| No Deforestation | 3.14 | 1185.70 |

**Table 2:** Carbon Stock and Social Value of Forest

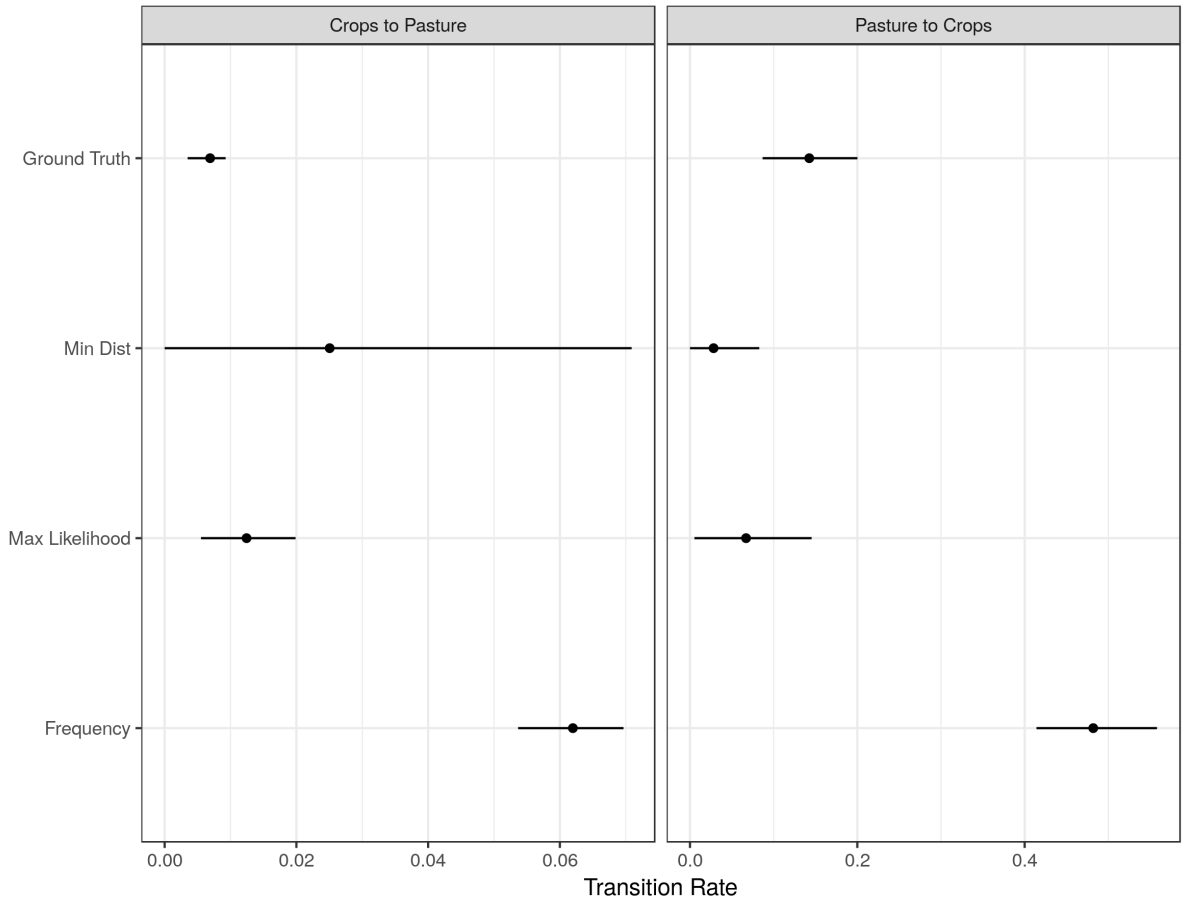



**Figure 1:** Time-invariant Transition Probabilities – Embrapa Validation Data

**Note:** *Ground Truth* data are the observed transition probabilities in the Embrapa test set, the *Frequency* estimator uses the GBM based land use classifications to estimate transitions, while *Min Dist* and *Max Likelihood* are the minimum distance and maximum likelihood HMM estimators for the transition rates. Error bars represent 95% confidence intervals based on subsampling. The results shown in this figure combine all years in the Embrapa test set, i.e. they assume time-invariant transition probabilities.

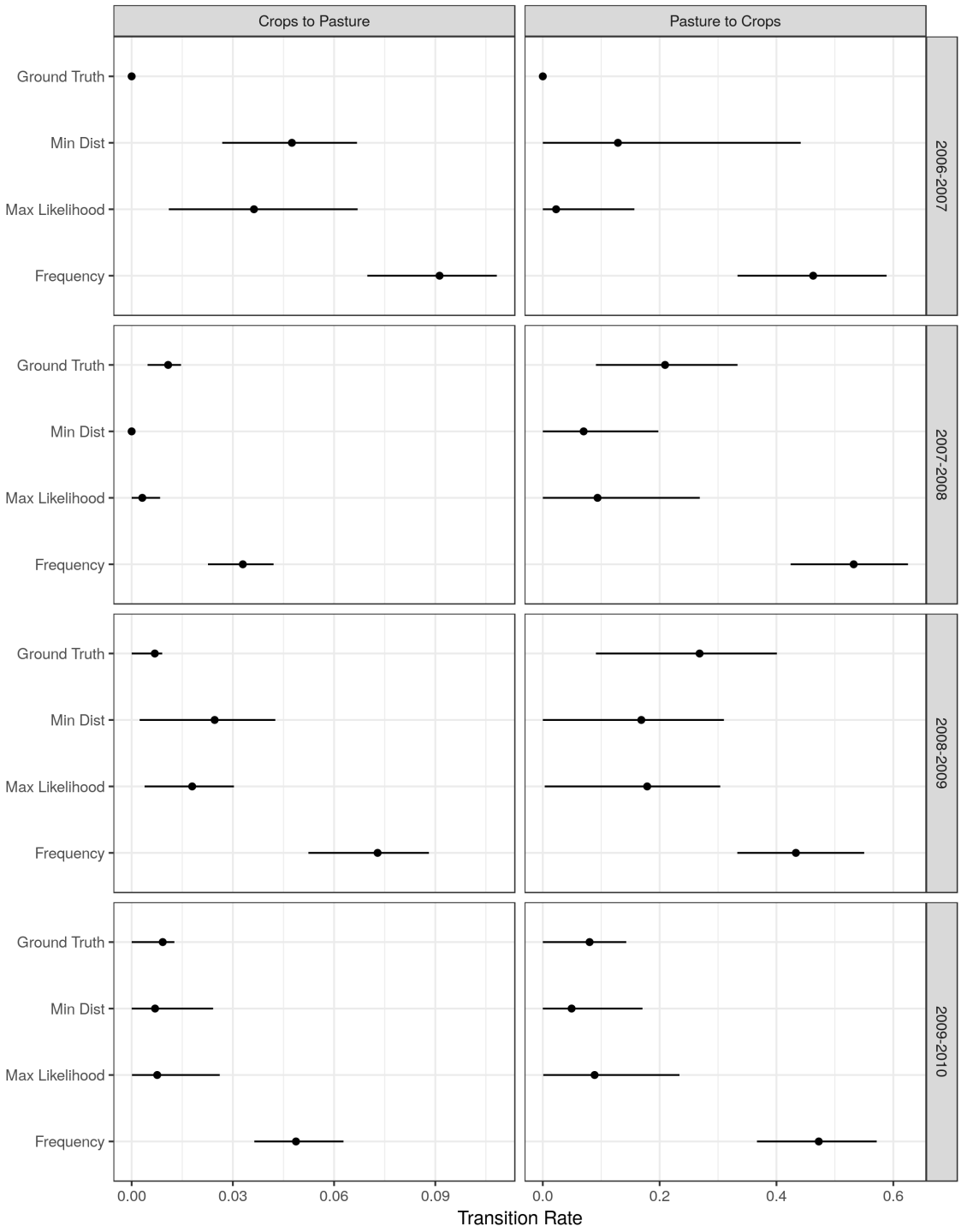



**Figure 2:** Time-varying Transition Probabilities – Embrapa Validation Data

**Note:** *Ground Truth* data are the observed transition probabilities in the Embrapa test set, the *Frequency* estimator uses the GBM based land use classifications to estimate transitions, while *Min Dist* and *Max Likelihood* are the minimum distance and maximum likelihood HMM estimators for the transition rates. Error bars represent 95% confidence intervals based on subsampling. The results shown in this figure combine assume time-varying transition probabilities.

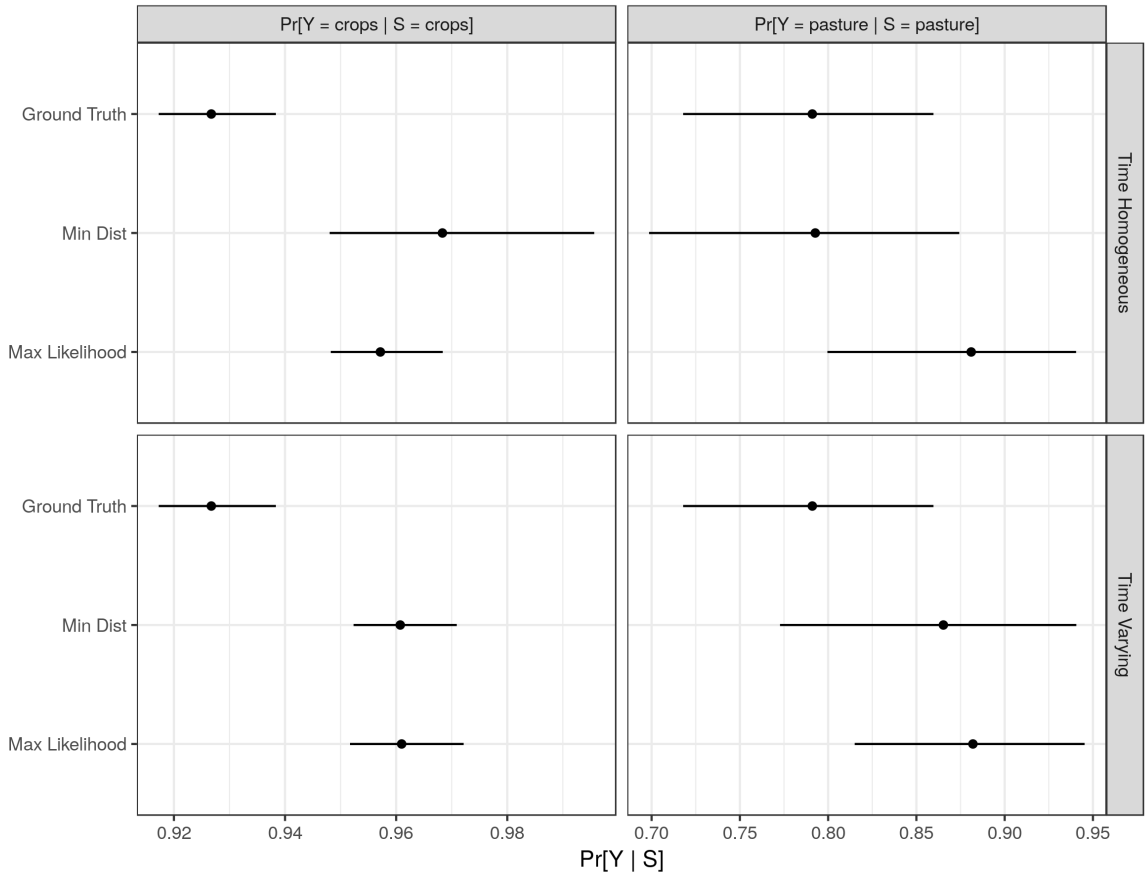



**Figure 3:** Misclassification Probabilities – Embrapa Validation Data

**Note:** *Ground Truth* corresponds to the misclassification probabilities from the "confusion matrix" comparing the Embrapa test set points and the GBM predictors. The *Min Dist* and *Max Likelihood* correspond to the minimum distance and maximum likelihood HMM estimates of the misclassification probabilties. Error bars represent 95% confidence intervals based on subsampling. The top panel presents the results based on the restricted model with time-invariant transition probabilities; and the bottom figure, the misclassifications based on the model with time-varying transition probabilities.

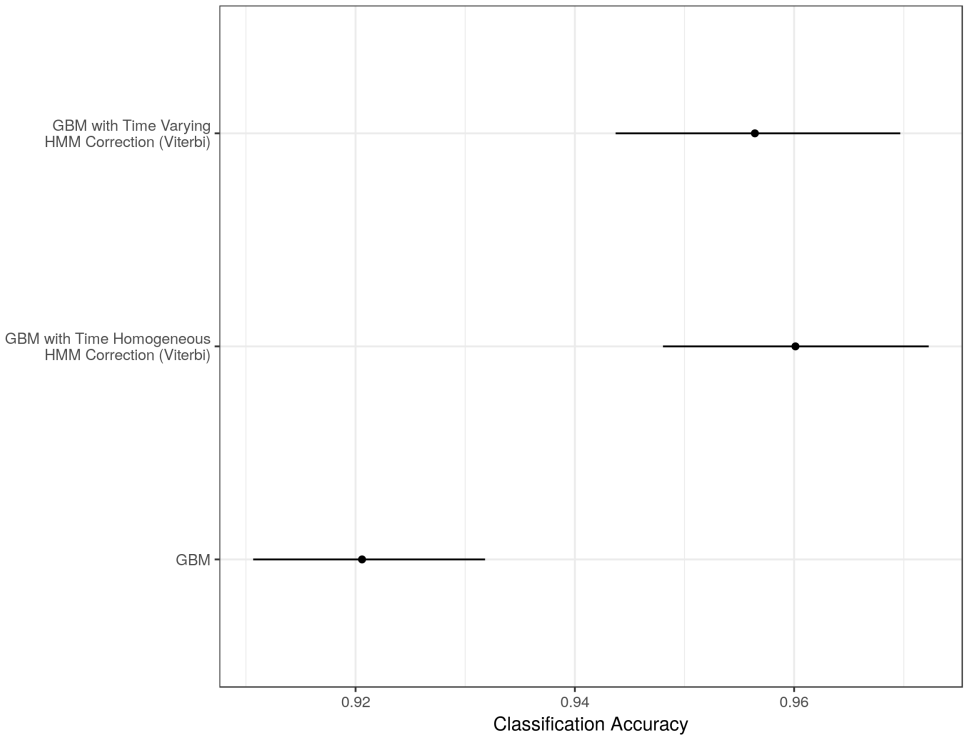
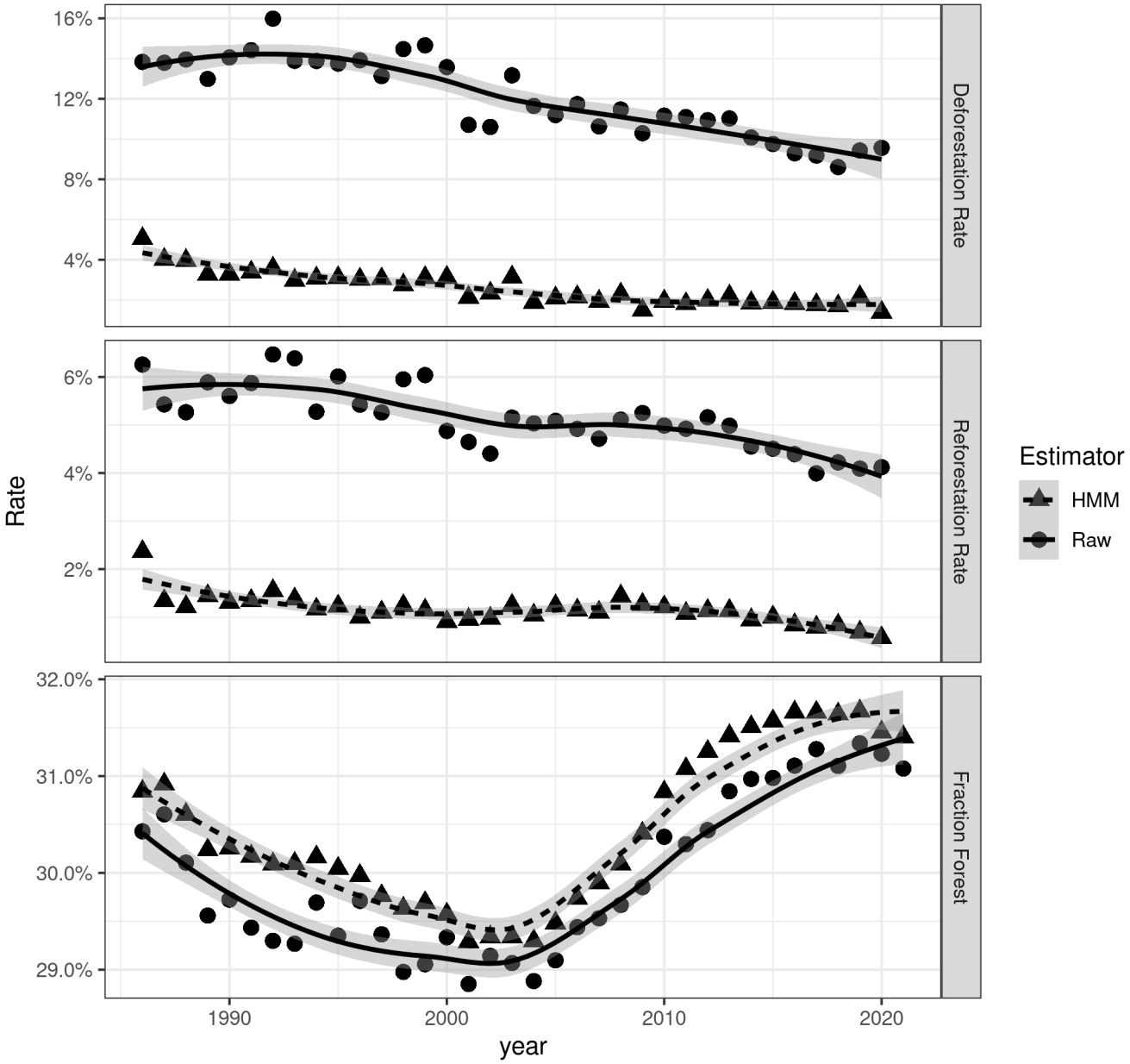



**Figure 4:** Classification Accuracy of GBM and HMM-Viterbi methods in the Embrapa Validation Data

**Note:** *GBM* corresponds to the accuracy (i.e, the fraction of correctly predicted points) in the test set of the GBM classifier. The *GBM with Time Homogeneous HMM Correction (Viterbi)* and the *GBM with Time Varying HMM Correction (Viterbi)* correspond to the accuracy of the classifications in the test set based on the Viterbi method, after applying the HMM (maximum likelihood estimator) correction assuming time-homogeneous and time-varying transitions, respectively.




Points reflect the HMM parameters aggregated over all of the tiles
(where the tile-specific deforestation rates are weighted by the fraction forest and the reforestation rates are weighted by the fraction not-forest.) Lines reflect a Loess trend.

**Figure 5:** Atlantic Forest Trends Over Time