A Functional EM Algorithm for Panel Count Data with Missing Counts

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Abstract
Panel count data is recurrent events data where counts of events are observed at discrete time points. Panel counts naturally describe self-reported behavioral data, and the occurrence of missing or unreliable reports is common. Unfortunately, no prior work has tackled the problem of missingness in this setting. We address this gap in the literature by developing a novel functional EM algorithm that can be used as a wrapper around several popular panel count mean function inference methods when some counts are missing. We provide a novel theoretical analysis of our method showing strong consistency. Extending the methods in (Balakrishnan et al., 2017; Wu et al., 2016), we show that the functional EM algorithm recovers the true mean function of the counting process. We accomplish this by developing alternative regularity conditions for our objective function in order to show convergence of the population EM algorithm to the true mean function. We prove strong consistency of the M-step, thus giving strong consistency guarantees for the finite sample EM algorithm. We present experimental results for synthetic data, synthetic missingness on real data, and a smoking cessation study, where we find that participants may underestimate cigarettes smoked by approximately 18.6\% over a 12 day period.

1. Introduction

A major goal in behavioral medicine is to identify the temporal patterns of risk factors that may prevent an individual from successfully modifying a health-related behavior. In smoking cessation, for example, it would be valuable to know the times of day, locations, and other contextual factors such as smoking opportunity (Kirchner et al., 2013) that may precipitate a lapse back to smoking. This knowledge could guide the design and timing of mobile interventions to prevent lapse and prolong abstinence (Rehg et al., 2017). A basic task in this context is to infer when smoking occurs, and this can be framed mathematically as modeling the counting process of a repeated negative event. Estimating the low-order moment functions of the counting process, such as the mean and variance functions, can then provide the desired characterization of a health-related behavior at the cohort or population-level.

While methods have been developed for automatically detecting smoking events via wearable sensors (Saleheen et al., 2015), the most common and widely-used measurement approach is self-report via Ecological Momentary Assessment (EMA), in which a participant responds to prompts and enters data via a smartphone app (Shiffman et al., 2008). An EMA can be randomly-triggered by the app, or it can be initiated by the participant (for example, following a smoking event). For recurrent events such as smoking, participant-initiated EMAs are vulnerable to false negatives due to systematic non-compliance (Stone and Shiffman, 2002). For example, a moment of high stress that precipitates a smoking lapse may similarly result in a failure to self-report the lapse.

In comparison to participant-initiated EMAs, random EMAs provide a less-biased data collection paradigm and have consequently been used in a wide variety of behavioral studies (Shiffman et al., 2007; Piasecki et al., 2011; O’Connell et al., 1998). In this approach, a participant is prompted 3-4 times a day at random times. Note that since the EMA times will not generally co-occur with the events of interest, participants will report the cumulative number of events since the last EMA. For example, they will be asked how many cigarettes they smoked or how many alcoholic drinks they consumed since the last prompt. Therefore, random EMA responses take the form of panel count data (Kalbfleisch and Lawless, 1985)(Sun and Kalbfleisch, 1995). In panel count data, the exact times of a counting process are not observed, and instead only the cumulative number of events since the last observation are measured, where the observation times are assumed to be random according to some unknown distribution.

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A key step in analyzing panel count data at the population level, in order to reveal the temporal pattern of smoking behaviors, is the computation of the mean function of the counting process. The mean function is a powerful tool because it converts the complex, discrete patterns of smoking counts from a population of participants (see Fig. 1) into a succinct and temporally-continuous summary of the smoking behavior over time (see Fig. 3). Periods of time in which smoking is infrequent across the population will manifest in mean function slopes which are locally near zero, while periods of high smoking activity will manifest in large slopes. These patterns can be referenced from the start of the study (to provide global context) or from the start of each week, or even each day, in order to study seasonal effects. However, the patterns of missingness which are inherent in EMA data pose a significant challenge for the asymptotically unbiased estimation of the mean function.

There are several possible conditions under which EMA data can be missing. First, when the mobile app delivers an EMA, it may be ignored by the user, or opened and then abandoned such that no data is collected. Second, the mobile app itself may decide to postpone the triggering of an EMA for any one of several reasons (e.g. privacy mode activated, battery low, phone off, user is driving). While EMAs are triggered randomly, the random process is constrained so there is a minimum temporal spacing between two EMAs, in order to keep participant burden at an acceptable level. Thus if EMAs are postponed or ignored too many times, then it will not be possible to trigger the full set of EMAs for the day, resulting in missing EMAs.

From the perspective of mean function estimation, missing EMAs cause a problem when they result in an inaccurate count of the total number of cigarettes smoked between intervals. Due to recall bias, as the interval between EMAs grows, participants are increasingly unlikely to report accurate counts. Behavioral scientists have historically developed heuristic imputation schemes to adjust for missing counts (Hallgren and Witkiewitz, 2013), but these procedures aren’t guaranteed to provide an unbiased estimator of the mean function. This paper presents the first self-contained and systematic treatment of the missing data problem for panel count data, by providing an EM algorithm for imputation and theoretical guarantees for asymptotic performance.

Our primary contribution is a functional Expectation-Maximization (EM) algorithm which can be used as a wrapper around standard non-parametric mean function estimators to compensate for missing data. In each case, the E-step uses estimates from a fitting method to fill in missing data, and the M-step calls that fitting method to estimate a mean function. This work can be viewed as extending several classic non-parametric methods (Wellner et al., 2000; Lu et al., 2007), as well as the baseline-only version of a semi-parametric method (Wang et al., 2013) for mean function estimation, to the setting of missing data.

The lack of ground truth for quantifying the quality of imputations in real-world settings is a barrier to evaluation, and it amplifies the importance of providing theoretical performance guarantees. We prove the strong consistency of our EM algorithm, in the context of wrapping the non-parametric MLE (NPMLE) of (Wellner et al., 2000). Our proof leverages recent results (Balakrishnan et al., 2017; Wu et al., 2016) showing consistency of the EM algorithm for parametric models, and addresses the extension of this approach to the non-parametric setting. In doing so we address three challenges: (1) For population EM, we propose a novel regularity condition on the E-step for recovery of the mean function and show that it is satisfied and leads to the same convergence rate. (2) In the finite sample setting, we use work from (Balakrishnan et al., 2017) to bridge the sample and population EM algorithms. This requires an extension of the proof from (Wellner et al., 2000) of strong consistency of the NPMLE. (3) Our M-step lacks a closed form, unlike the case in (Balakrishnan et al., 2017), making it difficult to obtain a uniform bound on the difference between the sample and population M-steps as a function of the sample size. By varying the sample size at each iteration, we show that we can still achieve strong consistency. We note that while (Balakrishnan et al., 2017; Wu et al., 2016) show uniform consistency that is not strong, we show strong consistency that is not uniform. The task of achieving both simultaneously is left to future work.

After showing strong consistency, we simulate missingness on a popular panel count tumor dataset and show that the estimates under missing data are close to those under complete data. We then apply our method to EMA data from a smoking cessation study and analyze the under-reporting by participants.

This paper makes three main contributions: (1) We propose an algorithm to estimate the mean function for panel count data under a novel missing data model; (2) We prove that this algorithm asymptotically recovers the true mean function; (3) We evaluate our method on simulated and real-world datasets. Our analysis of smoking data suggests that participants underestimate cigarettes smoked when asked to...
recall over a gap of 24 hours or longer.

2. Related Work

Panel count data analysis has a long history in nonparametric statistics, but our missing data problem has not been addressed in that literature or in machine learning. The closest related works to ours are (Wang et al., 2013; Wellner et al., 2000; Lu et al., 2007). These papers share our focus on estimating the mean function from panel count data. However, none of these works address a missing data model which can account for missing EMAs. (Wang et al., 2013) develop an EM approach under a much more limited missingness model which assumes that the total counts for each participant are known prior to data analysis. This makes their method unsuitable for analyzing real world data with missing EMAs. However, two strengths of their method are that they can incorporate baseline covariate information, and they relax the standard assumption of independence between observation times and the counting process.

Neither of (Wellner et al., 2000; Lu et al., 2007) handle missing counts, and thus cannot be applied directly to our setting. We propose an EM algorithm for missing data where we can wrap any one of (Wang et al., 2013; Wellner et al., 2000; Lu et al., 2007), by using the prior method to compute the M-step. (Wellner et al., 2000) provides the first strong theoretical guarantees for a mean function estimator in the panel count setting. (Lu et al., 2007) improve upon their rate of convergence by using spline mean functions. We use some of the tools from (Wellner et al., 2000) to prove that our finite sample M-step approaches the population M-step in large samples. But in order to prove consistency, we additionally show that the population EM algorithm recovers the true mean function, and that M-step consistency can bridge the sample and population EM algorithms.

Many of the other papers in the literature focus on either extending to the semi-parametric setting, relaxing assumptions in either the non-parametric or parametric setting, or improving estimation under specific distributional assumptions. They do not address missing data. (Wellner et al., 2007) extended (Wellner et al., 2000) to the semi-parametric setting. (Huang et al., 2006) analyzed panel count with informative observation times and subject-specific frailty, and (Hua et al., 2014) proposed using a smooth semi-parametric estimator to handle over-dispersion in panel count data. (Ding et al., 2018) proposed using a squared Gaussian process intensity function.

Because many of the methods in the panel count literature build off of the maximum pseudo-likelihood and maximum likelihood estimators of (Wellner et al., 2000) for both the objective function and the proof strategies, we show theory based on applying our algorithm to their NPMLE. However, the high-level proof strategy likely applies to all methods we use. We describe how we think the theory could be extended to the other methods after presenting the theory based on (Wellner et al., 2000).

EM Theory the other relevant area is recent work showing convergence of the EM algorithm to the true parameter (Balakrishnan et al., 2017; Wu et al., 2016). In (Balakrishnan et al., 2017), they show that under initialization within a sufficiently small ball around the true parameter and certain regularity conditions, population EM converges to the true parameter. Further, if one can uniformly bound the distance between the sample and population M-steps, one can show a finite-sample bound on EM that depends on the number of iterations and the sample size. (Wu et al., 2016) improve on their results (the original arxiv version of (Balakrishnan et al., 2017) was in 2014) by weakening the required regularity conditions, and replacing the requirement of uniform convergence of the M-step with three concentration inequalities: this is often easier to prove. We base our population guarantees on (Wu et al., 2016). For the sample guarantees, (Wu et al., 2016) assumes that one can calculate norms for differences between estimates directly, which may not be possible when they are an expectation over some unknown distribution. Thus, we base our sample guarantees on (Balakrishnan et al., 2017), as the sample setting of (Balakrishnan et al., 2017) is easier to extend to the non-parametric setting.

Point Process Missing Data Outside of the panel count setting, missing data has some treatment in the temporal point process literature, particularly in the Hawkes process setting. (Linderman et al., 2017) treat three types of missingness in the marked network Hawkes setting: a) some marks are hidden b) some vertices in the network are hidden and c) some intervals are missing. In (Shelton et al., 2018), they treat the marked Hawkes process setting where some events are fully observed, while others are interval censored but with marks present.

3. Model

3.1. Complete Data

Let \( N = \{N(u) : u \geq 0\} \) be a univariate counting process. We want to estimate its true mean function \( \Lambda^*(u) = EN(u) \) over a study window \([0, \tau]\). Let \( K \) be the random number of observations for a participant. Let \( T = (T_1, \cdots, T_K) \in \mathbb{R}^K \) be a random vector of observation times, with \( T_0 = 0 \). Let \( \Delta N = (\Delta N_1, \cdots, \Delta N_K) \) be the vector of count increments: \( \Delta N_j = N(T_j) - N(T_{j-1}) \). With complete data, for each participant \( i = 1, \cdots, n \) we observe \( \bar{Y} = (\Delta N, T, K) \in \mathcal{N} \times \mathcal{T} \times \mathcal{K} \). \( \mathcal{N}, \mathcal{T}, \mathcal{K} \) is the sample space.

Let \( \mathbb{P}_n; \mathbb{P} \) denote the empirical and true measures on \( \mathcal{N} \times \mathcal{T} \times \mathcal{K} \), respectively. For a measurable function \( f \),
Figure 1. Raw cigarette counts smoked since the previous observation. Observations occur at random times of day. We want to convert this to a mean function of cumulative cigarettes smoked, as in figure 3. We must deal with the fact that some of these counts are missing or unreliable.

\[
P_n f = \frac{1}{n} \sum_{i=1}^{n} f(Y_i) \quad \text{and} \quad P f = \int f \, dP.
\]

Under a non-homogeneous Poisson process assumption, the complete data sample log-likelihood (excluding constants) is

\[
l_n(Y|\Lambda) = n \mathbb{P}_n \left( \sum_{j=1}^{K} \Delta N_j \log[\Delta \Lambda(T_j)] - \Lambda(T_K) \right)
\]

and the population log-likelihood is

\[
l(\Lambda) = P \left( \sum_{j=1}^{K} \Delta N_j \log[\Delta \Lambda(T_j)] - \Lambda(T_K) \right)
\]

The goal is to estimate the mean function consistently even when the Poisson process assumption is violated.

3.2. Missing Data

Unlike previous work, we assume certain observations \( \Delta N_j \) are missing. Instead of observing a complete vector \( \Delta N \in \mathbb{R}^K \), each observation \( \Delta N_j \) is missing completely at random w.p. \( \epsilon \in [0, 1] \). Let \( \tau \in \{0, 1\}^K \) be the missingness pattern, where \( \circ \) takes the value 0 but is written differently to represent missingness. Let \( s = 1 - \tau \) be the complement of \( \tau \), so that \( s_j = 1 \) if \( \Delta N_j \) is missing. Let \( \Delta N^r = \Delta N \odot \tau \) and \( \Delta N^s = \Delta N \odot s \), where \( \odot \) represents elementwise product. Then \( \Delta N = \Delta N^r + \Delta N^s \), and we must observe \( \Delta N^r \) while \( \Delta N^s \) is unknown. Let \( Z \equiv \Delta N^s \) represent our missing data vector, and let \( Z \) be the space of values for our missing data. Then \( Y = (\Delta N^r, T, K) \), and \( Y, Z \in \mathcal{N} \times \mathcal{T} \times \mathcal{K} \times \mathcal{Z} \) gives us the observed and missing parts of the data, respectively.

In this case \( P_n \) and \( P \) are now the empirical and true measures, respectively, for \( \mathcal{N} \times \mathcal{T} \times \mathcal{K} \times \mathcal{Z} \).

4. EM Algorithm

Let \( f_{\Lambda}(y, z) \) be the complete joint density of \( (Y, Z) \), and \( p_{\Lambda}(y) \) be its marginalization. Let \( k_{\Lambda}(y|z) \) be the conditional density of \( y \) given \( z \). Define the population \( Q \)-function (population E-step) as

\[
Q(\Lambda'|\Lambda) = \int_Y \left( \int_{Z(y)} \log(f_{\Lambda}(y, z)) k_{\Lambda}(z|y) \right) p_{\Lambda}(y) \, dy
\]

and the sample or empirical \( Q \)-function (sample E-step) as

\[
Q_n(\Lambda'|\Lambda; \{Y_i\}) = \frac{1}{n} \sum_{i=1}^{n} \mathbb{E}_\Lambda[\log f_{\Lambda}(y_i, z_i)|Y_i]
\]

For the population EM algorithm we are interested in repeatedly maximizing the population \( Q \)-function over a convex set \( \Theta \) until convergence as follows

\[
Q(\Lambda^{(t+1)}|\Lambda^{(t)}) = \arg \max_{\Lambda' \in \Theta} Q(\Lambda'|\Lambda^{(t)})
\]

here \( \Lambda^{(t)} \) denotes the estimate at iteration \( t \). For the sample EM algorithm we optimize over a convex set \( \Theta_n \), where \( \{\Theta_n\} \) is a sieve: a sequence of nested sets \( \Theta_1 \subset \Theta_2 \subset \cdots \) such that \( \cup_{n=1}^{\infty} \Theta_n \) is dense in \( \Theta \) according to some norm. The sample \( M \)-step repeatedly applies

\[
Q_n(\Lambda^{(t+1)}|\Lambda^{(t)}; \{Y_i\}) = \arg \max_{\Lambda' \in \Theta_n} Q_n(\Lambda'|\Lambda^{(t)}; \{Y_i\})
\]

4.1. E-Step

We define the population and sample \( Q \) functions for our setting. Let \( \Delta \Lambda(T_j) = \Lambda(T_j) - \Lambda(T_{j-1}) \). The population \( Q \)-function is

\[
Q(\Lambda'|\Lambda) = \mathbb{P} \left( \sum_{j=1}^{K} \Delta N^r_j \Delta \Lambda^{s_j}(T_j) \log[\Delta \Lambda'(T_j)] - \Lambda'(T_K) \right)
\]

The sample \( Q \)-function is

\[
Q_n(\Lambda'|\Lambda; \{Y_i\}) = \mathbb{P}_n \left( \sum_{j=1}^{K} \Delta N^r_j \Delta \Lambda^{s_j}(T_j) \log[\Delta \Lambda'(T_j)] - \Lambda'(T_K) \right)
\]

replacing missing counts with their mean function estimates.

4.2. M-Step

In the population \( M \)-step, we maximize the population \( Q \)-function over the set \( \Theta = \{\Lambda : [0, \tau] \rightarrow [0, \infty) | \Lambda \text{ is nondecreasing, } \Lambda(0) = 0, \Lambda(\tau) \leq U_{\text{all}}\} \). Here \( U_{\text{all}} \) is a uniform upper bound for all mean functions in this.
set of functions. In the sample $M$-step, we maximize the sample $Q$-function over a convex set $\Theta_n$ of monotonic functions with the same property that $0 \leq \Lambda(t) \leq \Lambda(\tau) \leq U_{all}$ with complexity that increases with $n$. Using (Wellner et al., 2000), this is non-decreasing step functions: it involves finding the NPMLE of the $Q$-function via a modified iterative convex minorant procedure (Jongbloed, 1998). For (Lu et al., 2007) $\Theta_n$ is monotone polynomial splines with the number of knots increasing with $n$. For (Wang et al., 2013) it is also step functions, although the maximization technique differs.

4.3. Algorithm

We show the sample EM algorithm. The population EM algorithm is similar.

1. Initialize an estimate of the mean function $\Lambda^0$. Let $t = 0$.
2. (E-step): Compute $Q_n(\Lambda|\Lambda^{(t)}; \{Y_t\})$ using the current mean function estimate.
3. (M-step): Find $\Lambda^{(t+1)} = \arg \max_{\Lambda \in \Theta_n} Q_n(\Lambda|\Lambda^{(t)}; \{Y_t\})$ using one of the techniques referenced.
4. Repeat steps (2) and (3) until convergence.

5. Theory

We define the assumptions in 5.1. In 5.2 we define some measures, distances, and a quasi-inner product. In 5.3 we state two technical lemmas showing that certain regularity conditions hold. These are based on regularity conditions in (Wu et al., 2016), but the second lemma allows us to relax a regularity conditions that is difficult to verify in our setting. We prove in proposition 1 that given sufficiently close initialization, each iteration of population EM gives a contraction, bringing the estimated mean function closer to the true one. We use this in theorem 1 to show that population EM converges to the true parameter with linear convergence.

We then move to sample-based theory, and show in proposition 2 that the sample M-step is a strongly consistent estimator of the population M-step. Theorem 2, our main result, states that the distance between the current EM iterate and the true mean function is bounded by two terms: one describes the effect of the population EM algorithm to the true mean function, and one is the sum of distances between sample and population M-steps. In corollary 1, we show that by choosing the number of EM iterations and drawing a different number of samples at each iteration, the estimator can get arbitrarily close to the true mean function.

5.1. Assumptions

We make the following assumptions. Similar assumptions were made in (Wellner et al., 2000; Lu et al., 2007; Wang et al., 2013), although (Wang et al., 2013) relaxes assumption 1.

1. The counting process $N$ is independent of $K$ and $T$, the number of observations and their times.
2. The observation times are random variables taking values in the bounded set $O[T] = [\tau_0, \tau]$ where $0 < \tau_0 < \tau$ and $\tau \in (0, \infty)$
3. There exists $k_0 > 0$ s.t. $P(K \leq k_0) = 1$
4. The true mean function satisfies $\Lambda^*(u) \leq U$ for some $U \in (0, \infty)$ and $\Lambda^*(u) = \sum N(u), 0 \leq u < \infty$ and $U \leq U_{all}$
5. The true mean function $\Lambda^*$ has bounded $r$th derivative in $O[T]$ with $r > 1$. The first derivative has a positive lower bound in $O[T]$.
6. The function $M_0$ defined by

$$M_0(Y; \Lambda) = \sum_{j=1}^{K} \Delta N_j^{\tau_j} \Delta \Lambda(T_j)^{\tau_j} \log(\Delta N_j^{\tau_j} \Lambda(T_j)^{\tau_j})$$

has finite integral

$$P(M_0(Y; \Lambda)) < \infty$$

for any mean function s.t. $\Lambda(\tau) < \infty$ and any missingness pattern $\tau$.
7. $N(t) \leq U_{all}$ for $t \in [0, \tau]$.
8. The observation times are $\alpha$-separated. That is, $P(T_j - T_{j-1} \geq \alpha) = 1$ for some $\alpha > 0$ and all $j = 1, \cdots, K$.
9. Our observations $\Delta N_j$ are missing completely at random w.p. $\epsilon > 0$.

5.2. Measures, Distance Metrics, and Quasi-Inner Product

We define measures which are used to construct distance metrics between mean functions. We then define a quasi-inner product that is used to show regularity conditions for our population theory.

\footnote{this is not strong, and doesn’t imply at least a constant first derivative/superlinear function in general. Consider $\Lambda^*(t) = t^{1/2}$ over $[0, \tau]$. The derivative $\frac{1}{2\sqrt{t}} \geq \frac{1}{2\tau^{3/2}}$, but this function is sublinear.}
Define

$$
\mu(B) = \mathbb{E}\{\sum_{j=1}^{K} 1_B(T_j)\}
$$

$$
\mu_2(B_1 \times B_2) = \mathbb{E}\{\sum_{j=1}^{K} 1_{B_1(T_{j-1})} 1_{B_2(T_j)}\}
$$

where $B, B_1, B_2$ are the intersection of Borel sets in $\mathbb{R}$ with $[0, \tau]$. Then $\mu(B)$ is the expected number of observations in the set $B$, $\mu_2(B_1 \times B_2)$ is the expected number of cases where one observation is in $B_1$ and the next is in $B_2$. Let

$$
\|\Lambda_1 - \Lambda_2\| = \left[ \int_0^\tau \int_0^\tau |\Lambda_1(v) - \Lambda_1(u) - (\Lambda_2(v) - \Lambda_2(u))^2 d\mu_2(u,v)\right]^{1/2}
$$

$$
= \left\{ P\sum_{j=1}^{K} (\Delta \Lambda_1(T_j) - \Delta \Lambda_2(T_j))^2 \right\}^{1/2}
$$

(2)

this is the $d_2$ metric defined in (Wellner et al., 2000). Under assumption 3, convergence in this norm implies convergence in $L^2(\mu) = [\int |\Lambda_1(u) - \Lambda_2(u)|^2 d\mu(u)]^{1/2}$.

We base our theory on convergence in (2), implying convergence in $L^2(\mu)$.

Now define the function

$$
\langle \nabla Q(\Lambda^{(l)}|\Lambda), \Lambda'\rangle = \lim_{\eta \downarrow 0} \frac{Q(\Lambda^{(l)} + \eta \Lambda'|\Lambda) - Q(\Lambda^{(l)}|\Lambda)}{\eta}
$$

$$
= P\left( \sum_{j=1}^{K} \frac{\Delta N(T_j)^{s_j} \Delta \Lambda(T_j)^{s_j}}{\Delta \Lambda_j} - 1 \right)(\Delta \Lambda_j^{s_j})
$$

(3)

We do not claim that this corresponds to a valid inner product, but it is closely related to the inner products used in (Wu et al., 2016; Balakrishnan et al., 2017): we use it similarly. Their inner product is a directional derivative of the Q-function in the direction of a parameter vector. This is the right Gateaux derivative of the Q-function in the direction of a mean function, generalizing their object to infinite dimensions. We show that the equality in eqn (10) holds in appendix A.1. Gradient stability and local uniform strong concavity explicitly refer to types of Lipschitz gradient and strong concavity conditions in (Wu et al., 2016). Here they may not, but we use them similarly and use the same terminology.

5.3. Population Theory

We first state two lemmas for regularity conditions for our population Q-function. With these, we can prove that each iteration of population EM gives us a contraction and brings us closer to the true mean function. Lemma 1 is essentially the same as the gradient stability condition of (Wu et al., 2016). Lemma 2 is related to the local uniform strong concavity condition of (Wu et al., 2016), but they studied Q-functions with a quadratic dependence on parameters, allowing them to achieve a quadratic lower bound on $Q(\Lambda^*|\Lambda) - Q(\Lambda'|\Lambda) + \langle \nabla Q(\Lambda^*|\Lambda), \Lambda' - \Lambda^* \rangle$. They then use that quadratic lower bound along with their gradient stability condition to derive a contraction. In our setting the log-likelihood does not have quadratic dependency on the mean function, and thus a quadratic lower bound is difficult to show. However, by allowing a 'slack' term that can be summed with the terms in lemma 1, we still achieve a contraction. Lemma 2 shows this lower bound holds, and is the key technical step in the paper that allows us to apply (Wu et al., 2016) to our setting: it gives some robustness to potential violations of their quadratic bound assumption.

**Lemma 1.** (Gradient Stability) there exists $\gamma_1 > 0, r > 0$ so that for $\Lambda \in B_r(\Lambda^*)$, we have

$$
\langle \nabla Q(\Lambda^*|\Lambda) - \nabla Q(\Lambda^*|\Lambda^*), \Lambda' - \Lambda^* \rangle \leq \gamma_1 \|\Lambda - \Lambda^*\|\|\Lambda' - \Lambda^*\|
$$

Here $\gamma_1$ depends on $\epsilon$ (missingness probability) and $c > 0$. The latter is the uniform lower bound on increments of the true mean function.

**Proof.** Appendix A.2

**Lemma 2.** (Local Almost Uniform Strong Concavity) there exists $\nu > 0, \gamma_2 > 0, 0 < r \leq R$ such that for $\Lambda' \in B_R(\Lambda^*), \Lambda \in B_r(\Lambda^*)$

$$
Q(\Lambda^*|\Lambda) - Q(\Lambda'|\Lambda) + \langle \nabla Q(\Lambda^*|\Lambda), \Lambda' - \Lambda^* \rangle \geq \nu \|\Lambda' - \Lambda^*\|^2 - \gamma_2 \|\Lambda' - \Lambda^*\|\|\Lambda - \Lambda^*\|
$$

Here $\nu, \gamma_2$ depend on $c, b, c$, where $b > 0$ is a uniform upper bound on increments of mean functions in $\Theta$.

**Proof.** Appendix A.3

**Proposition 1.** (Population EM Contraction) Let $\Lambda^*$ be the true mean function and $c$ be a uniform lower bound on the increments $\Delta \Lambda_j^*$. There exists radii $0 < r \leq R$ and $\gamma_1, \gamma_2, \nu$ so that if $\gamma = \gamma_1 + \gamma_2, 0 < \gamma < \nu$ and for any $\Lambda \in B_r(\Lambda^*) \cap \Theta$ and $\Lambda' \in B_R(\Lambda^*) \cap \Theta$, if $Q(\Lambda'|\Lambda) \geq Q(\Lambda^*|\Lambda)$,

$$
\|\Lambda' - \Lambda^*\| \leq \frac{\gamma}{\nu} \|\Lambda - \Lambda^*\|
$$

**Proof.** See appendix A.4.
If we move up the $Q(\Lambda' | \Lambda)$ function past the true function $\Lambda^*$, we get a contraction. This is similar to proposition 3.2 in (Wu et al., 2016).

**Theorem 1.** (Population EM Convergence to True Parameter) Suppose $0 < r \leq R$ and $0 < \gamma < \nu$ such that the previous proposition holds. Take the EM sequence $\Lambda(t+1) = \arg\max_{\Lambda' \in B_R(\Lambda^*) \cap \Theta} Q(\Lambda' | \Lambda)$ and $\Lambda^0 \in B_r(\Lambda^*) \cap \Theta$. Then

$$\|\Lambda(t) - \Lambda^*\| \leq \left(\frac{\gamma}{\nu}\right)^t \|\Lambda(0) - \Lambda^*\|$$

The proof is in appendix A.5. At each iteration, we move towards the true function by a multiplicative factor of $\left(\frac{\gamma}{\nu}\right)$. This is similar to theorem 3.1 in (Wu et al., 2016) and the proof details are nearly identical.

### 5.4. Sample Theory

To prove convergence of the sample EM algorithm to the true mean function, we need the sample $M$-step to be a strongly consistent estimator of the population $M$-step

**Proposition 2.** Let $M_n(\Lambda) = \arg\max_{\Lambda' \in \Theta_n} Q_n(\Lambda' | \Lambda)$ and $M(\Lambda) = \arg\max_{\Lambda' \in \Theta} Q(\Lambda' | \Lambda)$. Then $\|M_n(\Lambda) - M(\Lambda)\| \to 0$ a.s.

**Proof.** See appendix B.1. \qed

To prove this, we extend the strong-consistency proof of the NPMLE of (Wellner et al., 2000) to the $M$-step.

We now state the main result of the paper.

**Theorem 2.** Suppose $0 < r \leq R$ and $0 < \gamma < \nu$ such that the population contractivity holds. Let $n_1, n_2, \cdots, n_t$ be a sequence of sample sizes. Take the EM sequence $\Lambda(t+1) = \arg\max_{\Lambda' \in B_R(\Lambda^*) \cap \Theta_{n_{t+1}}} Q_{n_{t+1}}(\Lambda' | \Lambda(t))$ and $\Lambda^0 \in B_r(\Lambda^*) \cap \Theta$. Then

$$\|\Lambda(t) - \Lambda^*\| \leq \left(\frac{\gamma}{\nu}\right)^t \|\Lambda(0) - \Lambda^*\|$$

$$+ \sum_{k=0}^{t-1} \|M_{n_k}(\Lambda(k)) - M(\Lambda(k))\|$$

**Proof.** See appendix B.2 \qed

The proof follows the proof of theorem 5 of (Balakrishnan et al., 2017) closely. They show and use uniform consistency of the sample $M$-step. This is difficult to do in our case because the $M$-steps do not have a closed form solution. For the next corollary, which gives strong consistency, we allow different sample sizes at each iteration.

**Corollary 1.** For any $\eta > 0$ and initialization $\Lambda^0 \in B_r(\Lambda^*)$, there exists $t > 0$ and a sequence $0 < n_1, \cdots, n_t$ s.t. if we take the EM sequence $\Lambda(t+1) = \arg\max_{\Lambda' \in B_R(\Lambda^*) \cap \Theta_{n_{t+1}}} Q_{n_{t+1}}(\Lambda' | \Lambda(t))$ then

$$\|\Lambda(t) - \Lambda^*\| < \eta$$

a.s.

**Proof.** take $t$ sufficiently large that $\left(\frac{\gamma}{\nu}\right)^t r < \frac{\eta}{\nu}$, and take each $n_k$ large enough that $\|M_{n_k}(\Lambda(k)) - M(\Lambda(k))\| \leq \frac{\eta}{n_k \nu}$. \qed

### 5.5. Extending to Other Methods

It should be possible to extend this theory to other methods. Most non-parametric panel count methods have the same objective function and same $\Theta$, but $\Theta_n$ is different. For instance, in (Lu et al., 2007), the objective function is the same, but $\Theta_n$ are now monotone splines instead of monotone step functions. Thus, the $M$ step consistency needs to be proven again.

### 6. Experiments

We use the spef package (Wang and Yan, 2011; Chiou et al., 2019) for implementations of panel count methods. Here we show results wrapping the AEE method of (Wang et al., 2013) and describe two experiments on real data. In the appendices we wrap and compare to other methods. In appendix C we provide additional synthetic experiments.

#### 6.1. Real Data with Synthetic Missingness

We analyze a dataset of bladder tumors (Byar, 1980): the blaTum dataset in the spef package. This has 85 patients with counts of tumors taken at appointment times. We create...
missingness artificially by deleting intervals completely at random w.p. 0.2. We then initialize $\Lambda^{(0)}$ by replacing the missing data with $\text{Pois}(5)$ random variables and fitting AEE. We bootstrap 1000 times, and plot the sample mean of our learned mean functions under complete data, the corrupted initialization, and our EM algorithm as a wrapper to AEE. Appendix D has additional experiments.

Fig 2 compares inference procedures from complete data and those with missing data using our wrapper. Our wrapper, while it starts the mean function far from that learned with complete data, moves much closer to the latter.

6.2. Smoking Cessation Study

We analyze a recent smoking cessation study with the EMA question: "since the last assessment, how many cigarettes did you smoke?" We have 125 participants tracked over 10-12 day, with 3-4 EMAs targeted, delivered at random times. Based on discussion with psychologists, we consider intervals of longer than 24 hours to be missing, but use them to initialize our model. In this experiment, unlike the previous one, we lack a ground truth on the true values of our missing data.

Fig 3 shows the results from bootstrapping 1000 times and fitting two models: one treating these long intervals as valid, and one treating them as missing where we run our procedure. These long intervals make up 5.7% of observations. The learned mean function from our wrapper ends the study at 51 cigarettes, while that from applying AEE to the data naively ends it at 43, a difference of 18.6%. Based on discussions with behavioral scientists leading this data collection study, we assume that participants respond to the EMA question by reflecting on the last EMA they have completed, rather than the last EMA they were prompted to complete but missed. This suggests that the number of cigarettes smoked is underestimated when the gap between completed EMAs is large. As this is not a formal hypothesis test, it motivates that deriving test statistics based on this method will be important in order to compare whether treating long intervals as missing data learns significantly different mean functions from applying these methods naively. This is challenging as the differences between fitted and true mean functions in norm do not converge to a normal distribution. However, there are test statistics based on weighting (Balakrishnan et al., 2009) that could be extended to this setting.

7. Discussion

In this paper we analyze panel count data mean function estimation under a novel missing model. We develop an algorithm, show its asymptotic properties, and apply it to two datasets including a smoking cessation study, where we find that participants may underestimate their cigarettes smoked over intervals longer than 24 hours.

For future work, an important extension is developing test statistics. (Balakrishnan et al., 2009; Zhao et al., 2011; Balakrishnan and Zhao, 2011) do this in panel count data settings, but we would need to extend their work to the missing data setting. Other important extensions for the missing data setting include: semi-parametric estimators with baseline covariates and joint modeling with internal time-varying covariates. Finally, finite sample guarantees as in (Wu et al., 2016; Balakrishnan et al., 2017) would be interesting.

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A. Proofs Related to Theorem 1

A.1. Proof of Equality in Equation 10

We start with the numerator

\[ Q(\Lambda^{(l)} + \eta \Lambda' | \Lambda) - Q(\Lambda^{(l)} | \Lambda) = P\left( \sum_{j=1}^{K} \Delta N_j^* \Delta \Lambda_j^* \log \left( \Delta \Lambda_j^{(l)} + \eta \Delta \Lambda_j' \right) - (\Lambda_K' + \eta \Lambda_K^*) \right) \]

\[ - P\left( \sum_{j=1}^{K} \Delta N_j^* \Delta \Lambda_j^* \log \left( \Delta \Lambda_j^{(l)} \right) - (\Lambda_K') \right) \]

\[ = P\left( \sum_{j=1}^{K} \Delta N_j^* \Delta \Lambda_j^* \log \frac{\Delta \Lambda_j^{(l)} + \eta \Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} - \eta \Lambda_K^* \right) \]

Now consider

\[ \lim_{\eta \downarrow 0} \frac{\Delta \Lambda_j^{(l)} + \eta \Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} = \lim_{\eta \downarrow 0} \left( \frac{\Delta \Lambda_j^{(l)} + \eta \Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} \right)^{1/\eta} \]

\[ = \lim_{\eta \downarrow 0} \left( 1 + \frac{\Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} \right)^{1/\eta} \]

\[ = \log \exp \left( \frac{\Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} \right) \]

\[ = \frac{\Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} \]

We next need to show that we can pull the limit as \( \eta \downarrow 0 \) under integrals. There are two relevant terms: \( \frac{P(\sum_{j=1}^{K} \Delta N_j^* \Delta \Lambda_j^* \log \Delta \Lambda_j^{(l)} + \eta \Delta \Lambda_j')}{\eta} \), which we can trivially handle by pulling \( \eta \) outside the integral, and

\[ \frac{P(\sum_{j=1}^{K} \Delta N_j^* \Delta \Lambda_j^* \log \Delta \Lambda_j^{(l)} + \eta \Delta \Lambda_j')}{\eta} = P\left( \sum_{j=1}^{K} \Delta N_j^* \Delta \Lambda_j^* \log \frac{\Delta \Lambda_j^{(l)} + \eta \Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} \right) \]

Noting that \( \frac{1}{\eta} \log \frac{\Delta \Lambda_j^{(l)} + \eta \Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} \) is monotone increasing to \( \frac{\Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} \) as \( \eta \downarrow 0 \), we can apply the monotone convergence theorem to pull the limit under the integral. Then

\[ \lim_{\eta \downarrow 0} \frac{Q(\Lambda^{(l)} + \eta \Lambda' | \Lambda) - Q(\Lambda^{(l)} | \Lambda)}{\eta} = P\left( \sum_{j=1}^{K} \Delta N_j^* \Delta \Lambda_j^* \log \frac{\Delta \Lambda_j^{(l)} + \eta \Delta \Lambda_j'}{\Delta \Lambda_j^{(l)}} - \Lambda_K' \right) \]

\[ = P\left( \sum_{j=1}^{K} \left( \frac{\Delta \Lambda_j^*}{\Delta \Lambda_j^{(l)}} - 1 \right)(\Delta \Lambda_j') \right) \]

A.2. Proof of Lemma 1

Denote \( \Lambda_j \equiv \Lambda(T_j) \). We first show that the term inside the integral is bounded. Since the true mean function has a uniform lower bound on its first derivative over the study time and there is a lower bound on observation spacing, \( \Delta \Lambda_j^* \) has a uniform lower bound \( c > 0 \). Further, since \( \Lambda, \Lambda^* \in \Theta \), there is some uniform upper bound \( b > 0 \) over increments of all mean
functions. Now
\[
\sum_{j=1}^{K} s_j \left( \frac{\Delta \Lambda_j - \Delta \Lambda_j^*}{\Delta \Lambda_j^*} \right) (\Delta \Lambda_j' - \Delta \Lambda_j^*) \leq \sum_{j=1}^{k_0} 2b_j^2 c < \infty
\]
then any integral of this over \(T \times K \times Z\) will also be finite, and we can apply Fubini’s theorem to such integrals. Then recalling that \(\epsilon > 0\) is the MCAR probability,
\[
\langle \nabla Q(\Lambda^*|\Lambda) - \nabla Q(\Lambda^*|\Lambda^*), \Lambda' - \Lambda^* \rangle = P \left[ \sum_{j=1}^{K} s_j \left( \frac{\Delta \Lambda_j - \Delta \Lambda_j^*}{\Delta \Lambda_j^*} \right) (\Delta \Lambda_j' - \Delta \Lambda_j^*) \right]
\]
\[
\leq \epsilon \left[ P \left( \sum_{j=1}^{K} \left( \frac{\Delta \Lambda_j - \Delta \Lambda_j^*}{\Delta \Lambda_j^*} \right)^2 \right)^{1/2} \right]^{1/2}
\]
Here we used Fubini’s theorem to pull out \(\epsilon\). Applying the CS inequality for inner products in \(l^2\), and finally applying the CS inequality for expectations gives us the result. The first term on rhs is then:
\[
P \left( \sum_{j=1}^{K} \left( \frac{\Delta \Lambda_j - \Delta \Lambda_j^*}{\Delta \Lambda_j^*} \right)^2 \right)^{1/2} \leq \frac{1}{c} P \left[ \sum_{j=1}^{K} (\Delta \Lambda_j - \Delta \Lambda_j^*)^2 \right]^{1/2}
\]
This gives us
\[
P \left[ \sum_{j=1}^{K} s_j \left( \frac{\Delta \Lambda_j - \Delta \Lambda_j^*}{\Delta \Lambda_j^*} \right) (\Delta \Lambda_j' - \Delta \Lambda_j^*) \right] \leq \frac{\epsilon}{c} ||\Lambda - \Lambda^*|| ||\Lambda' - \Lambda^*||
\]
and thus
\[
\langle \nabla Q(\Lambda^*|\Lambda) - \nabla Q(\Lambda^*|\Lambda^*), \Lambda' - \Lambda^* \rangle \leq \frac{\epsilon}{c} ||\Lambda - \Lambda^*|| ||\Lambda' - \Lambda^*||
\]

A.3. Proof of Lemma 2

Proof. We state one additional technical assumption. We assume that both \(\sum_{j=1}^{K} \tau_j [\Delta N_j \log \frac{\Delta \Lambda_j^*}{\Delta \Lambda_j^*} - (\Delta \Lambda_j^* - \Delta \Lambda_j') (1 - (\frac{\Delta N_j}{\Delta \Lambda_j^*} - 1))]\) and \(\sum_{j=1}^{K} s_j \Delta \Lambda_j \log \frac{\Delta \Lambda_j^*}{\Delta \Lambda_j^*} - (\Delta \Lambda_j^* - \Delta \Lambda_j') (1 - (\frac{\Delta \Lambda_j}{\Delta \Lambda_j^*} - 1))]\) are integrable over \(N \times T \times K \times Z\) with respect to the measure \(P\).

Denote
\[
I = P\left[ \sum_{j=1}^{K} \tau_j [\Delta N_j \log \frac{\Delta \Lambda_j^*}{\Delta \Lambda_j^*} - (\Delta \Lambda_j^* - \Delta \Lambda_j') (1 - (\frac{\Delta N_j}{\Delta \Lambda_j^*} - 1))] \right]
\]
\[
II = P\left[ \sum_{j=1}^{K} s_j \Delta \Lambda_j \log \frac{\Delta \Lambda_j^*}{\Delta \Lambda_j^*} - (\Delta \Lambda_j^* - \Delta \Lambda_j') (1 - (\frac{\Delta \Lambda_j}{\Delta \Lambda_j^*} - 1))] \right]
\]
the desired result is given by
\[
I + II \geq \nu ||\Lambda' - \Lambda^*||^2 - \gamma_2 ||\Lambda' - \Lambda^*|| ||\Lambda - \Lambda^*||
\]
We first lower bound \(I\), the terms for complete data. Let \(h(x) = x(\log x - 1) + 1\). By Taylor expanding \(\log (y + 1)\) at \(y = 0\), and then plugging in \(x = y - 1\), we can obtain \(h(x) = \frac{1}{2}(x - 1)^2 + o((x - 1)^2)\). Note that this implies \(h(x) \geq \frac{1}{2}(x - 1)^2\)
for \( x \) in a ball around 1, so that if we let \( x = \frac{\Delta^*}{\Lambda^*} \)

\[
I = P\left[ \sum_{j=1}^{K} \tau_j [\Delta N_j \log \frac{\Delta^*_j}{\Delta^*_j} - (\Delta^*_j - \Delta^*_j)(1 - (\frac{\Delta N_j}{\Delta^*_j} - 1))] \right]
\]

\[
= P\left[ \sum_{j=1}^{K} \tau_j [\Delta^*_j \log \frac{\Delta^*_j}{\Delta^*_j} - (\Delta^*_j - \Delta^*_j)] \right]
\]

\[
= (1 - \epsilon)P\left[ \sum_{j=1}^{K} \Delta^*_j h(\frac{\Delta^*_j}{\Delta^*_j}) - \epsilon P\left[ \sum_{j=1}^{K} \Delta^*_j h(\frac{\Delta^*_j}{\Delta^*_j}) \right] \right]
\]

\[
\geq \frac{1}{3}P\left[ \sum_{j=1}^{K} \Delta^*_j (\frac{\Delta^*_j}{\Delta^*_j} - 1)^2 \right] - \epsilon P\left[ \sum_{j=1}^{K} \Delta^*_j h(\frac{\Delta^*_j}{\Delta^*_j}) \right]
\]

\[
= \frac{1}{3}P\left[ \sum_{j=1}^{K} \Delta^*_j (\frac{\Delta^*_j}{\Delta^*_j} - 1)^2 \right] - \epsilon P\left[ \sum_{j=1}^{K} \Delta^*_j h(\frac{\Delta^*_j}{\Delta^*_j}) \right]
\]

\[
\geq \frac{1}{3b} \| \Lambda - \Lambda^* \|^2 - \epsilon \left[ \sum_{j=1}^{K} \Delta^*_j h(\frac{\Delta^*_j}{\Delta^*_j}) \right] \quad (11)
\]

where again \( b \) is a uniform upper bound on the increments of any mean function and we used Fubini’s theorem to pull out \( 1 - \epsilon \), which we can do because we assumed that the terms inside \( I \) were integrable. A very similar bound was given in (Balakrishnan et al., 2009), although they have \( \frac{1}{6} \) instead of \( \frac{1}{3} \). Any positive constant less than \( \frac{1}{2} \) will work but the ball will need to adjusted accordingly.

The term \( II \) is difficult to deal with by itself. However, it also has a coefficient of \( \epsilon \). Summing it with the part with coefficient \( -\epsilon \) in (11), we have

\[
II - \epsilon P\left[ \sum_{j=1}^{K} \Delta^*_j h(\frac{\Delta^*_j}{\Delta^*_j}) \right] = \epsilon P\left[ \sum_{j=1}^{K} (\Delta^*_j - \Delta^*_j)(1 - (\frac{\Delta N_j}{\Delta^*_j} - 1))] \right]
\]

\[
= \epsilon P\left[ \sum_{j=1}^{K} (\Delta^*_j - \Delta^*_j)(\frac{\Delta^*_j}{\Delta^*_j}) \right] - \epsilon P\left[ \sum_{j=1}^{K} \frac{\Delta^*_j}{\Delta^*_j} (\frac{\Delta^*_j}{\Delta^*_j} - 1)] \right]
\]

\[
= \epsilon P\left[ \sum_{j=1}^{K} \frac{\Delta^*_j}{\Delta^*_j} (\frac{\Delta^*_j}{\Delta^*_j} - 1)] \right] - \epsilon P\left[ \sum_{j=1}^{K} \frac{\Delta^*_j}{\Delta^*_j} (\frac{\Delta^*_j}{\Delta^*_j} - 1)] \right]
\]

\[
\geq -\epsilon P\left[ (\sum_{j=1}^{K} (\frac{\Delta^*_j}{\Delta^*_j} - 1)]^2 \right] \sum_{j=1}^{K} \Delta^*_j^2 \frac{\Delta^*_j}{\Delta^*_j} (\frac{\Delta^*_j}{\Delta^*_j} - 1)]^2 \right]^{1/2}
\]

\[
\geq -\epsilon b \| \Lambda - \Lambda^* \|^2 \left[ \sum_{j=1}^{K} \Delta^*_j^2 \frac{\Delta^*_j}{\Delta^*_j} (\frac{\Delta^*_j}{\Delta^*_j} - 1)]^2 \right]^{1/2} \quad (12)
\]

where in the last two steps we applied Cauchy Schwarz twice (once in \( l^2 \) and once for expectations) to get a negative lower
bound instead of a positive upper bound. Let 
\[
x = \frac{\Delta \Lambda_j^*}{\Delta \Lambda_j} - 1
\]
We now investigate the term
\[
P\left[\sum_{j=1}^{K} \Delta \Lambda_j^2 \log \left(\frac{\Delta \Lambda_j^*}{\Delta \Lambda_j} - 1\right)\right]^{1/2} = P\left[\sum_{j=1}^{K} \Delta \Lambda_j^2 [(1 + x) \log (1 + x) + x]^2\right]^{1/2}
\]
\[
= P\left[\sum_{j=1}^{K} \Delta \Lambda_j^2 [(1 + x) - \frac{x^2}{2} + o(x^2)]^2\right]^{1/2}
\]
\[
= P\left[\sum_{j=1}^{K} \Delta \Lambda_j^2 \left(2x^2 + o(x^2)\right)\right]^{1/2}
\]
\[
\leq P\left[\sum_{j=1}^{K} \Delta \Lambda_j^2 \left(9x^2\right)^{1/2}\right]
\]
\[
= 3P\left[\sum_{j=1}^{K} \Delta \Lambda_j^2 \left(\frac{\Delta \Lambda_j^*}{\Delta \Lambda_j} - 1\right)^2\right]^{1/2}
\]
\[
= 3\|\Lambda - \Lambda'\| \quad (13)
\]
Putting together (11), (12), and (13) we obtain
\[
I + II \geq \frac{1}{3b}\|\Lambda - \Lambda^*\|^2 - 3\epsilon b\|\Lambda' - \Lambda^*\|\|\Lambda^* - \Lambda'\|
\]

### A.4. Proof of Population Contractivity

We first state and prove an important lemma obtained by combining the previous two

**Lemma 3.** Take \(\gamma = \gamma_1 + \gamma_2\). There exists \(0 < r \leq R, \gamma > 0, \nu > 0\) so that if \((\Lambda', \Lambda) \in B_R(\Lambda^*) \times B_r(\Lambda^*), \gamma < \nu\).

**Proof.** In a neighborhood of the true mean function, the inequalities found by taylor expanding the log terms hold. We then want \(\gamma < \nu\) to hold, which requires

\[
\gamma < \nu
\]
\[
3\epsilon b + \frac{\epsilon}{c} < \frac{1}{3b}
\]
\[
\epsilon (3b + \frac{1}{c}) < \frac{1}{3b}
\]
\[
\epsilon < \frac{1}{9b^2 + \frac{3\epsilon}{c}}
\]

thus if the largest possible increment of mean functions in the ball goes down or the uniform lower bound on increments of the true mean function goes up, we can allow a higher missingness probability. 

We now state the main proof of population contractivity. Denote

\[
V(\Lambda'|\Lambda) = Q(\Lambda'|\Lambda) - Q(\Lambda^*|\Lambda) - \langle \nabla Q(\Lambda^*|\Lambda), \Lambda' - \Lambda^* \rangle
\]
then
\[ 0 \leq Q(\Lambda' | \Lambda) - Q(\Lambda^* | \Lambda) \\
= V(\Lambda' | \Lambda) + \langle \nabla Q(\Lambda^* | \Lambda), \Lambda' - \Lambda^* \rangle \\
= V(\Lambda' | \Lambda) + \langle \nabla Q(\Lambda^* | \Lambda) - \nabla Q(\Lambda^* | \Lambda^*), \Lambda' - \Lambda^* \rangle + \langle \nabla Q(\Lambda^* | \Lambda^*), \Lambda' - \Lambda^* \rangle \\
\leq V(\Lambda' | \Lambda) + \langle \nabla Q(\Lambda^* | \Lambda) - \nabla Q(\Lambda^* | \Lambda^*), \Lambda' - \Lambda^* \rangle \text{ KKT conditions} \\
\leq -\nu \| \Lambda' - \Lambda^* \|^2 + \gamma \| \Lambda - \Lambda^* \| \| \Lambda' - \Lambda^* \| \text{ technical Lemmas} \\
\]

and rearranging terms and dividing both sides by \( \| \Lambda' - \Lambda^* \| \) gives the desired result. Note that we used \( \langle \nabla Q(\Lambda^* | \Lambda^*), \Lambda' - \Lambda^* \rangle \leq 0 \), which if \( \langle \cdot, \cdot \rangle \) were a valid inner product would be the KKT conditions. However since \( \langle \cdot, \cdot \rangle \) may not be a valid inner product, they must be checked specifically. (Wellner et al., 2000) does it in the sample case for the true log-likelihood: it is easy to verify that it still holds in the population case for \( Q \)-functions. Noting that \( \Lambda^* \) maximizes \( Q(\Lambda' | \Lambda^*) \), we have that \( Q(\Lambda^* + \eta(\Lambda' - \Lambda^*), \Lambda^*) - Q(\Lambda^* | \Lambda^*) \leq 0 \)

\[
\langle \nabla Q(\Lambda^* | \Lambda^*), \Lambda' - \Lambda^* \rangle = \lim \lim_{\eta \downarrow 0} Q(\Lambda^* + \eta(\Lambda' - \Lambda^*), \Lambda^*) - Q(\Lambda^* | \Lambda^*) \\
\leq 0
\]

### A.5. Proof of Theorem 1

By induction. It holds for \( t = 0 \). Assume it holds for \( t \geq 0 \). Then \( \Lambda^{(t)} \in B_r(\Lambda^*) \) and by definition \( Q(\Lambda^{(t+1)} | \Lambda^{(t)}) \geq Q(\Lambda^* | \Lambda^{(t)}) \). Applying population contractivity and the induction assumption,

\[
\| \Lambda^{t+1} - \Lambda^* \| \leq \frac{2}{\nu^t} \| \Lambda^t - \Lambda^* \| \\
\leq (\frac{2}{\nu})^{t+1} \| \Lambda^0 - \Lambda^* \|
\]

### B. Proofs Related to Theorem 2

#### B.1. Proof of Proposition 2

Our proof follows (Wellner et al., 2000) closely, but we have to handle the fact that we replace missing counts with the current mean function estimate’s increments, and also handle the fact that their proof that their population M-estimator is unique does not hold in our setting: we replace it by showing that the population objective function is strictly concave, and thus the M-estimator must be unique a.e.

Let

\[
m_{\Lambda'; \Lambda} = \sum_{j = 1}^{K} \Delta N_j \gamma_j \Lambda_j^t \log(\Delta \Lambda_j') - \Delta \Lambda_j'
\]

which is an individual participant’s sample \( Q \)-function, and let

\[
M(\Lambda' | \Lambda) = P m_{\Lambda'; \Lambda} \\
M(\Lambda' | \Lambda) = Q(\Lambda' | \Lambda) \\
M_{\text{in}}(\Lambda' | \Lambda) = P_n m_{\Lambda'; \Lambda} \\
M_{\text{in}}(\Lambda' | \Lambda) = Q_n(\Lambda' | \Lambda; \{ Y_i \})
\]

this is simply rewriting the \( Q \)-functions using empirical processes notation.

Let

\[
M(\Lambda) = \arg \max M(\Lambda' | \Lambda) \\
M_{\text{in}}(\Lambda) = \arg \max M_{\text{in}}(\Lambda' | \Lambda)
\]
these are the $M$-estimators (M-steps) for the population and sample $Q$-functions, given current parameters, respectively, and note that they are also mean functions and thus have increments $\Delta M_j$ and $\Delta M_{n,j}$ for the population and sample versions, respectively.

We need an upper envelope for the class of functions $M \equiv \{ m_{A',A} : A', A \in \Theta \}$. Since $g(x) = a \log x - x$ has max at $x = a$ for $a > 0$,

$$m_{A',A}(Y) \leq \sum_{j=1}^{K} \Delta N_{j}^{\tau_{j}} \log(\Delta N_{j}^{\tau_{j}})$$

$$= M_{0}(Y; \Lambda)$$

where $PM_{0}(Y; \Lambda) < \infty$ by assumption. Now since $M_{n}(\Lambda)$ maximizes $M_{n}(\Lambda')|A)$, we have $M_{n}(M_{n}(\Lambda)|A) \geq M_{n}((1-\eta)M_{n}(\Lambda) + \eta M(\Lambda)|A)$, which gives us

$$\lim_{n \to \infty} \frac{M_{n}((1-\eta)M_{n}(\Lambda) + \eta M(\Lambda)|A) - M_{n}(M_{n}(\Lambda)|A)}{\eta} \leq 0$$

(21)

and evaluating this limit using the same techniques as in A.1 gives us

$$\mathbb{P}_{n}(\sum_{j=1}^{K} \frac{\Delta N_{j}^{\tau_{j}}}{\Delta M_{n,j}(\Lambda)} - 1)(\Delta M_{j}(\Lambda) - \Delta M_{n,j}(\Lambda)) \leq 0$$

which can be written as

$$0 \geq \mathbb{P}_{n}\{\sum_{j=1}^{K} (\Delta N_{j}^{\tau_{j}} \frac{\Delta M_{j}(\Lambda)}{\Delta M_{n,j}(\Lambda)} + \Delta M_{n,j}(\Lambda))\} - \mathbb{P}_{n}\{\sum_{j=1}^{K} (\Delta M_{j}(\Lambda) + \Delta N_{j}^{\tau_{j}})\}$$

now the second term on the rhs converges a.s. by the SLLN and assumptions 2, 3, and 4 to

$$P(M_{K}(\Lambda)) + (1-\epsilon)P(\Lambda_{n}^{*}) + \epsilon P(\Lambda) \equiv C < \infty$$

(22)

here we know that $P(\Lambda_{n}^{*}) < \infty$ from the assumptions mentioned. That $P(M_{K}(\Lambda)) < \infty$ and $P(\Lambda) < \infty$ follows since $\Lambda, M(\Lambda) \in B_{R}(\Lambda^{*})$.

Hence it follows that for any subset $A$ of $t \in \mathbb{R}^{k} : 0 \leq t_1 \leq t_2 \leq \cdots \leq t_k$ and $T = (T_1, \cdots, T_K)$, we have, almost surely,

$$C \geq \lim_{n \to \infty} \sup \mathbb{P}_{n}\{\sum_{j=1}^{K} \Delta N_{j}^{\tau_{j}} \frac{\Delta M_{j}(\Lambda)}{\Delta M_{n,j}(\Lambda)} + M_{n,K}(\Lambda)\}$$

$$\geq \lim_{n \to \infty} \mathbb{P}_{n}\{1_{A}(T)\} \{\sum_{j=1}^{K} \Delta N_{j}^{\tau_{j}} \frac{\Delta M_{j}(\Lambda)}{\Delta M_{n,j}(\Lambda)} + M_{n,K}(\Lambda)\}$$

Define

$$\nu(B) = \mathbb{E}1_{B}(T)$$

(23)

which is the probability of the last observation happening in the set $B$. Let $S_{\nu} \equiv \text{supp}(\nu)$ and set $\tau \equiv \text{sup}(S_{\nu})$. Then letting $A = R^{k-1} \times [b, \tau]$ for every $b \in (0, \tau]$,

$$C \geq \lim_{n \to \infty} \sup \mathbb{P}_{n}\{1_{[b,\tau]}(T_{K})M_{n,K}(\Lambda)\}$$

(24)

$$\geq \lim_{n \to \infty} \sup \mathbb{P}_{n}\{M_{n}(\Lambda)(b)\}1_{[b,\tau]}(T_{K}) = \lim_{n \to \infty} \sup \mathbb{P}_{n}\{M_{n}(\Lambda)(b)\nu([b, \tau])\}$$

(25)

almost surely by the strong law of large numbers. There are then two cases: one where $\nu([\tau]) > 0$ and the other where there exists $0 < b < \tau$ arbitrarily close to $\tau$ such that $\nu([b, \tau]) > 0$. The first case is where the probability of the last observation happening at study end time is non-zero, while the second is where it is zero, but arbitrarily small intervals
where $m$ Thus theorem A.1 in (Wellner et al., 2000) (one-side Glivenko Cantelli) yields

$$\limsup_{n \to \infty} M_n(\Lambda) = \frac{C}{\nu(\{\tau\})} < \infty$$

and hence the functions are a.s. bounded on $[0, \tau]$. Since the sequence of functions $\{M_n(\Lambda)(u, \omega) : u \in [0, \tau]\}$ is uniformly bounded for $n$ sufficiently large, by Helly’s selection theorem $\{M_n(\Lambda)(\cdot, \omega)\}$ has a subsequence $\{M_{n'}(\Lambda)(\cdot, \omega)\}$ converging to a monotonically increasing $\Lambda' = \Lambda'_1$ defined on $[0, \tau]$ and taking values on $[0, \frac{C}{\nu(\{\tau\})}]$. Consider the class of functions

$$\mathcal{M}_\tau \equiv \{m_{\Lambda', \Lambda} : \Lambda' \in \Theta_\tau\}$$

where

$$\Theta_\tau \equiv \{\Lambda' \in \Theta : \Lambda'(\tau) \leq \frac{C}{\nu(\{\tau\})} + 1\}$$

note that $\Theta_\tau$ is compact for the (pseudo)-metric $\| \cdot \|$. This follows since we can also apply Helly’s selection theorem to any sequence in $\Theta_\tau$ to show sequential compactness, and sequential compactness in metric spaces implies compactness. Moreover, the function $\Lambda' \to m_{\Lambda', \Lambda}(Y_t)$ is upper semi-continuous in $\Lambda'$ for $P$ for almost all $Y_t$ (by the same argument as (Wellner et al., 2000)). Further $m_{\Lambda', \Lambda}(Y) \leq M_0(Y; \Lambda)$ for all $Y$ and $\Lambda' \in \Theta_\tau$, and $P(M_0(Y; \Lambda)) < \infty$ by assumption. Thus theorem A.1 in (Wellner et al., 2000) (one-side Glivenko Cantelli) yields

$$\limsup_{n \to \infty} \sup_{\Lambda' \in \Theta_\tau} (P_n - P)m_{\Lambda', \Lambda} \leq 0 \text{ a.s.}$$

Since $M_n(M(\Lambda)|\Lambda) \to M(M(\Lambda)|\Lambda)$ a.s. by the strong law of large numbers and $M_n(M(\Lambda)|\Lambda) \leq M_n(M_n(\Lambda)|\Lambda)$, it follows that

$$M(M(\Lambda)|\Lambda) \leq \liminf_{n \to \infty} M_n(M_n(\Lambda)|\Lambda)$$

and from (26) and (29) it follows that

$$\limsup_{n' \to \infty} M_{n'}(M_{n'}(\Lambda)|\Lambda) = \limsup_{n' \to \infty} \sup_{n} \frac{P_n - P}{m_{\Lambda', \Lambda}(\cdot)} \en
$$

$$\leq \limsup_{n' \to \infty} \sup_{n} \frac{P_{M_{n'}(\Lambda), \Lambda}}{m_{\Lambda', \Lambda}} \text{ by (29)}$$

$$\leq P(m_{\Lambda', \Lambda})$$

for any subsequence $M_{n'}(\Lambda)$ converging almost surely to $\Lambda'$ on $[0, \tau]$; this follows from the upper semi-continuity of $\Lambda' \to P(m_{\Lambda', \Lambda})$ which follows from Theorem A.1 in (Wellner et al., 2000) along with pointwise convergence of $M_{n'}(\Lambda)$ on $[0, \tau]$. Combining (30) and (33) we have

$$0 \leq M(\Lambda'|\Lambda) - M(M(\Lambda)|\Lambda)$$

however $M(\Lambda)$ is a maximum of $M(\Lambda'|\Lambda)$. Thus if $M(\Lambda'|\Lambda)$ has an a.e. unique maximizer, $M(\Lambda) = \Lambda'$. We thus need to show uniqueness. It suffices to show that $M(\Lambda'|\Lambda)$ is strictly concave.

Note

$$M(\frac{\Lambda_1 + \Lambda_2}{2} | \Lambda) = P\left(\sum_{j=1}^{K} \Delta N_{j} \Lambda_j \log \frac{\Delta \Lambda_{1, j} + \Delta \Lambda_{2, j}}{2} - \left[\frac{\Delta \Lambda_{1, j} + \Delta \Lambda_{2, j}}{2}\right]\right)$$

$$\geq P\left(\sum_{j=1}^{K} \Delta N_{j} \Lambda_j \log \sqrt{\Delta \Lambda_{1, j} \Delta \Lambda_{2, j}} - \left[\frac{\Delta \Lambda_{1, j} + \Delta \Lambda_{2, j}}{2}\right]\right) \text{ AM-GM inequality}$$

$$= \frac{1}{2} M(\frac{\Lambda_1}{2} | \Lambda) + \frac{1}{2} M(\frac{\Lambda_2}{2} | \Lambda)$$
We claim for any 1000
We generate
We prove by induction. First, this holds for 300
we divide by the total time points by 920
learned models at specific points. To do so, for each bootstrap replicate, we add a small amount of noise ±1e − 0 to the observed time points for identifiability purposes, take all of these time points, and take a subset. We originally have 920 time points and so creating 1000 bootstrap replicates will lead to approximately 920, 000 time points. In order to reduce this we divide by the total time points by 300 and randomly select that many so that we have approximately 3, 000 time points at which we evaluate each function in order to form a mean and marginal confidence intervals.

B.2. Proof of Theorem 2
We claim for any t > 0,

\[ \|\Lambda^{(t+1)} - \Lambda^*\| \leq \frac{\gamma}{2^t} \|\Lambda^{(t)} - \Lambda^*\| + \|M_{n_{t+1}}(\Lambda^{(t)}) - M(\Lambda^{(t)})\| \]

We prove by induction. First, this holds for t = 1.

\[ \|\Lambda^{(1)} - \Lambda^*\| \leq \|M(\Lambda^{(0)}) - \Lambda^*\| + \|M_{n_1}(\Lambda^{(0)}) - M(\Lambda^{(0)})\| \leq \frac{\gamma}{2} \|\Lambda^{(0)} - \Lambda^*\| + \|M_{n_1}(\Lambda^{(0)}) - M(\Lambda^{(0)})\| \]

Now assume holds true for t > 0. Then for t + 1,

\[ \|\Lambda^{(t+1)} - \Lambda^*\| \leq \|M(\Lambda^{(t)}) - \Lambda^*\| + \|M_{n_{t+1}}(\Lambda^{(t)}) - M(\Lambda^{(t)})\| \leq \frac{\gamma}{2} \|\Lambda^{(t)} - \Lambda^*\| + \|M_{n_{t+1}}(\Lambda^{(t)}) - M(\Lambda^{(t)})\| \]

Now iterating we have

\[ \|\Lambda^{(t)} - \Lambda^*\| \leq \left(\frac{\gamma}{2}\right)^t \|\Lambda^{(0)} - \Lambda^*\| + \sum_{k=0}^{t-1} \|M_{n_{k+1}}(\Lambda^{(k)}) - M(\Lambda^{(k)})\| \]

C. Synthetic Analysis
C.1. Square Root Synthetic Experiment
We generate synthetic panel count data from an inhomogeneous Poisson processes with mean functions \( \Lambda^*(u) = u^{1/2} \), \( \Lambda^*(u) = u^2 \). We use 100 trajectories, each with 30 observations and for each observation set it to missing with probability 0.1. We initialize the mean function \( \Lambda^{(0)} \) by replacing the missing data with \( \text{Pois}(5) \) random variables and fitting a model.

We generate 1000 Monte Carlo runs and create Monte Carlo marginal confidence intervals from those runs.

Fig 4 compares the true mean function against AEE wrapped with our method vs AEE directly on the corrupted data. Taking the corrupted data as given learns highly biased results, while wrapping AEE with our algorithm reduces bias substantially for the square root experiment and learns close to the true mean function for the quadratic experiment.

D. Further Analysis of Bladder Tumor Dataset
D.1. Comment on Mean and Confidence Intervals
In order to form the mean and marginal confidence intervals in the case of step functions, we need to evaluate the 1000 learned models at specific points. To do so, for each bootstrap replicate, we add a small amount of noise ±1e − 6 to the observed time points for identifiability purposes, take all of these time points, and take a subset. We originally have 920 time points and so creating 1000 bootstrap replicates will lead to approximately 920, 000 time points. In order to reduce this we divide by the total time points by 300 and randomly select that many so that we have approximately 3, 000 time points at which we evaluate each function in order to form a mean and marginal confidence intervals.
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Figure 4. Mean+95% Monte Carlo CIs of 1000 runs, synthetic datasets: 20% missingness using AEE wrapped with our method. Black/solid is the true mean function. Red/dotted is initialization with missing data set to Poisson(5) values, which is very far from the true mean function. Blue/dashed is our EM algorithm initialized at red. (a) $\Lambda^*(u) = \sqrt{u}$ a square root mean function (b) $\Lambda^*(u) = u^2$ a quadratic mean function

D.2. Additional Experiment

We perform an additional experiment, where we vary the missingness probability with $\epsilon = 0.1, 0.2, 0.3, 0.4$. We do so for each of the five following methods: the NPMPLE of (Wellner et al., 2000), the smoothed MPLs and MLs estimators of (Lu et al., 2007), and the AEE and AEEX methods of (Wang et al., 2013). Note that we do not wrap the NPMLE of (Wellner et al., 2000), which is the model where we show $M$-step theory, as the SPEF package does not contain it. Since we show that bias is relatively low but increasing as a function of the missingness probability for five methods, we expect the same for the NPMLE.

The results of the first experiment are shown in figure 5. The bias for $\epsilon = 0.1$ is almost non-existent, it is low for $\epsilon = 0.2$, and it goes up for $\epsilon = 0.3$ and $0.4$. Note that $30 - 40\%$ missingness is large, and it is unsurprising that there is some bias. Further, in all cases it is much lower than the initialization with corrupted data shown in figure 2.
Figure 5. Results for mean and 95% CIs for 1000 bootstrap replicates for bladder tumor dataset, with the missingness probability $\epsilon$ set to $\epsilon = 0.1, 0.2, 0.3, 0.4$. We see that for $\epsilon = 0.1$ there is almost no bias relative to the complete data model, and for $\epsilon = 0.2$ it is low. For $\epsilon = 0.3, 0.4$ the bias increases substantially. Note that 30-40% probability of missingness is very large, and some bias is to be expected, but it is still far less than the initialization in figure 2. The methods wrapped with our method are (a) MPL of (Wellner et al., 2000) (b) AEE of (Wang et al., 2013) (c) AEEX of (Wang et al., 2013) (d) MPLs of (Lu et al., 2007) note that for this we need to reduce the time axis slightly as spline models cannot interpolate far past the region where they have values in learning (e) MLs of (Lu et al., 2007), same issue.