Classification under
Nuisance Parameters
and
Generalized Label Shift
in
Likelihood-Free Inference



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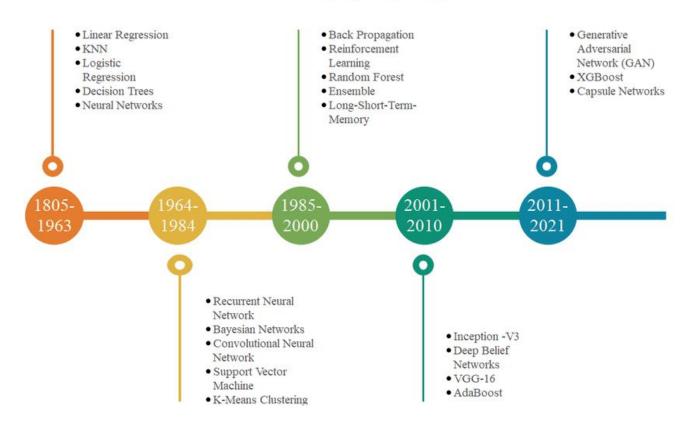


M. Doro (Padova)

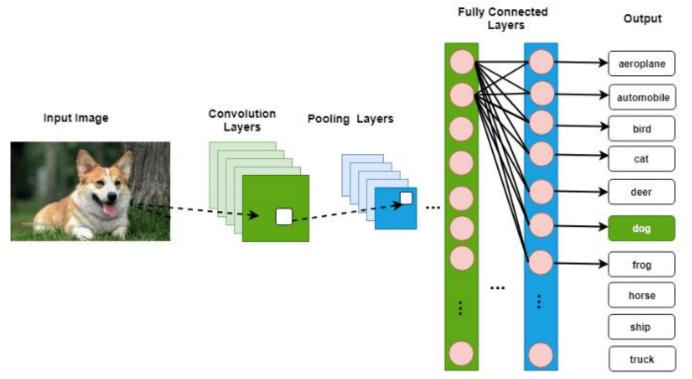


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Machine Learning & Deep Learning Algorithms Development Timeline



Machine Learning Revolution



Goal in Supervised Learning

Given measurements $(\mathbf{X}_1, Y_1), \dots, (\mathbf{X}_n, Y_n)$, learn a model to predict Y_i based on \mathbf{X}_i

construct g to obtain good predictions

$$g(\mathbf{X}_{n+1}) \approx Y_{n+1}, \ldots, g(\mathbf{X}_{n+m}) \approx Y_{n+m}$$

$$R(g) = \mathbb{E}\left[(Y - g(\mathbf{X}))^2 \right]$$

Standard Assumption: i.i.d.



If data is not i.i.d., new assumptions are necessary

Information Sciences 649 (2023) 119612



- [Total Dataset Shift] $H_{0,D}: P_{X,Y}^{(1)} = P_{X,Y}^{(2)}$
- [Feature Shift] $H_{0,F}: P_{X}^{(1)} = P_{X}^{(2)}$
- [Response Shift] $H_{0,R}: P_Y^{(1)} = P_Y^{(2)}$
- [Conditional Shift Type 1] $H_{0,C1}: P_{X|Y}^{(1)} = P_{X|Y}^{(2)}$ ($P_{Y}^{(2)}$ almost surely) [Conditional Shift Type 2] $H_{0,C2}: P_{Y|X}^{(1)} = P_{Y|X}^{(2)}$ ($P_{X}^{(2)}$ almost surely)

A unif

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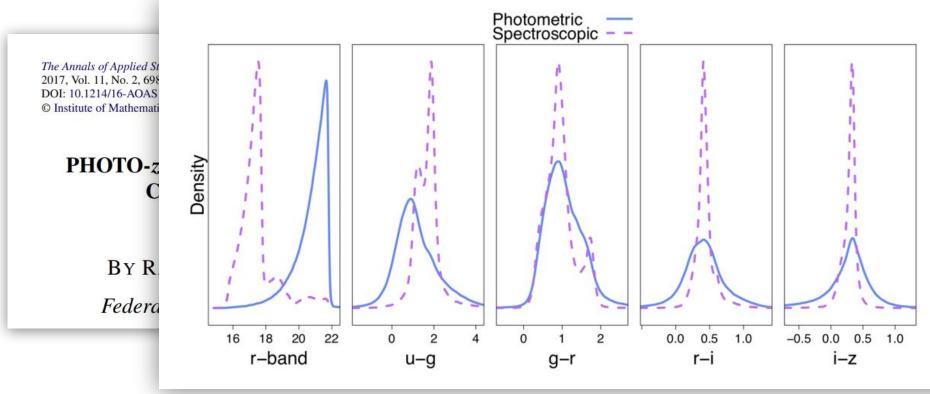
b Department of Statistics, Federal University of São Carlos, Brazil

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Example: Y|x is the same



Example: X|y is the same

Journal of Machine Learning Research 20 (2019) 1-33

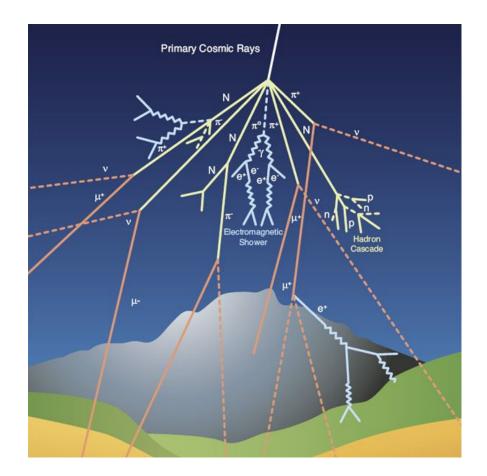
Submitted 7/18; Revised 2/19; Published 4/19

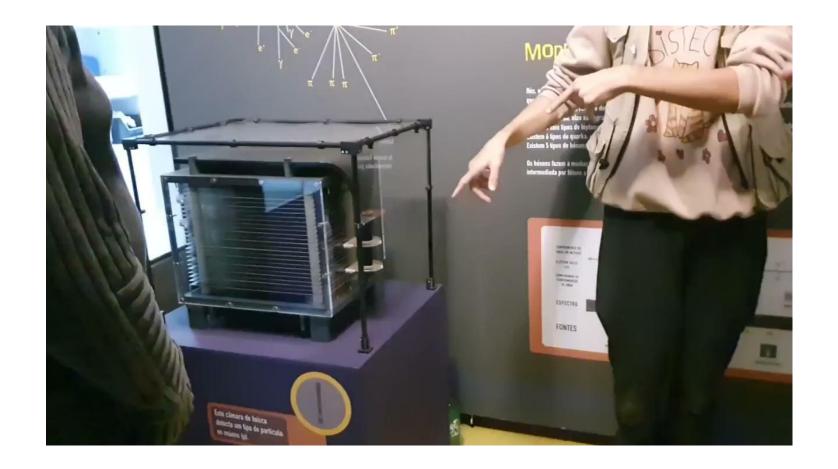
Quantification Under Prior Probability Shift: the Ratio Estimator and its Extensions

Afonso Fernandes Vaz Rafael Izbicki Rafael Bassi Stern

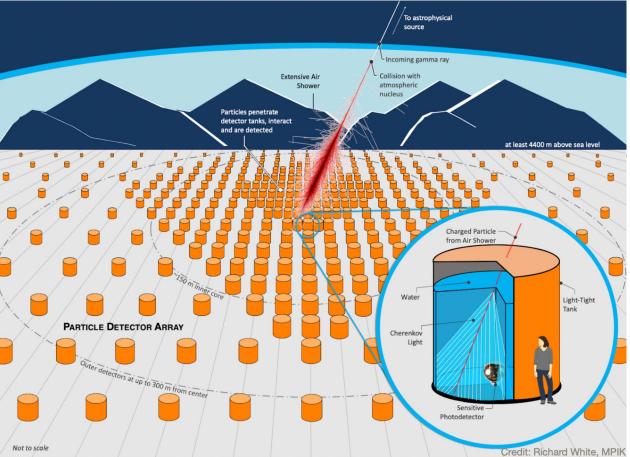
Department of Statistics Federal University of São Carlos São Carlos, SP 13565-905, Brazil AFONSOFVAZ@GMAIL.COM RAFAELIZBICKI@GMAIL.COM RBSTERN@GMAIL.COM

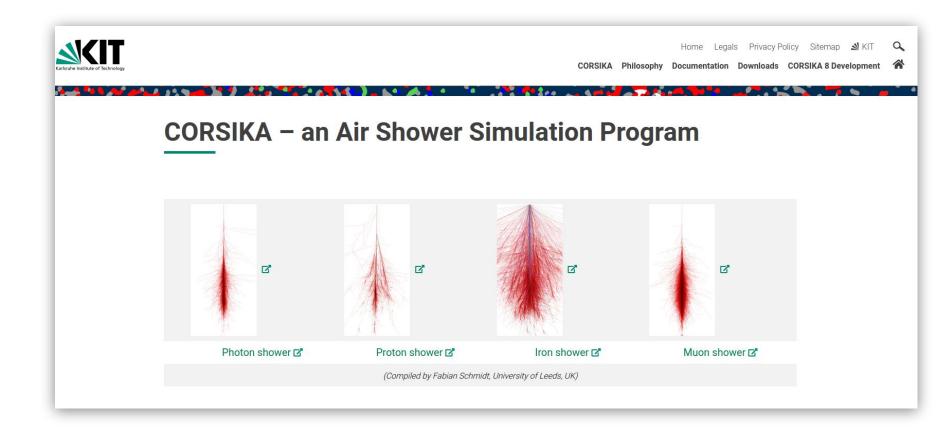
This work









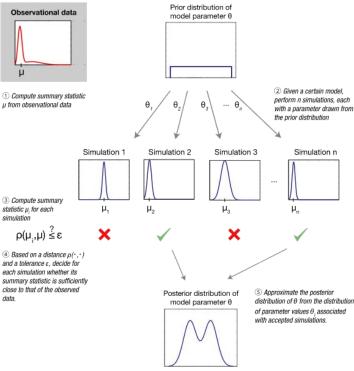


In terms of Statistics:

mechanistic model: $\theta = (Y, \nu) \mapsto X$

$$\{(Y_i,\mathbf{x}_i)\}_{i=1}^B$$

Likelihood-Free Inference (Simulator-Based Inference) Observational data Prior distribution of prior distrib

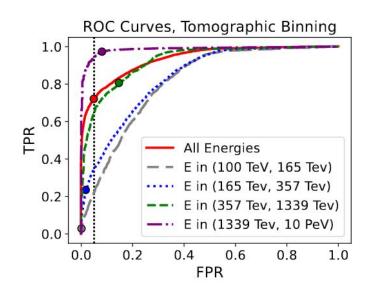


Source: wikipedia

P(Y=1|x) leads to invalid uncertainty quantification

$$\{(Y_i, \mathbf{x}_i)\}_{i=1}^B$$

ROC Curves are not valid



Summarizing so far

mechanistic model:
$$\theta = (Y, \nu) \mapsto X$$

$$\{(Y_i, \mathbf{x}_i)\}_{i=1}^B$$

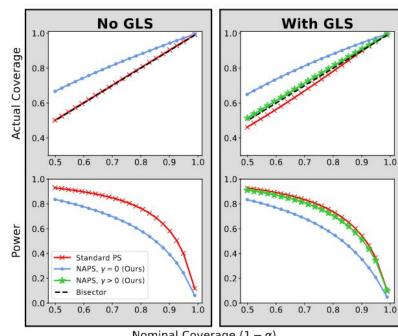
P(Y=1|x): invalid uncertainty quantification

$$\mathbb{P}_{\text{target}}(Y \in R_{\alpha}(\mathbf{X})) \ge 1 - \alpha$$

Generalized Label Shift (GLS)

$$p_{\text{train}}(\mathbf{x}|y,\boldsymbol{\nu}) = p_{\text{target}}(\mathbf{x}|y,\boldsymbol{\nu})$$

$$\mathbb{P}_{\text{target}}(Y \in R_{\alpha}(\mathbf{X}))$$



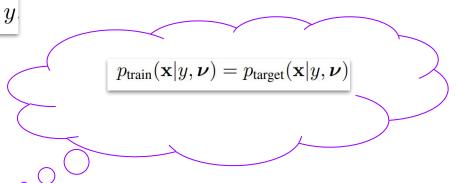
Nominal Coverage $(1 - \alpha)$

Method

$$H_{0,y}: Y = y$$
 versus $H_{1,y}: Y \neq y$

$$\lambda(\mathbf{x}) = \mathbb{P}_{\mathrm{train}}(Y = y|\mathbf{x})$$

$$W_{\lambda}(C; y, \boldsymbol{\nu}) := \mathbb{P}_{target}(\lambda(\mathbf{X}) \leq C|y, \boldsymbol{\nu})$$



Monotonic Classifier

$$W_{\lambda}(C; y, \boldsymbol{\nu}) := \mathbb{P}_{target}(\lambda(\mathbf{X}) \leq C|y, \boldsymbol{\nu})$$

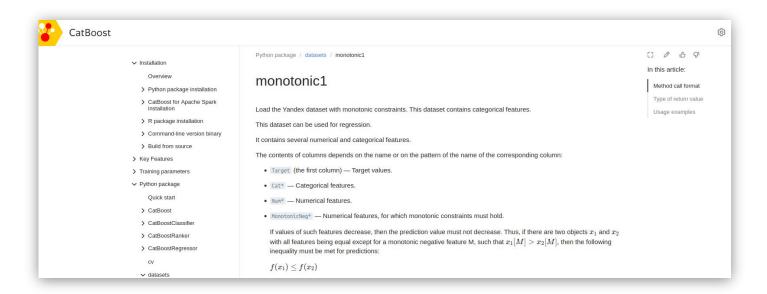
We learn $W_{\lambda}(C; y, \nu)$ using a monotone regression that enforces that the rejection probability is a non-decreasing function of C. For each point i (i = 1, ..., B) in the calibration sample $\mathcal{T}' = \{(y_1, \nu_1, \mathbf{X}_1), ..., (y_B, \nu_B, \mathbf{X}_B)\}$ sampled from $p_{\text{train}}(\boldsymbol{\theta})\mathcal{L}(\mathbf{x}; \boldsymbol{\theta})$, with $\boldsymbol{\theta} = (y, \nu)$, we sample a set of K cutoffs from the empirical distribution of the test statistic λ . Then, we regress the random variable

$$Z_{i,j} := \mathbb{I}\left(\lambda(\mathbf{X}_i) \le C_j\right) \tag{13}$$

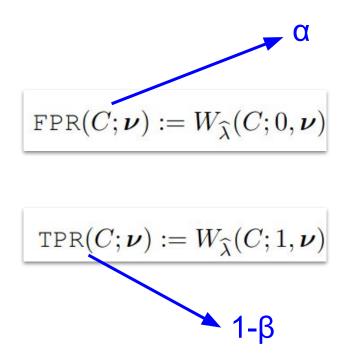
on y_i , ν_i and $C_{i,j}$ (= C_j) using the "augmented" calibration sample $T'' = \{(y_i, \nu_i, C_{i,j}, Z_{i,j})\}_{i,j}$, for $i = 1, \ldots, B$ and $j = 1, \ldots, K$, where K is our augmentation factor. See Algorithm 1 for details.

Monotonic Classifier

$$W_{\lambda}(C; y, \boldsymbol{\nu}) := \mathbb{P}_{target}(\lambda(\mathbf{X}) \leq C|y, \boldsymbol{\nu})$$



Controlling FPR or TPR



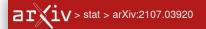
$$C_{\alpha} = \inf_{\boldsymbol{\nu} \in \mathcal{N}} \operatorname{FPR}^{-1}(\alpha; \boldsymbol{\nu}).$$

$$\widetilde{C}_{\alpha} = \sup_{\boldsymbol{\nu} \in \mathcal{N}} \mathtt{TPR}^{-1}(\alpha; \boldsymbol{\nu})$$

Controlling FPR or TPR, but with more power

$$C_{\alpha}^{*}(\mathbf{x}) = \inf_{\boldsymbol{\nu} \in S(\mathbf{x}; \gamma)} \{ \text{FPR}^{-1}(\beta; \boldsymbol{\nu}) \}$$

$$\beta = \alpha - \gamma$$



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[Submitted on 8 Jul 2021 (v1), last revised 19 Nov 2023 (this version, v8)]

Likelihood-Free Frequentist Inference: Bridging Classical Statistics and Machine Learning for Reliable Simulator-Based Inference

Niccolò Dalmasso, Luca Masserano, David Zhao, Rafael Izbicki, Ann B. Lee

Many areas of science make extensive use of computer simulators that implicitly encode intractable likelihood functions of complex systems. Classical statistical methods are poorly suited for these so-called likelihood-free inference (LFI) settings, especially outside asymptotic and low-dimensional regimes. At the same time, traditional LFI methods - such as Approximate Bayesian Computation or more recent machine learning techniques - do not guarantee confidence sets with nominal coverage in general settings (i.e., with high-dimensional data, finite sample sizes, and for any parameter value). In addition, there are no diagnostic tools to check the empirical coverage of confidence sets provided by such methods across the entire parameter space. In this work, we propose a unified and modular inference framework that bridges classical statistics and modern machine learning providing (i) a practical approach to the Neyman construction of confidence sets with frequentist finite-sample coverage for any value of the unknown parameters; and (ii) interpretable diagnostics that estimate the empirical coverage across the entire parameter space. We refer to the general framework as likelihood-free frequentist inference (LF2I). Any method that defines a test statistic can leverage LF2I to create valid confidence sets and diagnostics without costly Monte Carlo samples at fixed parameter settings. We study the power of two likelihood-based test statistics (ACORE and BFF) and demonstrate their empirical performance on high-dimensional, complex data. Code is available at this https://dimensional.complex data. Code is available at this https://dimensional.complex.

Controlling FPR or TPR, but with more power

Theorem 1 (Nuisance-aware cutoffs for FPR/TPR control). Choose a threshold $\alpha \in [0,1]$ and $\gamma \in [0,\alpha]$. Let $S_y(\mathbf{x};\gamma)$ be a valid $(1-\gamma)$ confidence set for $\boldsymbol{\nu}$ at fixed $y \in \{0,1\}$ according to Definition 3. Let $\lambda(\mathbf{X})$ be any test statistic that measures how plausible it is that \mathbf{X} was generated from $H_{0,y}$. Define the nuisance-aware rejection cutoff to be

$$C_{\alpha,y}^*(\mathbf{x}) = \inf_{\boldsymbol{\nu} \in S_y(\mathbf{x};\gamma)} \{ W_{\lambda}^{-1}(\beta; y, \boldsymbol{\nu}) \}, \tag{8}$$

where $\beta = \alpha - \gamma$, and W is the rejection probability in Definition 1. Then, for all $\nu \in \mathcal{N}$, we have FPR control:

$$\mathbb{P}_{target}\left(\lambda(\mathbf{X}) \le C_{\alpha,y}^*(\mathbf{X})|y,\boldsymbol{\nu}\right) \le \alpha \tag{9}$$

(maximum type-I error probability for $H_{0,y}$).

NAPS

Definition 2 (Nuisance-aware prediction set). A nuisance-aware prediction set (NAPS) is the set returned from a set-valued classifier $\mathbf{H}: \mathbf{x} \mapsto \{\emptyset, 0, 1, \{0, 1\}\}$ with

$$\mathbf{H}(\mathbf{x}; \alpha) = \left\{ y \in \{0, 1\} \mid \widehat{\tau}_y(\mathbf{x}) > C_{\alpha, y}^*(\mathbf{x}) \right\}, \quad (5)$$

where

$$C_{\alpha,y}^*(\mathbf{x}) = \inf_{\boldsymbol{\nu} \in S_y(\mathbf{x};\gamma)} \{ W_{\widehat{\tau}_y}^{-1}(\beta; y, \boldsymbol{\nu}) \}, \tag{6}$$

is the rejection cutoff, $\beta = \alpha - \gamma$ and $S_y(\mathbf{x}; \gamma)$ is a $(1 - \gamma)$ confidence set for ν defined by Equation 7.

NAPS

Theorem 2. Let $\mathbf{H}(\mathbf{x}; \alpha)$ be the nuisance-aware prediction set of Definition 2. Under GLS, for every $y \in \{0, 1\}$ and $\nu \in \mathcal{N}$

$$\mathbb{P}_{target}(Y \in \mathbf{H}(\mathbf{X}; \alpha) | y, \nu) \ge 1 - \alpha.$$

Moreover,

$$\mathbb{P}_{target}(Y \in \mathbf{H}(\mathbf{X}; \alpha)) \geq 1 - \alpha.$$

Summary

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Algorithm 1 Nuisance-aware prediction sets
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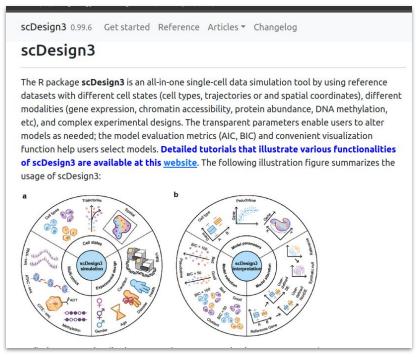
Input: training set $\mathcal{T} = \{(Y_i, \mathbf{X}_i)\}_{i=1}^B$; calibration set $\mathcal{T}' = \{(y_i, \boldsymbol{\nu}_i, \mathbf{X}_i)\}_{i=1}^{B'}$; observation \mathbf{x} ; miscoverage levels $\alpha \in (0, 1)$ and $\gamma \in [0, \alpha)$.

Output: Prediction set $H_{\alpha}(\mathbf{x})$ such that Equation 1 holds.

- 1: // Training
- 2: Estimate $\mathbb{P}_{\text{train}}(Y = y|\mathbf{X})$ with a probabilistic classifier
- 3: // Calibration
- 4: Estimate $W_{\tau_y}(C; y, \boldsymbol{\nu}) := \mathbb{P}_{\text{target}}(\tau_y(\mathbf{X}) \leq C|y, \boldsymbol{\nu})$ as detailed in Algorithm 2 by
 - i. Computing $\hat{\tau}_{v}(\mathbf{X})$ as in Equation 3 for all $\mathbf{X} \in \mathcal{T}'$;
 - ii. Constructing the augmented calibration set T'';
 - iii. Estimating $W_{\tau_y}(C;y,\boldsymbol{\nu})$ from \mathcal{T}'' via monotone regression.
- 5: // Inference
- 6: **for** $y \in \{0, 1\}$ **do**
- 7: Compute $\hat{\tau}_{u}(\mathbf{x})$ as in Equation 3
- 8: **if** $\gamma = 0$ then
 - $C^*_{\alpha,y}(\mathbf{x}) \leftarrow \inf_{\boldsymbol{\nu} \in \mathcal{N}} \{\widehat{W}_{\widehat{\tau}_{\boldsymbol{\nu}}}^{-1}(\alpha; y, \boldsymbol{\nu})\}$
- 10: **else**
- 11: Obtain a level- γ confidence set $S_y(\mathbf{x}; \gamma)$ for $\boldsymbol{\nu}$
- 12: $C_{\alpha,y}^*(\mathbf{x}) \leftarrow \inf_{\boldsymbol{\nu} \in S_y(\mathbf{x};\gamma)} \{\widehat{W}_{\widehat{\tau}_v}^{-1}(\alpha \gamma; y, \boldsymbol{\nu})\}$
- 13: end if
- 14: end for
- 15: $\mathbf{H}(\mathbf{x}; \alpha) \leftarrow \left\{ y \in \{0, 1\} \mid \widehat{\tau}_y(\mathbf{x}) > C^*_{\alpha, y}(\mathbf{x}) \right\}$
- 16: **return** $\mathbf{H}(\mathbf{x}; \alpha)$

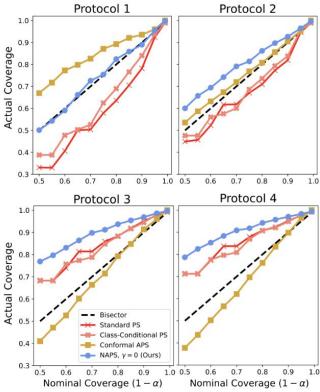
Application: Single-Cell RNA Sequencing

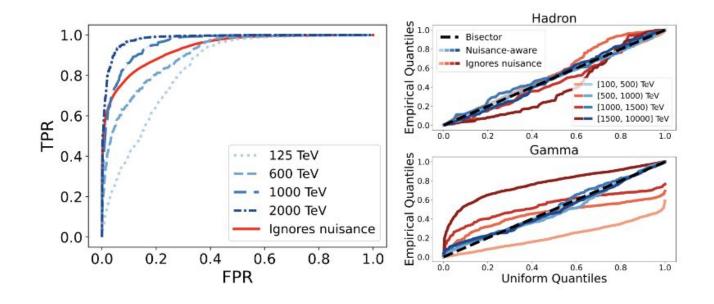
Goal: infer the cell's type (CD4+ vs Cytotoxic T-cells) from the observed gene count

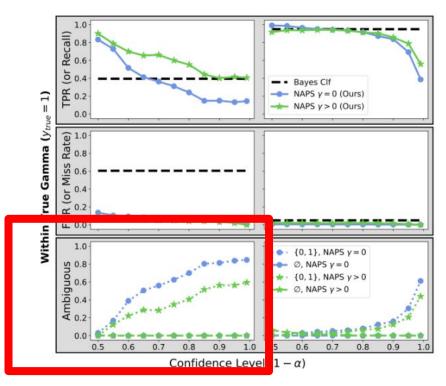


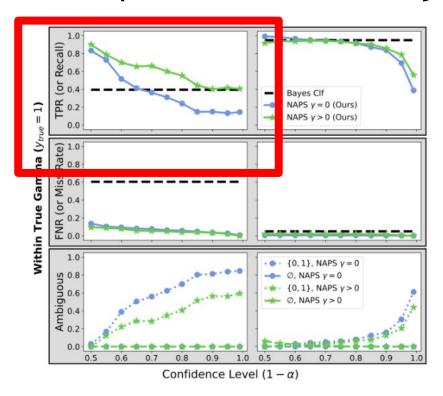
Song, et al Nat Biotechnol (2023)

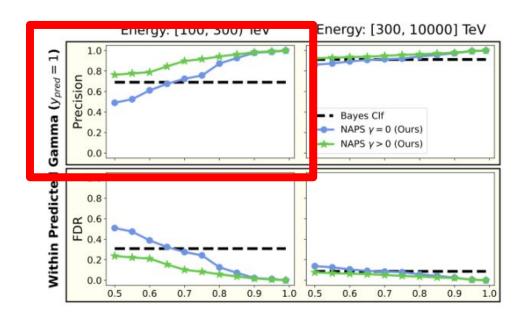
Application: Single-Cell RNA Sequencing











Final Remarks

- GLS models how (X,Y) changes
- Applications to SBI/LFI
- Can be used for classification if training data with (X,Y,v) is available

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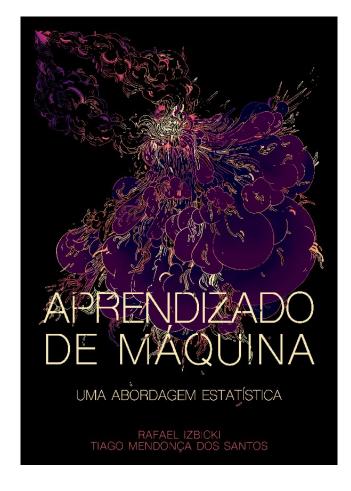
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[Submitted on 8 Feb 2024]

Classification under Nuisance Parameters and Generalized Label Shift in Likelihood-Free Inference

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Thanks!

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