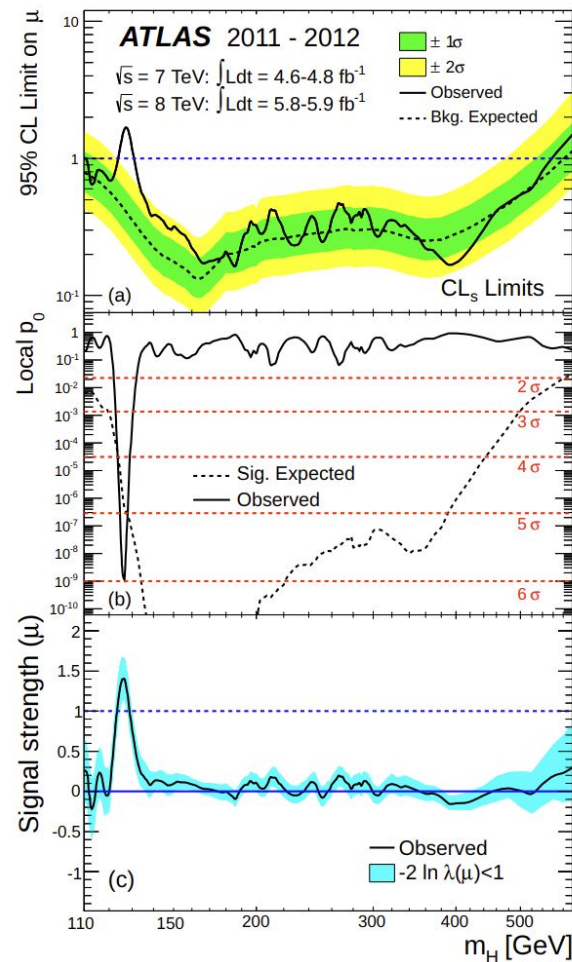

Introduction to statistics

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HASCO, Goettingen, 2024

Introduction

- Focusing on HEP statistics approaches
- **Quantum mechanics/field theory = statistical theory**
 - Needed for every interpretation
- Here we will go through
 - Basics of statistics
 - Hypotheses testing
 - Discovery and limit setting
 - Parameter estimation
 - Unfolding
- Should be able to understand these plots at the end of this presentation



<https://arxiv.org/abs/1207.7214>

Useful references

- G. Cowan, *Statistical Data Analysis*, Oxford University Press, 1998
 - Related: Cowan's Academic lectures: [indico link](#)
- F. James, *Statistical methods in experimental physics*, 2nd ed., World Scientific, 2006
- K. Cranmer, *Practical Statistics for the LHC*, <https://arxiv.org/abs/1503.07622>
- Cowan et al, *Asymptotic formulae for likelihood-based tests of new physics*, <https://arxiv.org/abs/1007.1727>

- Commonly used model for the binned likelihood fit in HEP: *HistFactory: A tool for creating statistical models for use with RooFit and RooStats*, <https://cds.cern.ch/record/1456844>

Basics

Frequentist statistics

- Probability = **outcomes of repeatable observations**

$$P(x) = \lim_{n \rightarrow \infty} \frac{\text{number of outcomes of } x}{n}$$

- I.e. we need **repeatable events**
- Does Higgs boson exist? Is the mass of the top quark between 172 and 173 GeV? ...?
 - It is **either true or false** but we do not know which
 - The frequentists tools tell us about outcomes of (hypothetical) **repeated experiments**
- The **preferred theories** (models, hypotheses, ...) are those for which our observations would be considered "usual"

Bayesian statistics

- Interpretation of probability extended to a degree of belief
 - The degree of belief is updated based on the observations
- Bayes' formula

Probability
observing data X ,
assuming the
hypothesis H

Prior probability
for hypothesis H

$$P(H|\vec{x}) = \frac{P(\vec{x}|H)\pi(H)}{\int P(\vec{x}|H)\pi(H) dH}$$

Normalisation, i.e. sum of all possible outcomes

Bayesian statistics example

- Assume 2% of the population have COVID19 in a given time
- The tests for COVID19 detect the virus in 90% of the cases and give false-positive (show positive result even when there is no COVID19 virus) in 5% of the cases
- The test result is positive, what is the probability that the person has the COVID19 virus?

We can use the Bayes' formula for this

- $P(H) = 0.02$ - this is the prior probability, i.e. before we do the test
- $P(x,H) = 0.9$ - i.e. if the person is positive, what is the likelihood of getting a positive result
- Normalisation = $0.9 \times 0.02 + 0.05 \times 0.98$ - i.e. has the virus and positive test + does not have virus and has a positive test
- Using the Bayes' formula:

$$\frac{0.9 \times 0.02}{0.9 \times 0.02 + 0.05 \times 0.98} \approx 24\%$$

- How would the probability change if the person would do another test and it came back positive?

Frequentist vs Bayesian

- Frequentist
 - **Limit of a long term frequency**
 - Do not need an infinite sample for the definition to be useful
 - **Sometimes no ensemble exists**
- Bayesian
 - **Probability is a degree of belief**
 - Intrinsically **subjective** (choice of the prior)
 - No golden rule for the **choice of priors**
- “Bayesians address the question everyone is interested in, by using assumptions no-one believes. Frequentists use impeccable logic to deal with an issue of no interest to anyone” - L. Lyons

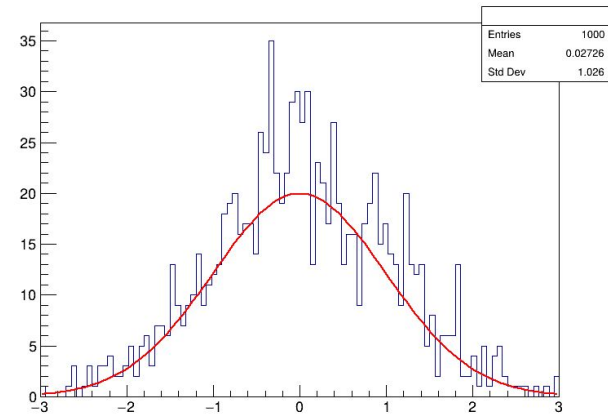
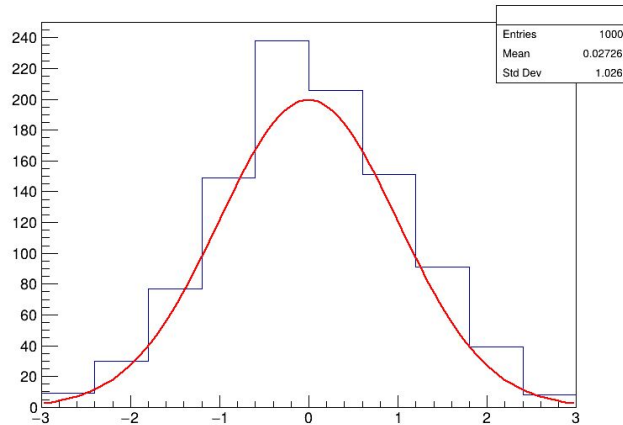
Binned vs unbinned - distributions

- Unbinned distributions

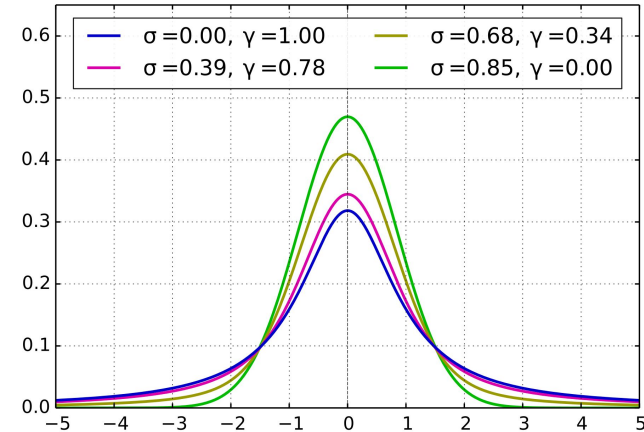
- Requires smooth distributions - i.e. PDF
 - Often not known
 - Can use approximations

- Binned distributions

- Approximate distributions
- Binning choice - **resolution vs available statistics**



Voigt function
Breit-Wigner x Gauss



Likelihoods

- What we want is probability of our model describing data (frequentist)
- I.e. “likelihood”:

$$P(\vec{x}|H)$$

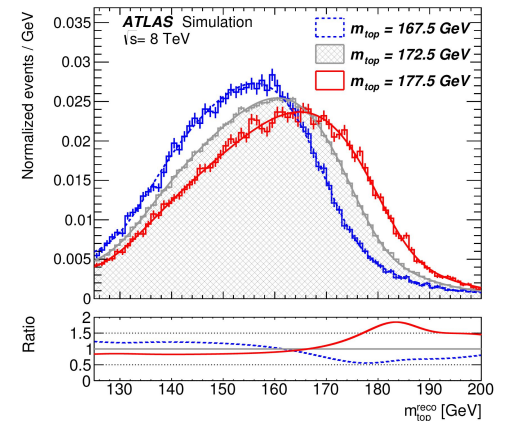
- **Binned-likelihood**

- **Probability per bin** and combine from all bins
 - No correlations \Leftrightarrow product of the per-bin likelihoods
- Often much simpler than unbinned
- Depends on binning choice (corrections might be needed)

- **Unbinned likelihood**

- **Probability per event** and combine for all events
 - No correlations \Leftrightarrow product over all events
- No bin-width effects
- Requires analytical (or approximate functions)

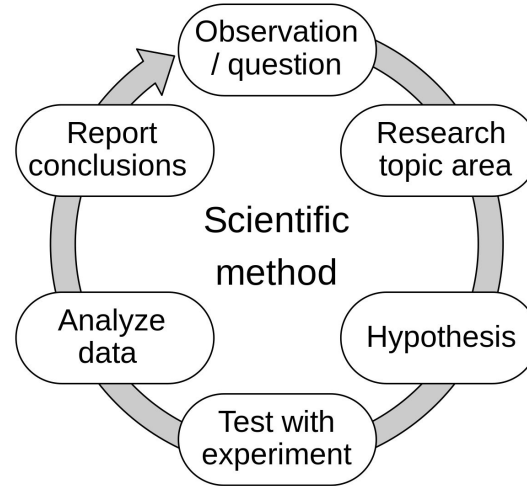
[Eur. Phys. J. C 79 \(2019\) 290](#)



Hypothesis testing

Definitions

- Hypothesis testing is a core of the scientific method

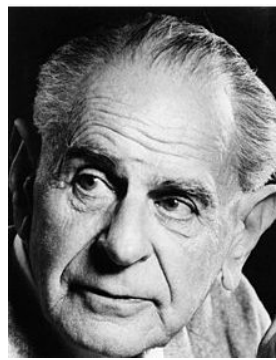


- **Hypothesis H** specifies the **probability for the data**, i.e., the outcome of the observation, x
- Possible values of data (x) form the sample space ("data space")
- The **probability for x given H** is also called the **likelihood of the hypothesis, written $L(x|H)$** .
 - E.g. The probability to observe N number of events with a given selection assuming the validity of the Standard Model

Hypothesis testing

How to confirm a hypothesis?

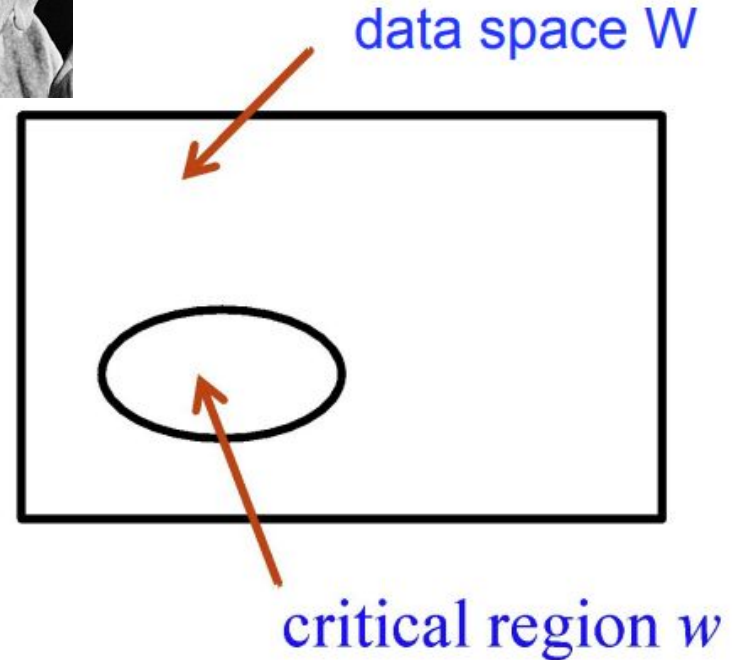
- Karl Popper: **You cannot!**
- But you **can reject a hypothesis!**



- Find a region, W , of the data space where the is only **small probability α to observe data x provided H_0 is true** - this is the “critical region”

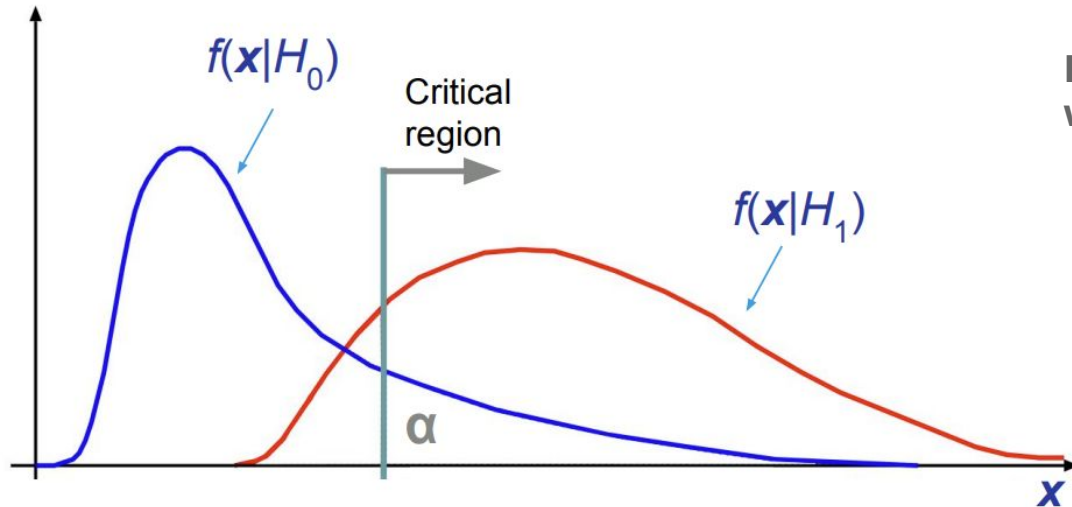
$$P(x \in W | H_0) \leq \alpha$$

- **Reject hypothesis if data is observed in W**
- α is called “size” or “**significance level**” of the test



How to select the critical region?

- Infinitely many critical regions for a given hypothesis
- No **unique way to select it**
- Can define an **alternative hypothesis** H_1
- Roughly speaking:
 - Choose the critical region so that the **probability of observing data under H_0 is low** and **probability of observing data under H_1 is high**



Rejecting H_0 does not mean “ H_0 is wrong and H_1 is right”

- Frequentist - only outcome of repeated experiments
- Bayesian - depends on the priors

Type-I and type-II errors

- **Type-I error** (false negative)
 - **Reject hypothesis H_0 if it is true**
 - Maximum probability for this is α

$$P(x \in W \mid H_0) \leq \alpha$$

- **Type-II error** (false positive)
 - **Accept hypothesis H_0 if it is false and H_1 is true**
 - Occurs with probability β

$$P(x \in S - W \mid H_1) = \beta$$

- $1 - \beta$ is called the “power” of the test

True negative



False positive



False negative



True positive



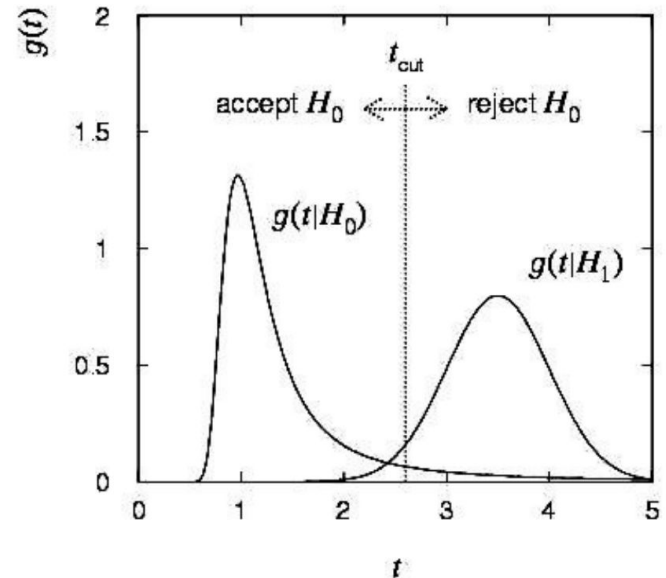
Test statistics

- Assume that for **each event we have a collection of numbers**
 - Number of jets, leptons, MET value, ..., have multiple bins, ...
 - Data (x) will follow some joint PDF for the different observables
 - The critical region is **multidimensional** - cumbersome to work with
- Can define the **boundary** of the critical region using an equation of form

$$t(x_1, \dots, x_n) = t_{\text{cut}}$$

- Where $t(x_1, \dots, x_n)$ is the **scalar** test statistics

We have turned an N-dimensional problem to a 1-dimensional one!



Optimal choice for the test statistics

- How to choose the test statistics?
- **Neyman-Pearson lemma**: For a test of size α of the simple hypothesis H_0 , to obtain the highest power with respect to the simple alternative H_1 , choose the critical region W such that the likelihood ratio satisfies

$$\frac{P(\mathbf{x}|H_1)}{P(\mathbf{x}|H_0)} \geq k$$

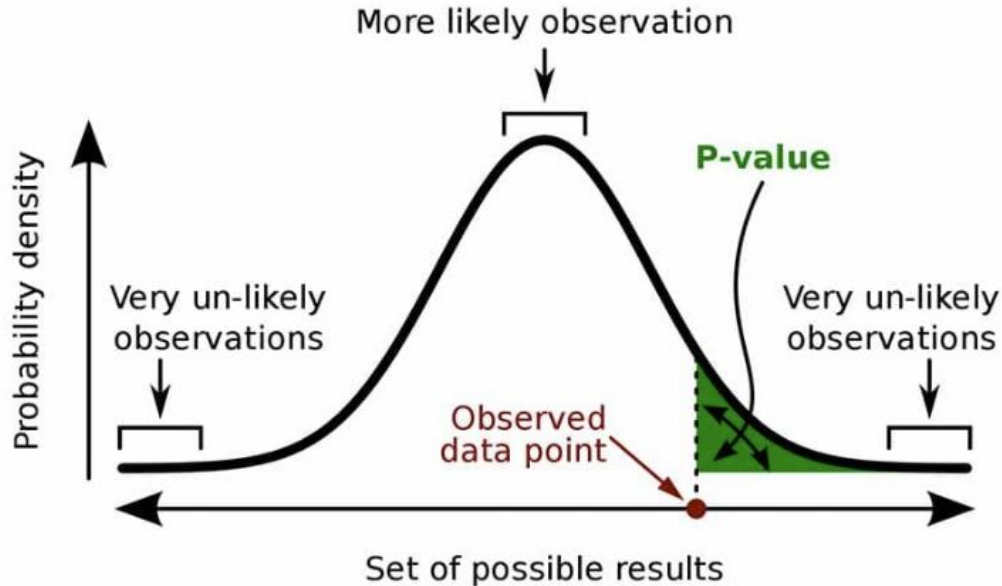
everywhere in W and is less than k else - k is a constant chosen such that the test has size α

- The **optimal scalar test statistics is then**

$$t(\mathbf{x}) = \frac{P(\mathbf{x}|H_1)}{P(\mathbf{x}|H_0)}$$

p-value

- Level of agreement (compatibility) of data and a given hypothesis (model) H
- p-value -> probability, under assumption of H , to observe data with **equal or lesser compatibility** with H relative to the data we got
 - **This is NOT a probability that H is true!**

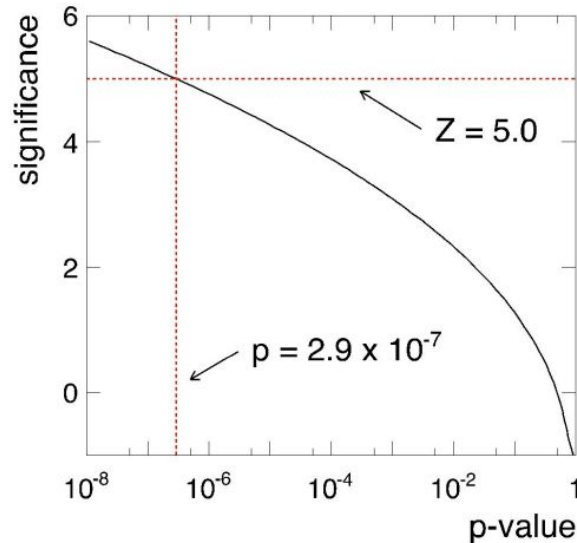
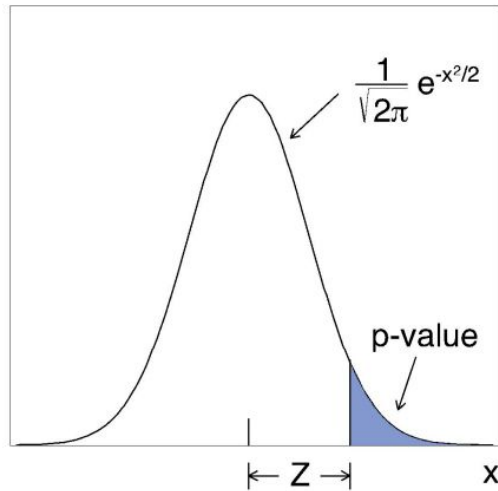


p-value and significance

- We can define the significance Z as the **number of standard deviations** (“sigmas”) that a Gaussian variable would fluctuate in one direction to give the same p-value

$$p = \int_Z^{\infty} \frac{1}{\sqrt{2\pi}} e^{-x^2/2} dx = 1 - \Phi(Z) \longrightarrow Z = \Phi^{-1}(1 - p)$$

Gaussian cumulative function

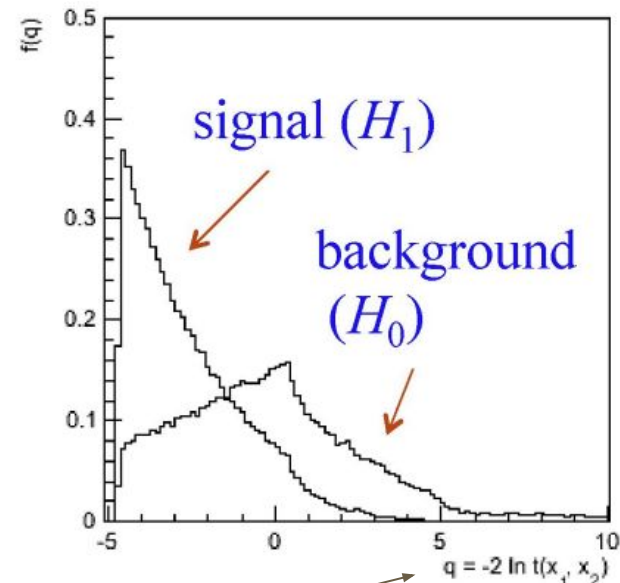


z (one tail)	p-value
1.00	0.16
2.00	0.023
3.00	0.0013
4.00	3.2e-05
5.00	2.9e-07
6.00	9.9e-10

Discovery significance

Discovery in HEP

- We want to discover new physics (BSM)
- Typically
 - Hypothesis H_0 , i.e. the “null hypothesis” is the SM prediction
 - **“Background-only” hypothesis**
 - Alternative hypothesis H_1 is your favourite model
- We know what to do
 - Find the $P(x, H_0)$ and $P(x, H_1)$, i.e. the ***likelihood***
 - **Build the test statistics** using the ratios
 - **Calculate the p-value**
 - **Reject/accept**
- How to get the PDF?
 - Use **MC simulation**
 - Need to get a distribution of the values
 - **Pseudo-experiments/toys!**

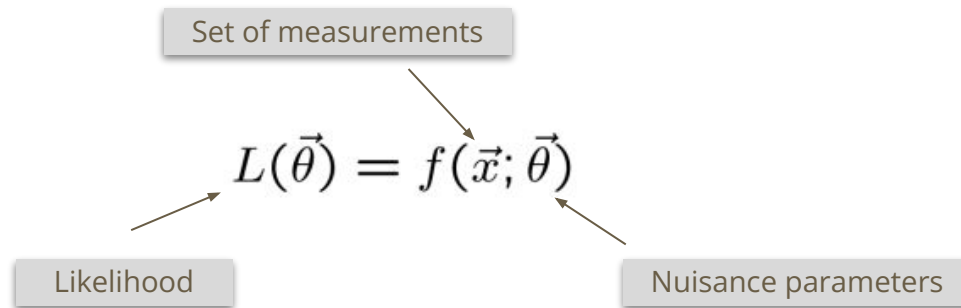


We usually use (-2 times) logarithm of the ratio

Let's add systematics

- So far, only considered statistical uncertainty
- In reality, many **systematic uncertainties affect the predictions**
- Can add the **systematics into the likelihood**
 - Define “*signal strength*”, μ , as $n = \mu \cdot s + b$
 - $\mu = 1$ means cross-section as predicted by the model
 - Add “*nuisance parameters*” to the likelihood
 - Parameters that impact the likelihood, but we are not interested in them, e.g. systematic uncertainties
 - Usually, “*subsidiary*” or “*auxiliary*” measurements are used to constrain NPs

$$\mu = \frac{\sigma_{obs.}}{\sigma_{pred.}}$$



Commonly used model

- More and more common approach for including systematics in HEP statistical analysis:
 - include **systematic uncertainties as unknown parameters in the model**
 - **nuisance parameters** modifying expectations in a **parametric** way
 - **nuisance parameters constrained by subsidiary measurements**

- The binned profile-likelihood:

$$L(\vec{n} \mid \vec{\theta}, \vec{k}) = \prod_i P(n_i \mid S_i(\vec{\theta}, \vec{k}) + B_i(\vec{\theta}, \vec{k})) \times \prod_j G(\theta_j)$$

data → \vec{n} Poisson ↓ $P(n_i \mid \dots)$ Gaussian (or other pdf...) ↓ $G(\theta_j)$

constrained parameters: nuisance parameters (**NPs**) associated to systematic uncertainties

data events in bin i prediction in bin i (signal+background) constraint term for nuisance parameter j

unconstrained parameters: parameter of interest (**POI** or “ μ ”) + unconstrained nuisance parameters (e.g. background normalization parameters)

Profile-likelihood significance

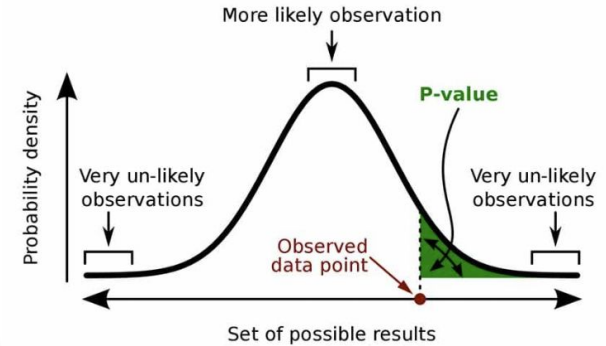
- Define test statistics

$$\lambda(\mu) = \frac{L(\mu, \hat{\theta})}{L(\hat{\mu}, \hat{\theta})}$$

Maximises L for a given fixed μ

Best fit μ

Likelihood value that maximises the likelihood for all parameters



- Observing new physics \Leftrightarrow excluding background-only hypothesis \Leftrightarrow excluding $\mu = 0$
- Only consider upward fluctuations

$$q_0 = \begin{cases} -2 \ln \lambda(0) & \hat{\mu} \geq 0 \\ 0 & \hat{\mu} < 0 \end{cases}$$

$$p_0 = \int_{q_{0,\text{obs}}}^{\infty} f(q_0|0) dq_0$$

Wald's approximation

- Running the **fit can take a long time**
- We need a PDF for the test statistics \Leftrightarrow many fits to toy data
 - For 5 sigma discovery we need $\sim 10^7$ toys!
- Luckily, there is a **powerful approximation** - Wald's approximation
- **For large n , the likelihood ratio is approximately chi-square distributed!**
 - Does not require the likelihood to be chi-square or gaussian distributed!

$$-2 \ln \lambda(\mu) = \frac{(\mu - \hat{\mu})^2}{\sigma^2} + \mathcal{O}(1/\sqrt{N})$$

$$\hat{\mu} \sim \text{Gaussian}(\mu', \sigma)$$

sample size

- Under this assumption, the significance is simply

$$Z = \Phi^{-1}(1 - p_0) = \sqrt{q_0}$$

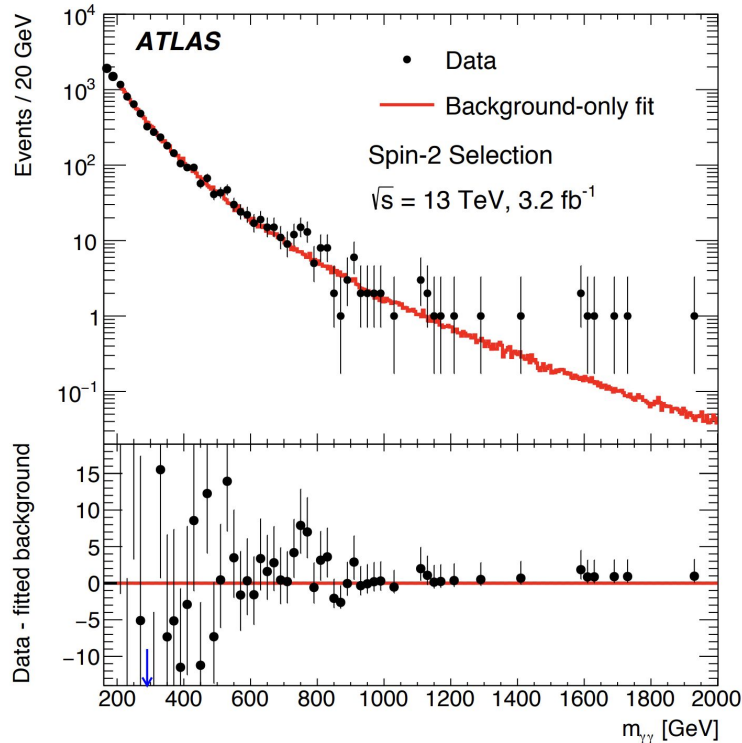
Usually a good approximation as long as number events in each bin is greater than ~ 10

- I.e. need to **run the fit only twice** - **unconditional** and **with μ fixed to 0**
 - Get the $-2 \ln L$ values for the fits and take the square root of the difference

Look-elsewhere effect

- What if we are looking for a resonance with an unknown mass and see an excess in some mass?
 - Should we just quote the **significance for that mass point**?

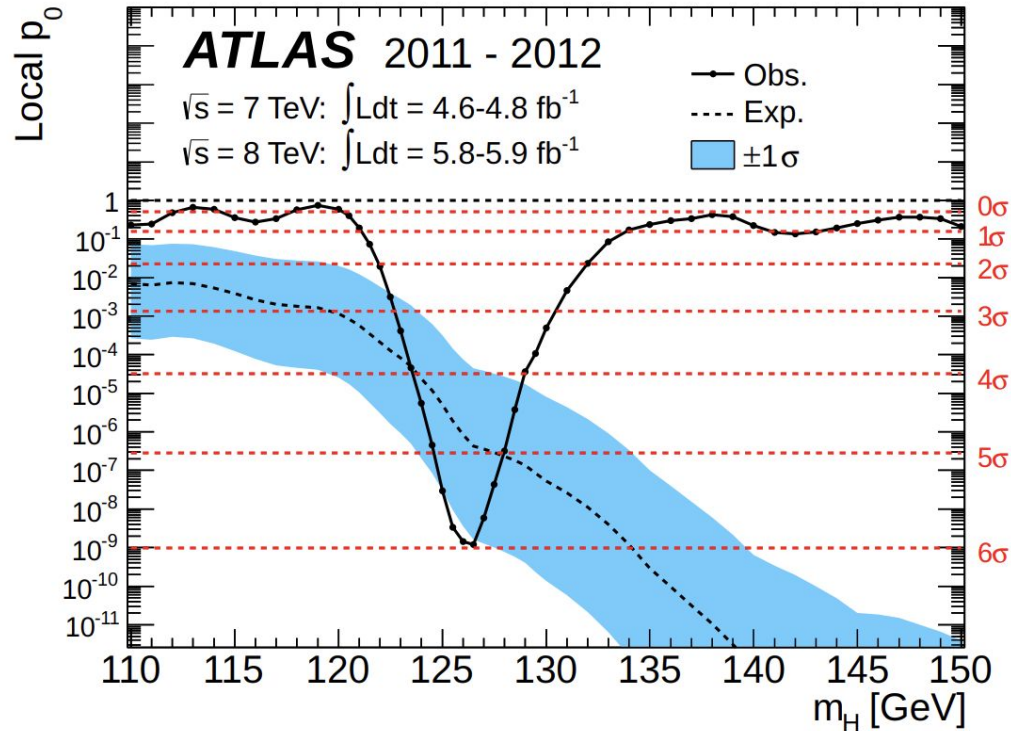
<https://arxiv.org/abs/1606.03833>



- Need to take into account the **"trials"**
 - We are **"testing" multiple bins**
 - We have more options to find an excess
 - **Need to correct for this!**
- Significance for a **fixed mass point** \Leftrightarrow local significance
- Significance for the **floating mass** \Leftrightarrow global significance
 - **Global significance \leq local significance**
- How to relate local significance to the global one?
 - **No simple recipe**
 - Need to **run toys**
 - Usually only 100s, not millions

Reading significance plots

<https://arxiv.org/abs/1207.7214>



- Dashed curve = "Expected" median p_0
 - p_0 for each mass of the SM Higgs boson - from MC
- Blue band = 1 sigma variations of the p_0 value
- Full line = "Observed" p_0 value from real data
- > 5 sigma at around $m_H = 125 \text{ GeV}$

Setting limits

Setting limits

- What if we do not see any significant excess?
 - We can **set limits!**
- What values of μ can be excluded with the observed data?
 - I.e. the **implied rate for a given μ would be very high for the observed data**
 - One-sided test - provide an “upper limit”
- Slightly modify the test statistics used for discovery
 - If μ comes out negative (unphysical) we can compare to the closest model with $\mu = 0$

$$\tilde{\lambda}(\mu) = \begin{cases} \frac{L(\mu, \hat{\theta})}{L(\hat{\mu}, \hat{\theta})} & \hat{\mu} \geq 0, \\ \frac{L(\mu, \hat{\theta})}{L(0, \hat{\theta})} & \hat{\mu} < 0. \end{cases} \quad \tilde{q}_\mu = \begin{cases} -2 \ln \tilde{\lambda}(\mu) & \hat{\mu} \leq \mu \\ 0 & \hat{\mu} > \mu \end{cases}$$

This is the test statistics commonly used (e.g. Higgs combinations)

Setting limits - continued

- **Settings limits** = finding the highest value of μ that results in p-value not smaller than γ
 - γ is **usually chosen as 0.05, i.e. 95% confidence level (CL)**
 - "What is the largest value of μ that is still compatible with the data?"

The diagram illustrates the formula for the p-value, $p_\mu = \int_{\tilde{q}_\mu}^{\infty} f(\tilde{q}_\mu | \mu, \hat{\theta}(\mu)) d\tilde{q}_\mu$. It includes several callout boxes: 'P-value for a given μ ' points to the entire formula; 'Test statistics' points to the variable \tilde{q}_μ in the integrand; 'Maximises likelihood for a fixed μ ' points to the estimated parameter $\hat{\theta}(\mu)$; and 'Observed value q_μ tilde' points to the lower limit of the integral.

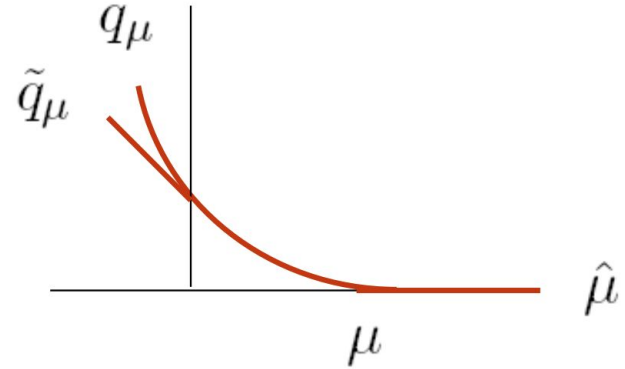
$$p_\mu = \int_{\tilde{q}_\mu}^{\infty} f(\tilde{q}_\mu | \mu, \hat{\theta}(\mu)) d\tilde{q}_\mu$$

- **Need to solve for μ**
 - Nasty integral equation
 - Can run **pseudo-experiments** to get the distribution of the test statistics
 - Find μ that leads to $p_\mu = 0.05$

Asymptotic limit settings

- Can use the Wald's approximation
 - The test statistics approaches chi-square

$$q_{\mu} = \begin{cases} \frac{(\mu - \hat{\mu})^2}{\sigma^2} & \hat{\mu} < \mu \\ 0 & \hat{\mu} > \mu \end{cases} \quad \tilde{q}_{\mu} = \begin{cases} \frac{\mu^2}{\sigma^2} - \frac{2\mu\hat{\mu}}{\sigma^2} & \hat{\mu} < \mu \\ \frac{(\mu - \hat{\mu})^2}{\sigma^2} & 0 \leq \hat{\mu} \leq \mu \\ 0 & \hat{\mu} > \mu, \end{cases}$$

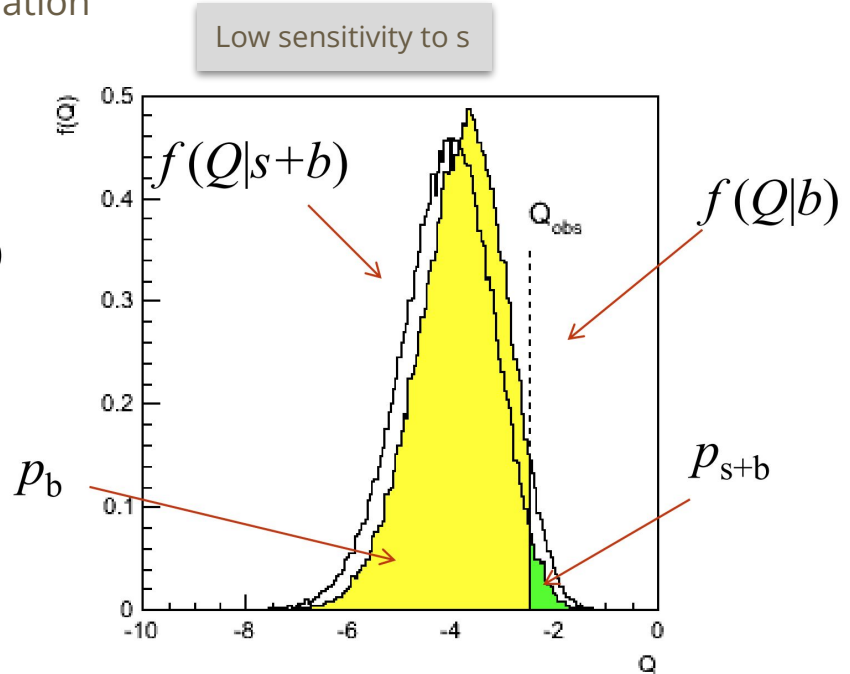
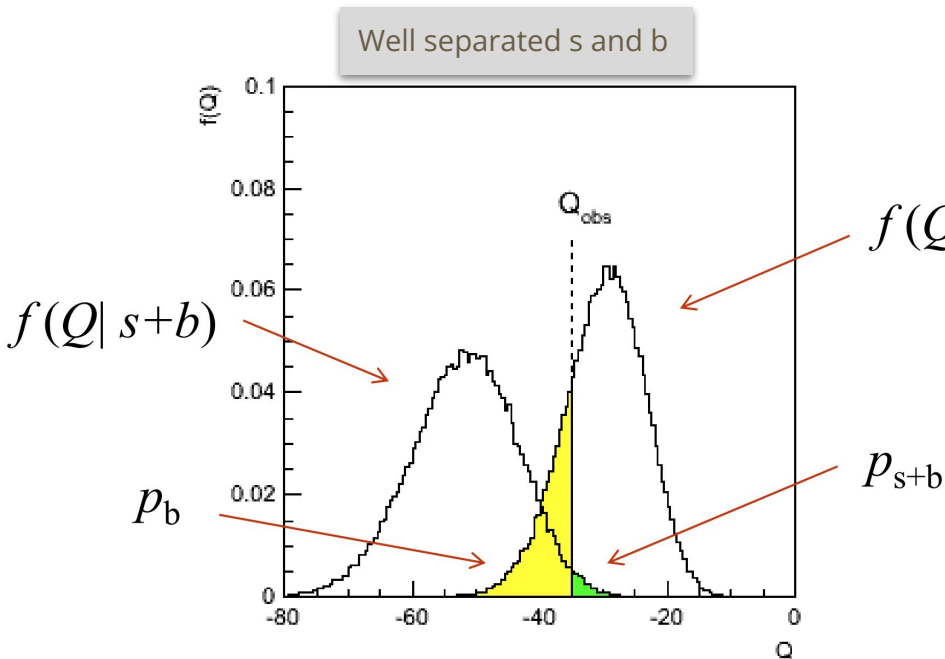


- **Limit estimation in practice (simplified)**

- Get the best fit value of μ and its uncertainty (more on this later)
 - Set μ to +2 sigma (approximately 95%) - this is a starting point of the iterative estimation
 - Calculate the p-value for this μ
 - If p-value too small, decrease μ , if p-value too large increase μ
 - Repeat!
 - Stop when the p-value is sufficiently close to 0.05
 - Usually requires O(10) fits
- **If the asymptotic approximation is not valid, have to use toy experiments**

The CLs issue

- Suppose we **have a low sensitivity to a particular signal**
 - Test statistics for **s+b** is **very similar to background-only**
 - There is non-negligible **probability to exclude s+b even when we have low sensitivity**
 - Can be caused by a downward fluctuation



The CLs procedure

[A. Read et al.](#)

- **Solution** to the issue: do not use only p-value for the s+b but divide by p-value for b-only

- **Define CLs**

$$CL_s = \frac{CL_{s+b}}{CL_b} = \frac{p_{s+b}}{1-p_b}$$

- **Reject s+b hypothesis if CLs < α**

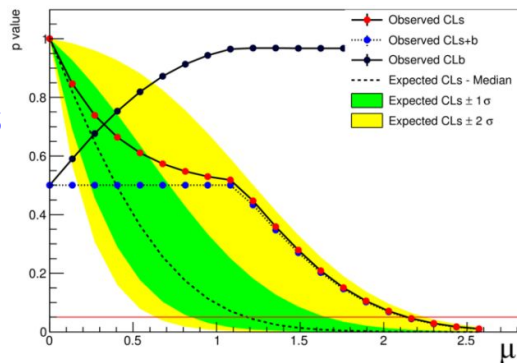
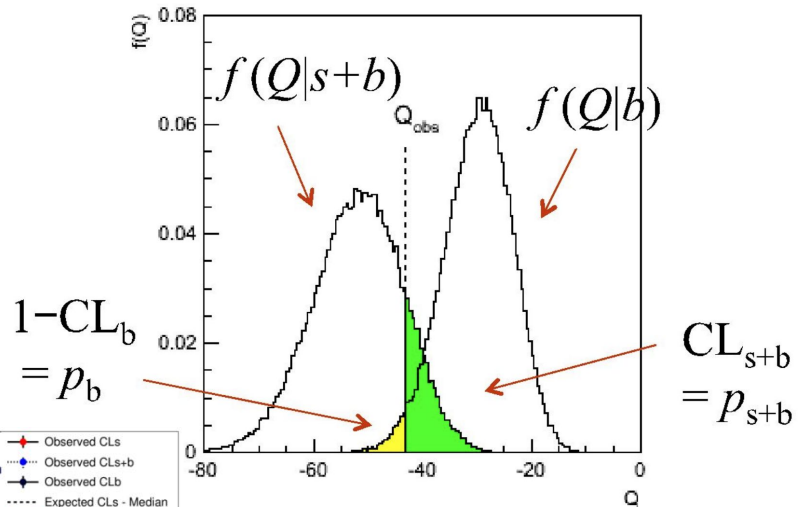
- Reduces “effective p-value”

- If low sensitivity

- Ratio of p-values

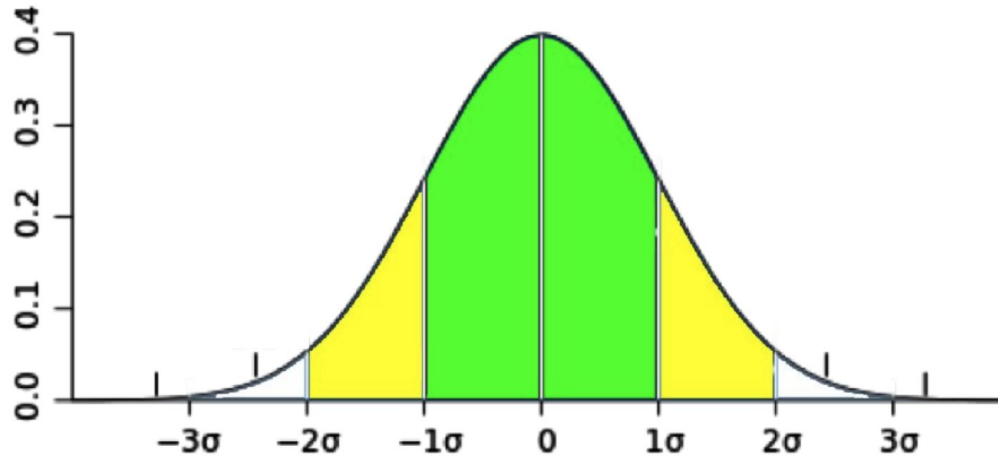
- Not liked by statisticians

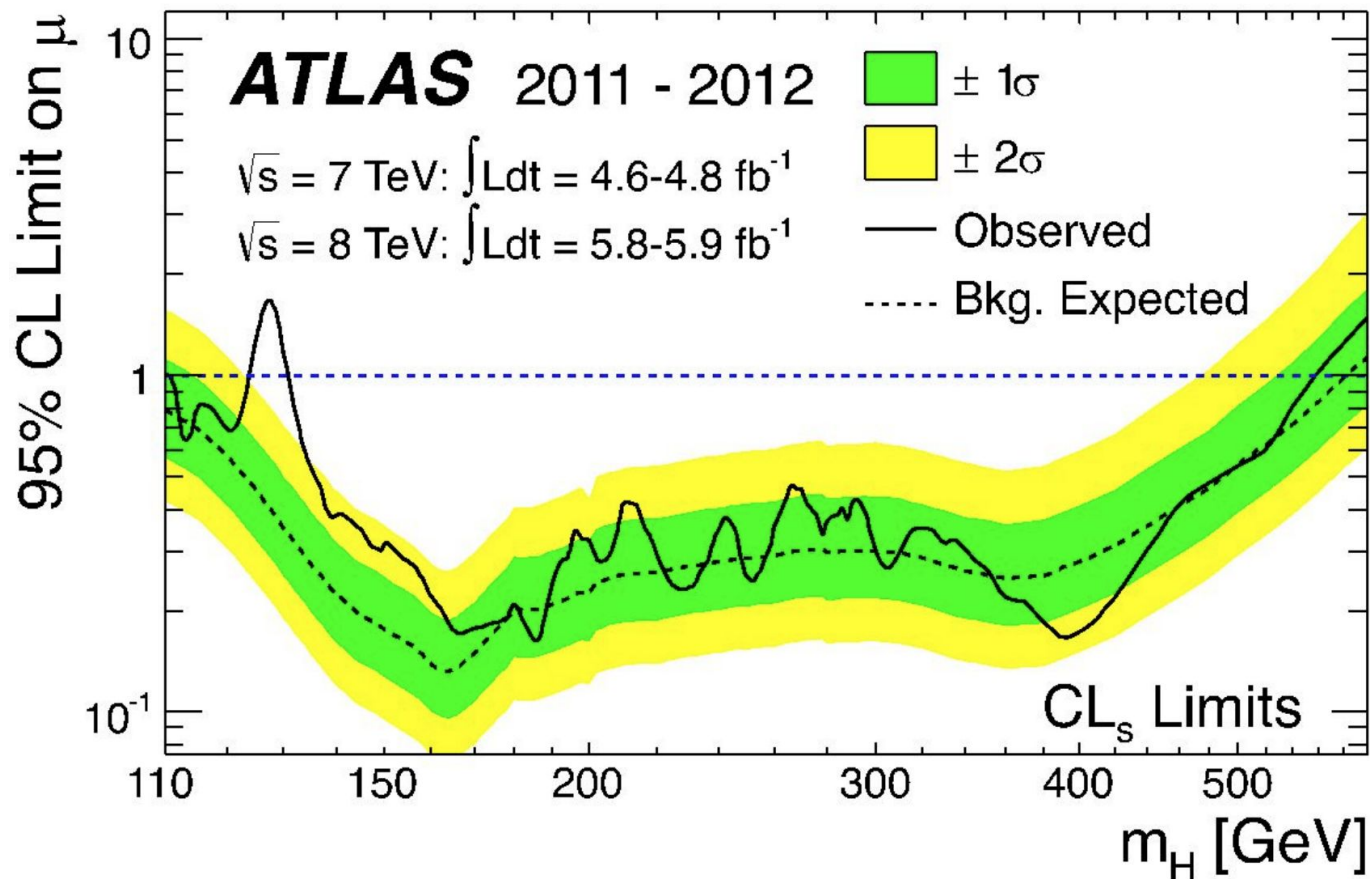
- **Used in almost all HEP searches**



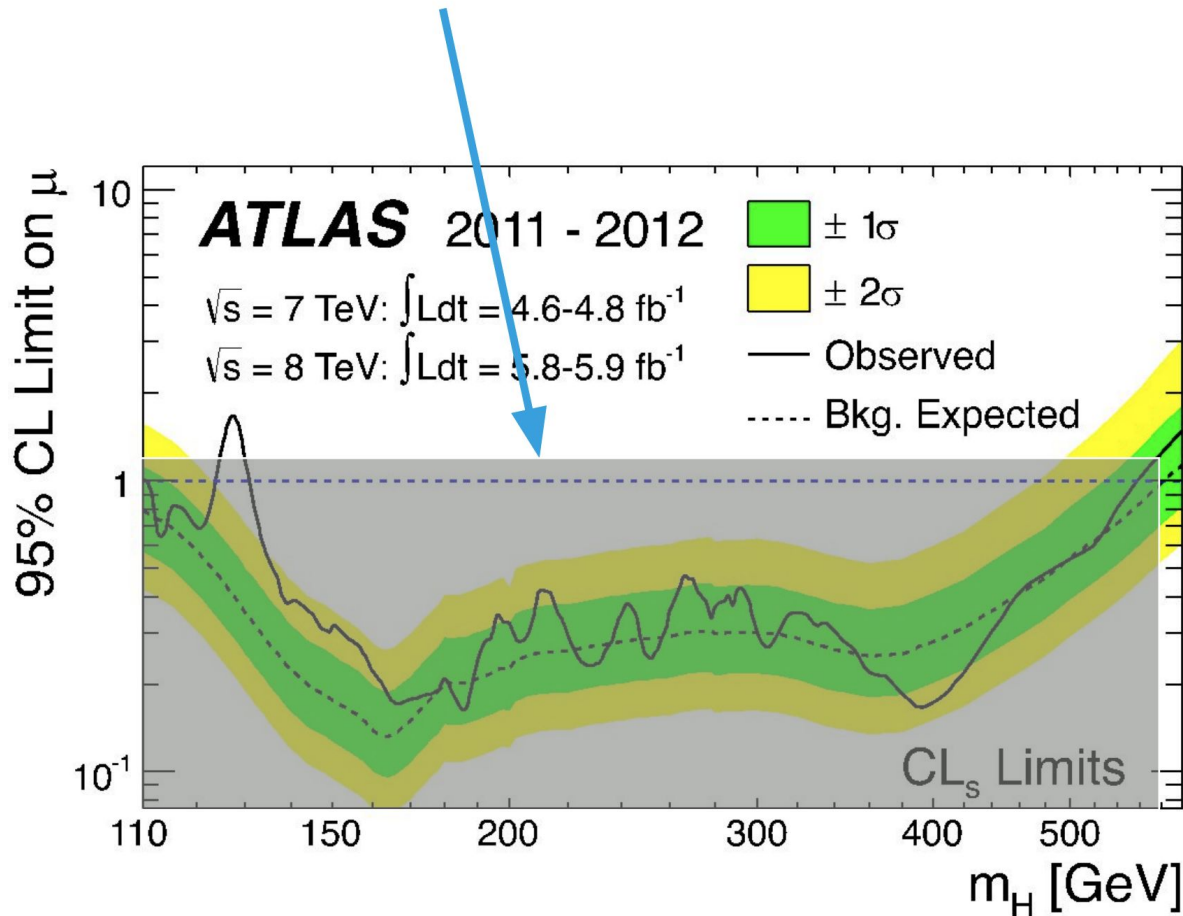
Expected limits

- **Expected limits** can be calculated using the MC prediction
 - Assume background only, what would be the limit on μ in case data = MC?
 - Can do it for several models, e.g. different masses of the Higgs boson
- Frequentist approach
 - Distribution of the p-value \Leftrightarrow distribution of the 95% CL limits
 - Can quote **median expected limit** and **$\pm 1(2)$ sigma variations**

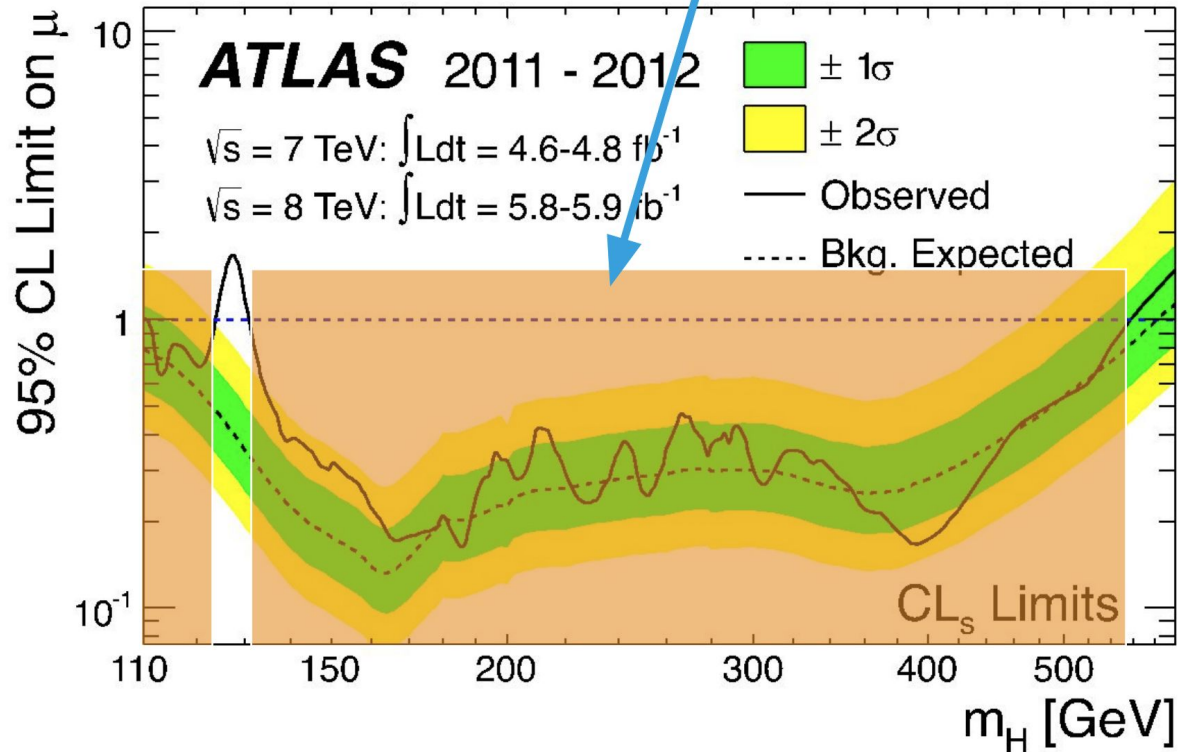




Expected excluded mass range



Observed excluded mass range



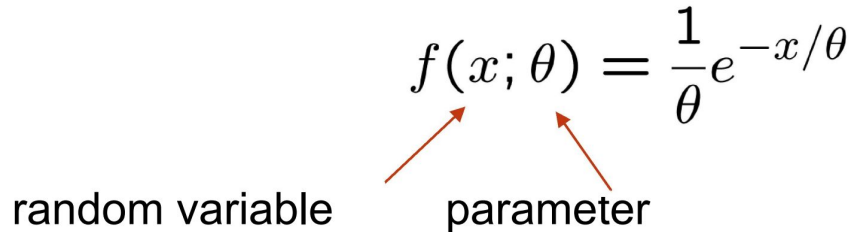
Parameter estimation

Estimators

- Often *not searching for a new process*
 - E.g. Measuring top-quark mass, CKM matrix elements, ...
- How to get the parameters from the model with their uncertainties?
- We need the PDF of the estimation
- **Parameters** are **constants of the estimator** that characterise the shape

$$f(x; \theta) = \frac{1}{\theta} e^{-x/\theta}$$

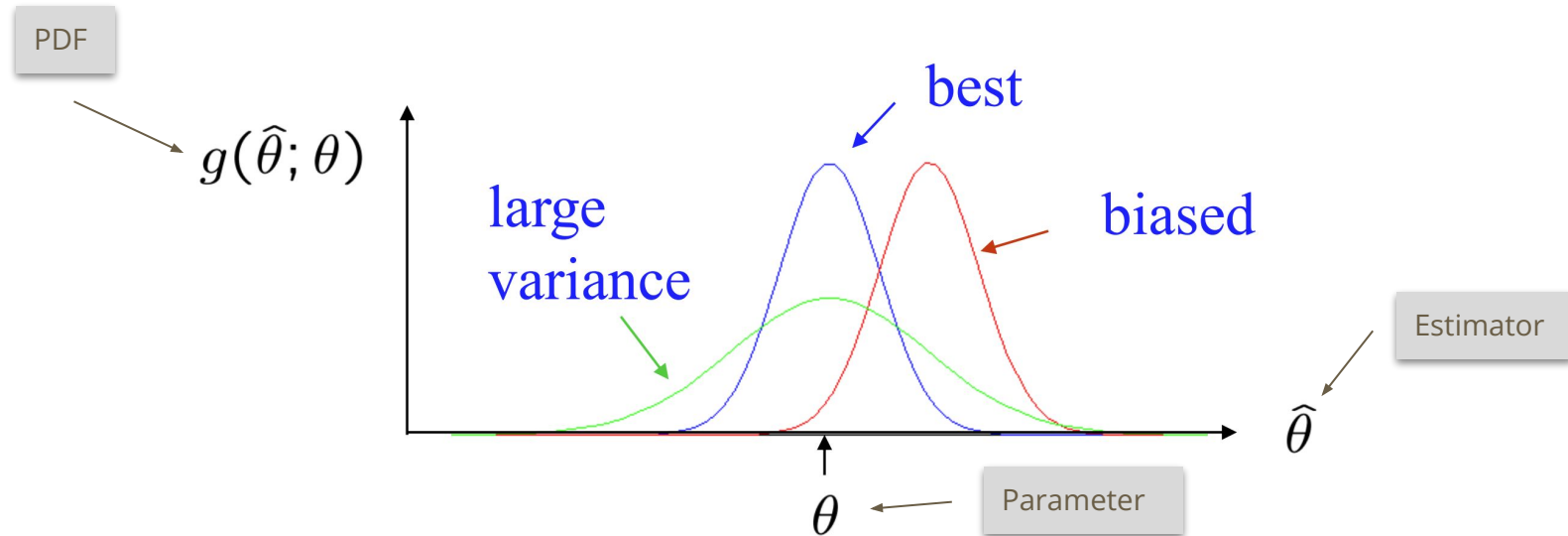
random variable parameter



- We want to **find some function of data to estimate the parameter(s)**: $\hat{\theta}(\vec{x})$
 - Estimator written with a hat

Estimators continued

- Repeating the measurement -> get PDF



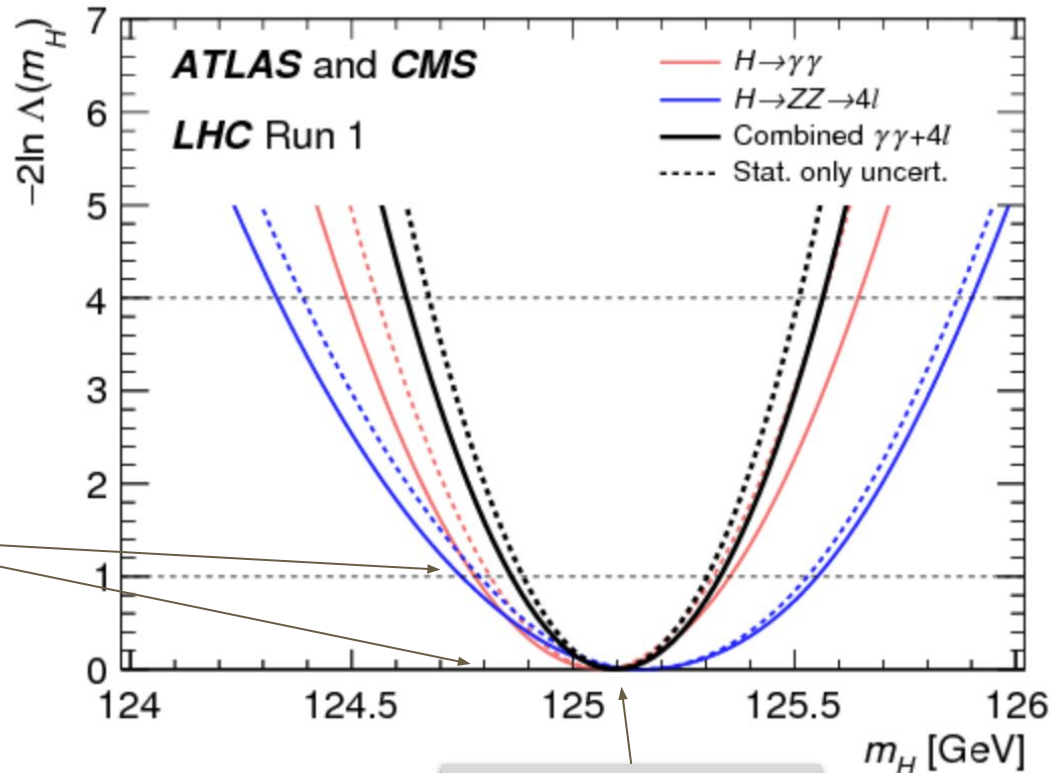
- We want unbiased estimator (bias = 0) with small variance (small statistical uncertainty)
 - **Generally: conflicting requirements**

Maximum-likelihood estimate

- **Maximum-likelihood estimate** \Leftrightarrow values of parameters that maximize the likelihood
 - Usually: use negative log likelihood
 - Frequentists statistics: **Minimise the NLL (i.e “fit”)**
 - Use minimiser tools, e.g. [Minuit](#)
 - Bayesian statistics: **Sample posterior likelihood**, using Markov-chain Monte Carlo (MCMC)
- If the hypothesized θ is close to the true value, then we expect a high probability to get data like that which we actually found
- **ML estimators are not guaranteed** to have any ‘optimal’ properties
 - **In practice they’re very good**
- **Uncertainty of the parameter?**
 - **Value of θ where the negative log likelihood shifts by one half** (1 sigma = 0.5, 2 sigma = 2, 3 sigma = 4.5, ...)
 - Motivated by the Normal distribution where shift of 0.5 happens at exactly 1 sigma

MINUIT

Example: Higgs mass measurement - <https://arxiv.org/abs/1503.07589>



Likelihood scan wider when systematic uncertainties are added (next slide)

Uncertainty

Best fit mass parameter

Adding systematic uncertainties

- **Nuisance parameters** (systematic uncertainties) can be added to the likelihood
 - Recall the common model $L(\vec{n} | \vec{\theta}, k) = \prod_i P(n_i | S_i(\vec{\theta}, k) + B_i(\vec{\theta}, k)) \times \prod_j G(\theta_j)$
- **Maximum-likelihood** \Leftrightarrow also the NPs get their best fit value and an uncertainty
 - **Covariance matrix** of all parameters (including NPs)
 - Can also get **correlations of the parameters** (“post-fit”)
 - Lot of physics in these values!

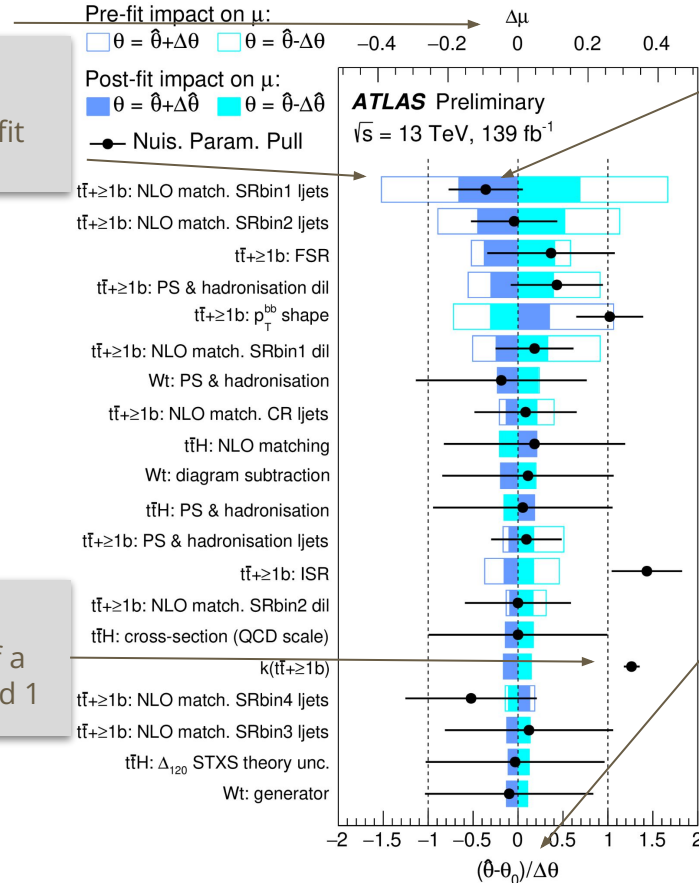
- The uncertainty (likelihood shifts by one half) includes stat+syst
 - **How to get an impact of individual sources of the uncertainties?**
 - Fix a given NP value to ± 1 sigma, repeat the minimisation and check impact on the parameter of interest
 - Repeat for all NPs
 - Stat-only uncertainty can be obtained by fixing all NPs to their fitted values and repeating the fit and getting the uncertainty on the POI

Reading pull/ranking plots ATLAS-CONF-2020-058

Impact of a given NP on the POI (ttH signal strength here). Full boxes \leftrightarrow post-fit impact, empty boxes \leftrightarrow pre-fit impact

NPs “ranked” by their impact on the POI

Some parameters do not have a Gaussian term (e.g. normalisation of a given background) \leftrightarrow centred around 1



Central value and uncertainty of a Nuisance parameter indicated with the black point and error bar

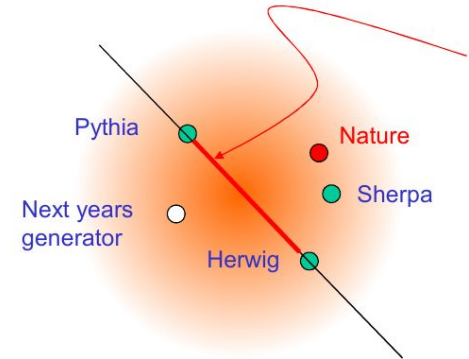
- Is the central value postfit different than 0 (“pull”)?
- Is the post-fit uncertainty smaller than prefit (“constraints”)?

In the model, most of the NPs have a Gaussian term in the likelihood \leftrightarrow can talk about “sigmas”.

Dangers of constraining systematic uncertainties

- Post-fit uncertainty smaller than prefit \Leftrightarrow **constraint**
 - Reduces total uncertainty - good!
 - **Is it reliable?**
 - Should the measurements have power to constrain a given uncertainty?
 - Is the measurements “better” than dedicated calibrations?
 - Are the variation granular enough?
- Usually: pass nominal and +/- 1 sigma variations
 - Interpolation/extrapolation to get **continuous** impact
 - Might not have enough freedom to fit the real shape
 - Systematic might not be granular enough
 - Propagating impacts from high statistic regions?

2-point variations especially problematic!

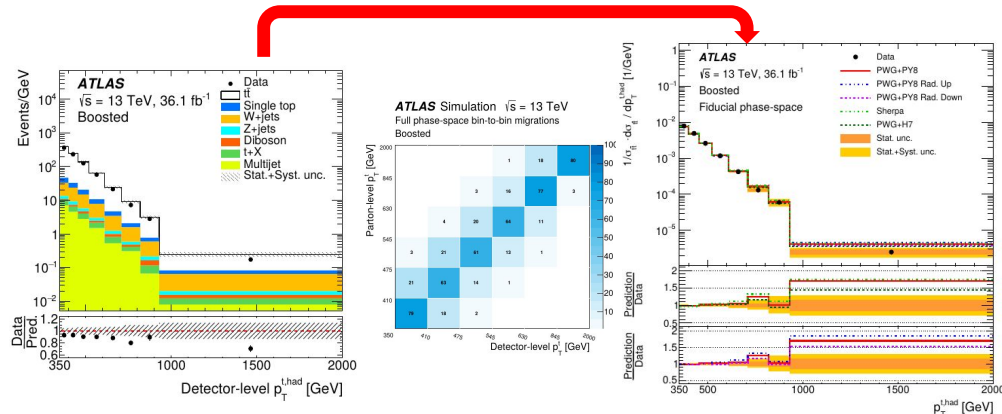


Unfolding

Slides from: Michele Pinamonti

What is *unfolding* about?

- **Unfolding** is:
 - *removal of detector resolution effects from observed distribution, to extract (our best-guess of) underlying true distribution*
 - i.e. extraction of a **differential cross-section**
- Can be done to extract:
 - **total-phase-space** or **fiducial-phase-space** cross-sections
 - cross-sections vs. variable defined at **particle-level** or at **parton-level**
- The unfolding problem can be essentially reduced to a **response-matrix-inversion** problem

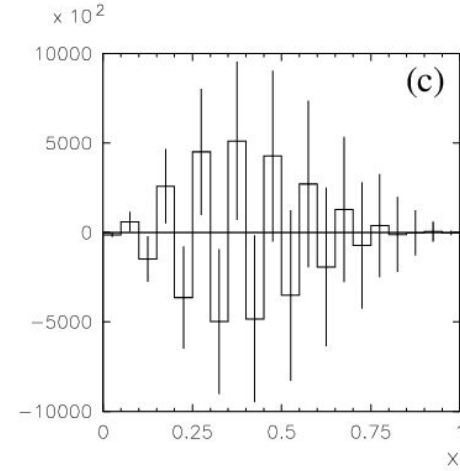
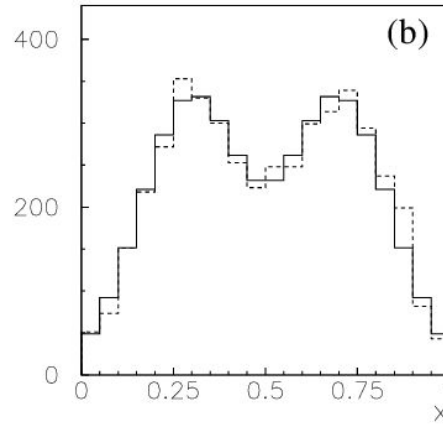
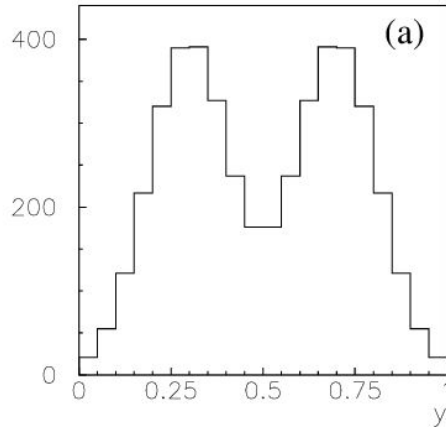


The regularization concept

“To regularize or not to regularize?
This is the question...”



- Most delicate point is the so-called **regularization**:
 - introduced to avoid **amplification of statistical fluctuations** in unfolded data (**oscillations**), happening when just **inverting** response matrix



- Regularization techniques always imply some level of **assumptions** \Rightarrow inevitable **bias**
 - Variance-bias optimisation

Tikhonov regularisation

- Recall the unfolding problem $A\vec{x} = \vec{b}$
- This can be reformulated as a **minimisation** problem (chi-square): $\chi^2 = (A\vec{x} - \vec{b})^T (A\vec{x} - \vec{b}) = \min$
 - Can minimise to find the best fit for \vec{x}
 - Can **impose some additional constraint** (will bias the result!)

$$L(\vec{x}) \equiv \chi^2(\vec{x}) + \Phi(\vec{x}) \rightarrow \min$$

- **Common choice** for the constraint: **second discrete derivative (Tikhonov)**

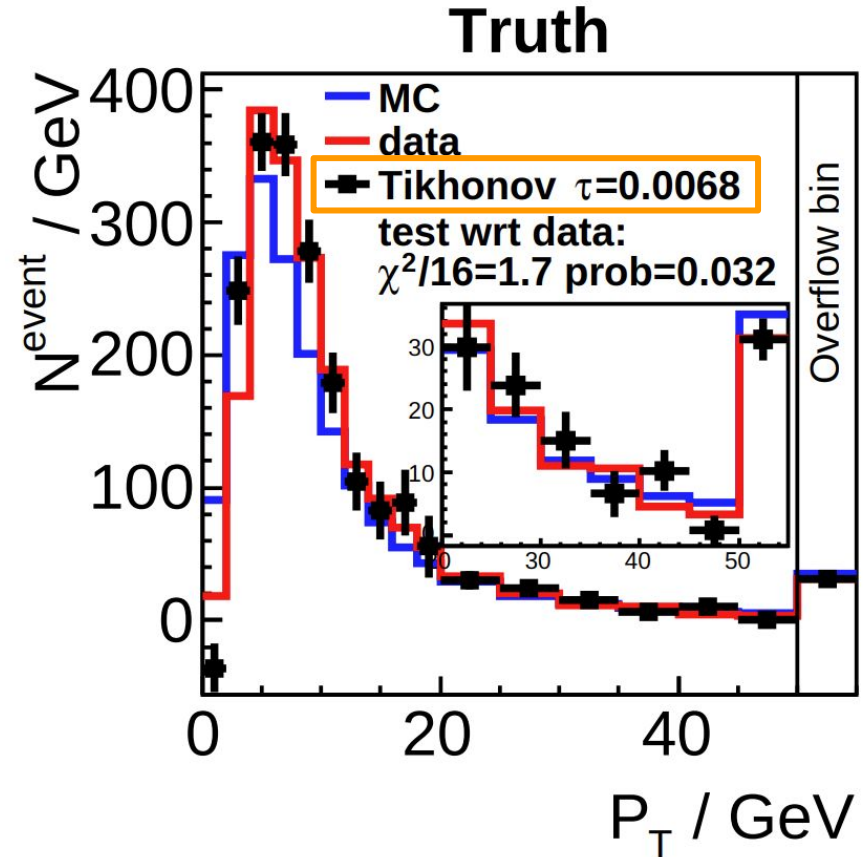
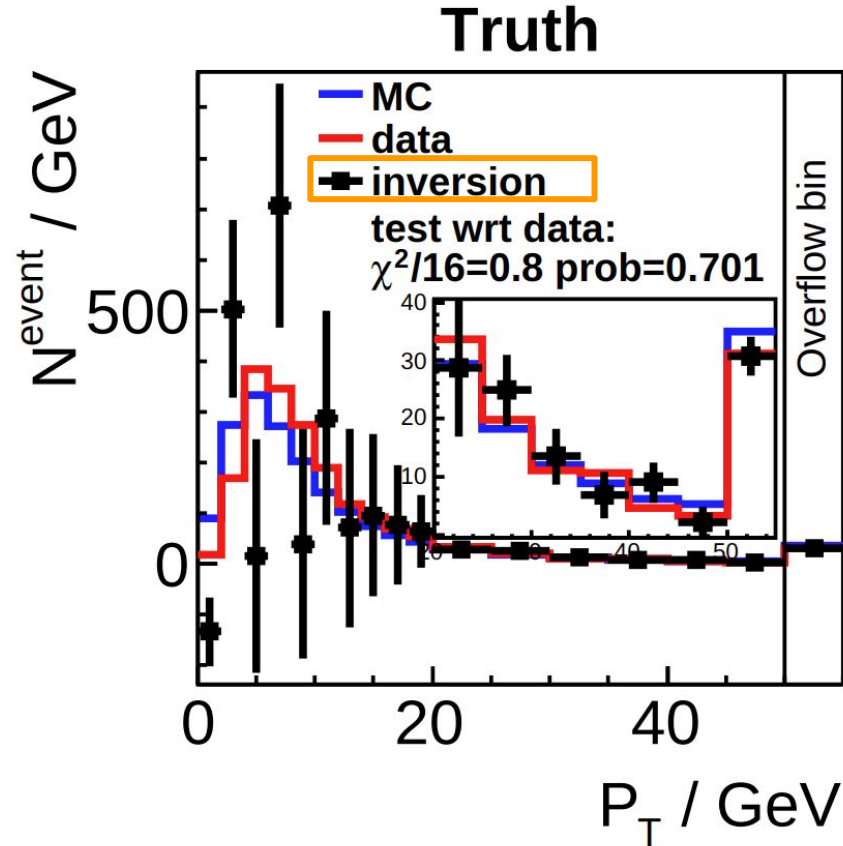
$$\Phi(\vec{x}) = \tau \sum_i (x_{i-1} - 2x_i + x_{i+1})^2$$

- Choice of $\tau \Leftrightarrow$ strength of the regularisation
- Different choices of $\Phi(\vec{x})$ possible - e.g. **SVD** $\longrightarrow A = U S V^T$
 - See e.g. <https://arxiv.org/abs/hep-ph/9509307>

Impact of regularisation

Taken from:

<https://arxiv.org/abs/1611.01927>



Iterative Bayesian Unfolding (IBU)

- Frequently used in high-signal measurements
- Uses Bayes theorem iteratively:

$$p(\mathbf{T}|\mathbf{D}, \mathcal{M}) \propto \mathcal{L}(\mathbf{D}|\mathbf{T}, \mathcal{M}) \cdot \pi(\mathbf{T})$$

posterior *likelihood* *prior*

true distribution points to $p(\mathbf{T}|\mathbf{D}, \mathcal{M})$
data ("reco") distribution points to $\mathcal{L}(\mathbf{D}|\mathbf{T}, \mathcal{M})$
response matrix points to $\mathcal{L}(\mathbf{D}|\mathbf{T}, \mathcal{M})$

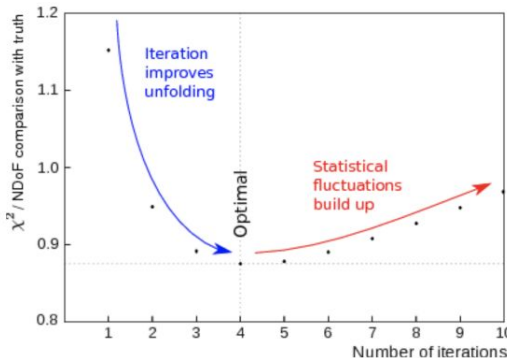
Systematics:

- not included in the formalism
- accessed via ensemble test

- prior based on theoretical prediction in first iteration
- following iterations use result of previous ones as prior



$$\begin{aligned} p_1(\mathbf{T}|\mathbf{D}) &\propto \mathcal{L} \cdot \pi(\mathbf{T}) \\ p_2(\mathbf{T}|\mathbf{D}) &\propto \mathcal{L} \cdot p_1(\mathbf{T}|\mathbf{D}) \\ p_3(\mathbf{T}|\mathbf{D}) &\propto \mathcal{L} \cdot p_2(\mathbf{T}|\mathbf{D}) \\ &\dots \end{aligned}$$



Regularization:

- achieved by stopping after a few iterations ($N_{\text{iter}} \rightarrow \infty \Rightarrow$ unregularized unfolding, i.e. matrix inversion)
- finding optimal stopping point is an important feature of using IBU

Thank you for your attention

Questions?

“If your experiment needs a statistician, you need a better experiment.”

— Ernest Rutherford

Simple example

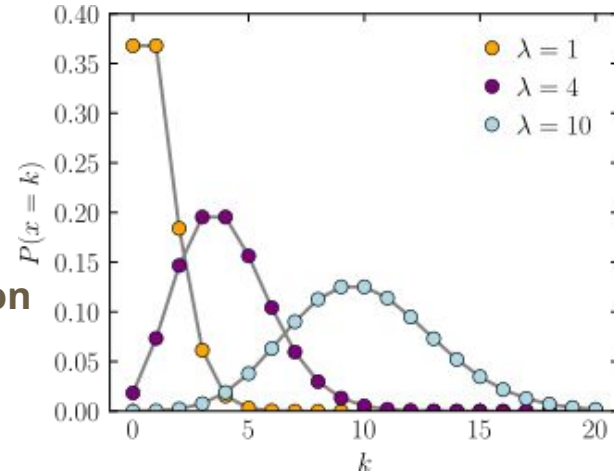
- Suppose we are doing a **counting experiment**
 - Predicted number of background events is **b**
 - Predicted number of signal events is **s**
 - Observed number of events will follow **Poisson distribution**

$$P(n|b) = \frac{b^n}{n!} e^{-b}$$

Background only

$$P(n|s+b) = \frac{(s+b)^n}{n!} e^{-(s+b)}$$

Signal + bkg



- We observe **n** instances of **\mathbf{x}**
- **Likelihoods for the hypotheses**

- Background only

$$L_b = \frac{b^n}{n!} e^{-b} \prod_{i=1}^n f(\mathbf{x}_i|b)$$

- Signal + bkg

$$L_{s+b} = \frac{(s+b)^n}{n!} e^{-(s+b)} \prod_{i=1}^n (\pi_s f(\mathbf{x}_i|s) + \pi_b f(\mathbf{x}_i|b))$$

(Prior) probabilities for an event to be signal or bkg

Simple example continued

- Define test statistics (**-2 logarithm of the likelihood ratio**)

Is constant, can be ignored

$$Q = -2 \ln \frac{L_{s+b}}{L_b} = -s + \sum_{i=1}^n \ln \left(1 + \frac{s f(\mathbf{x}_i|s)}{b f(\mathbf{x}_i|b)} \right)$$

- Let us assume we observe $Q = Q_{\text{obs}}$

e.g. $b = 100, s = 20$.

Suppose in real experiment Q is observed here.

- HEP standard**

- Claim **discovery at 5 sigma**
- Reject B-only hypothesis when p-value is $< 2.9 \times 10^{-7}$

