

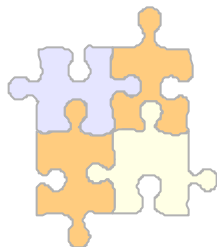
RooFit Tutorial – Fitting and Generating

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Overview

- WARNING - This tutorial is incomplete
 - Relevant parts of the retired 'advanced' tutorial have been moved here.

Generating Toy MC events



Prototyping your ToyMC off real data

Using RooMCStudy to efficiently generate (and fit) many samples

PDF generator interface has two invocation methods

- Regular

- All observables generated by the PDF

```
genData = pdf.generate(<observables>, numEvent) ;
```

- With prototype data

- Some observables modeled by a prototype dataset, other generated by PDF

```
RooDataSet protoData("D","D",<protoObservables>") ;  
// fill protoDataSet ;  
genData = pdf.generate(<genObservables>, protoData) ;
```

- *Generator cycles through dataset*, loading proto-observables in PDF.
- *PDF generates other observables* → *all correlations preserved*
- By default #events is also taken from proto dataset.
If overruled, generated dataset may not exactly reproduce
proto data, unless $\#events = n * \#proto\text{-}events$

Generating ToyMC for sin2beta fit

- CP/mixing PDF doesn't model per-event errors & tagCats
 - Must use prototype data when generating
- Where to get the prototype data for per-event errors etc...?
 - Pre-generate proto data with separate PDF

Add desired
#entries for
each tagCat
by hand

```
// Generate tagging categories
```

```
RoodataSet proto("pD","pD",tagCat) ;  
tagCat = "Lep" ; for (i=0;i<400 ;i++) proto.add(tagCat) ;  
tagCat = "Kao" ; for (i=0;i<1600;i++) proto.add(tagCat) ;  
tagCat = "NT1" ; for (i=0;i<250 ;i++) proto.add(tagCat) ;  
tagCat = "NT2" ; for (i=0;i<1500;i++) proto.add(tagCat) ;
```

Generate
per-event
errors from
separate PDF
(same #evts)

```
// Generate a set of event errors
```

```
RoobifurGauss gerr("gerr","error distribution",dterr,  
                  RooRealConstant::value(0.1),  
                  RooRealConstant::value(0.3),  
                  RooRealConstant::value(0.8)) ;  
RoodataSet *errdata = gerr.generate(dterr,proto.numEntries());
```

Add per-event
errors column
to proto data

```
// Add per-event error column to protoData  
proto.merge(errdata) ;
```

Generating ToyMC for sin2beta fit

- Where to get the prototype data for per-event errors etc...?
 - **Use actual distribution from data**

```
// Select per-event errors and tagCat from actual data
RooDataSet* protoData = cpData->reduce(RooArgSet(dterr, tagCat));
```

- Prototype data can be provided for *any* observable, *overriding the PDFs* intrinsic distribution
 - Example: force B^0/B^0 -bar distribution of actual data

```
// Select per-event errors, tagCat and tag flavour from data
RooDataSet* protoData =
    cpData->reduce(RooArgSet(dterr, tagCat, tagFlav));

// Generate deltat from pdf with tag flavour from data
RooDataSet* genData = cpPdf->generate(deltat, protoData)
```

- Generate ToyMC dataset that mimic all properties of data
 - Use prototype data for *everything except* dt and mB
 - Tagging breakdown, # B^0/B^0 bar, per-event errors, run numbers all taken from data

How to *efficiently* generate multiple sets of ToyMC?

- Use **RooMCStudy** class to manage generation and fitting
- Generating features
 - *Generator overhead only incurred once*
 - ® Efficient for large number of small samples
 - Optional Poisson distribution for #events of generated experiments
 - Optional automatic creation of ASCII data files
- Fitting
 - Fit with generator PDF or different PDF
 - Fit *results* (floating parameters & NLL)
automatically *collected in summary dataset*
- Plotting
 - Automated plotting for distribution of parameters, parameter errors, pulls and NLL

A RooMCStudy example

- Generating and fitting a simple PDF

```
// Setup PDF
RooRealVar x("x","x",-5,15) ;
RooRealVar mean("mean","mean of gaussian",-1) ;
RooRealVar sigma("sigma","width of gaussian",4) ;
RooGaussian gauss("gauss","gaussian PDF",x,mean,sigma) ;

// Create manager
RooMCStudy mgr(gauss,gauss,x,"","mhv") ;

// Generate and fit 1000 experiments of 100 events each
mgr.generateAndFit(1000,100) ;
RooMCStudy::run: Generating and fitting sample 999
RooMCStudy::run: Generating and fitting sample 998
RooMCStudy::run: Generating and fitting sample 997
...
```

The diagram illustrates the components of the `RooMCStudy` constructor call `mgr(gauss, gauss, x, "", "mhv")`. Callouts identify the following elements:

- Generator PDF:** Points to the first `gauss` argument.
- Generator Options:** Points to the `"mhv"` argument.
- Fitting PDF:** Points to the second `gauss` argument.
- Fitting Options:** Points to the `"mhv"` argument.
- Observables:** Points to the `x` argument.

A RooMCStudy example

- Plot the distribution of the value, error and pull of *mean*

```
// Plot the distrution of the value
```

```
RooPlot* mframe = mean.frame(-2,0) ;
```

```
mgr.plotParamOn(mframe) ;
```

```
mframe->Draw() ;
```

```
// Plot the distrution of the error
```

```
RooPlot* meframe = mgr.plotError(mean,0.,0.1) ;
```

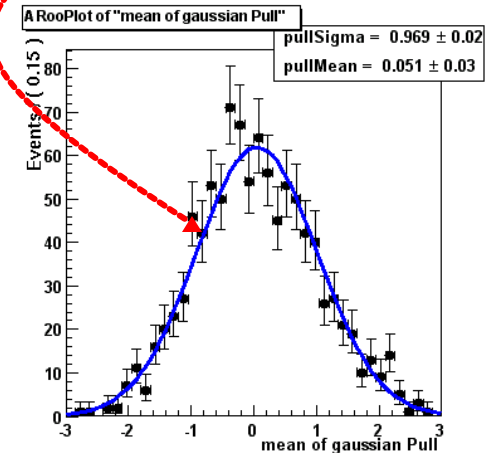
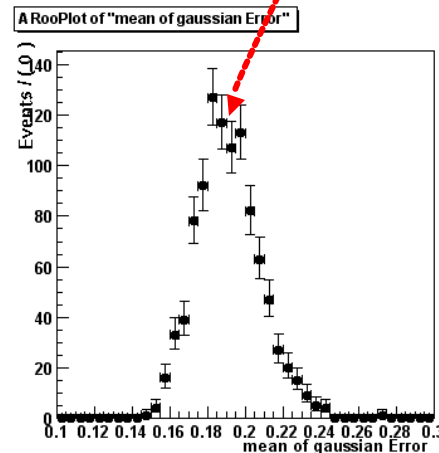
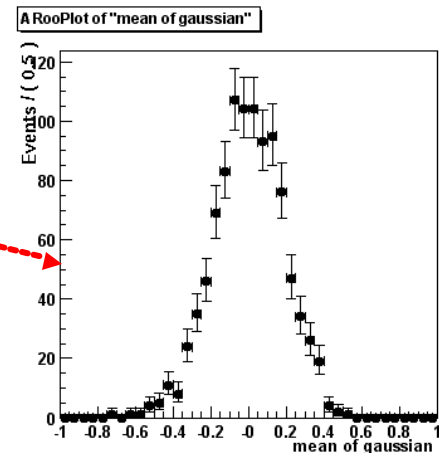
```
meframe->Draw() ;
```

```
// Plot the distrution of the pull
```

```
RooPlot* mpframe = mgr.plotPull(mean,-3,3,40,kTRUE) ;
```

```
mpframe->Draw() ;
```

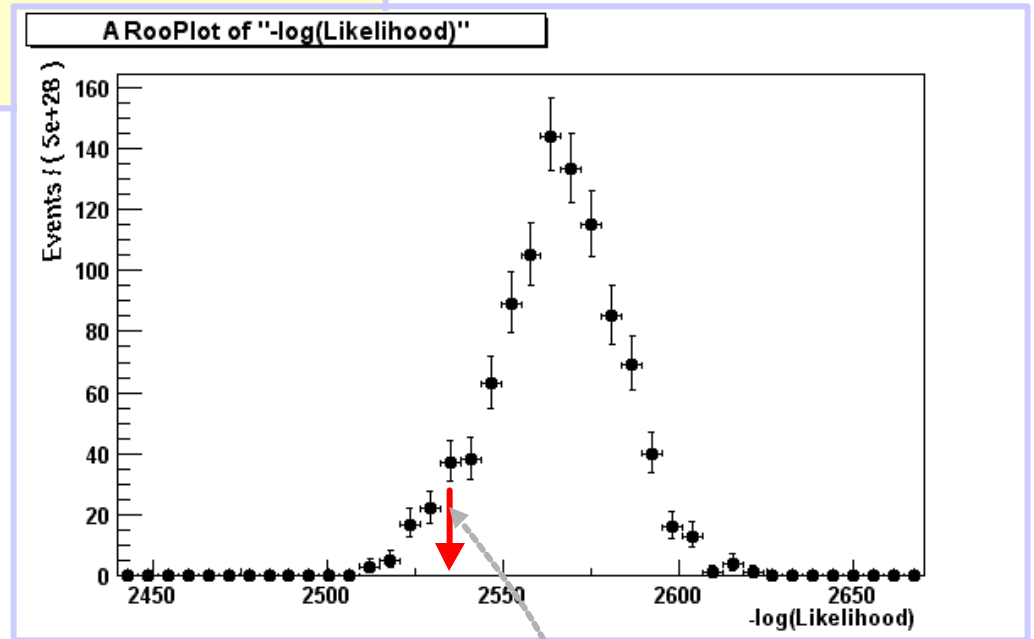
Add Gaussian fit



A RooMCStudy example

- Plot the distribution of $-\log(L)$

```
// Plot the distribution of the NLL  
mgr.plotNLL(mframe) ;  
mframe->Draw() ;
```



- All plots are regular **RooPlots** and can be further decorated
 - E.g add arrow indicating value of fit to actual data

A RooMCStudy example

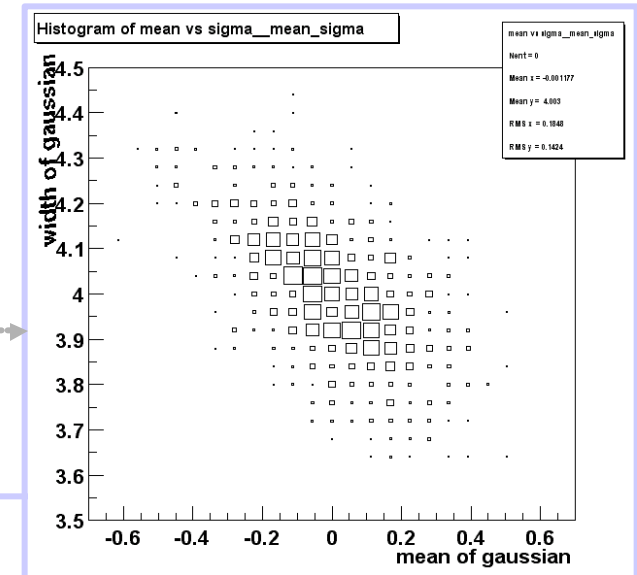
- For other uses, use summarized fit results in **RooDataSet** form

```
mgr.fitParDataSet().get(10)->Print("v") ;
```

```
RooArgSet::
```

```
1) RooRealVar::mean      :  0.14814 +/- 0.191 L(-10 - 10)
2) RooRealVar::sigma     :  4.0619 +/- 0.143 L(0 - 20)
3) RooRealVar::NLL       :  2585.1 C
4) RooRealVar::meanerr   :  0.19064 C
5) RooRealVar::meanpull  :  0.77704 C
6) RooRealVar::sigmaerr  :  0.14338 C
7) RooRealVar::sigmapull :  0.43199 C
```

```
TH2* h = mean.createHistogram("mean vs sigma",sigma) ;
mgr.fitParDataSet().fillHistogram(h,RooArgList(mean,sigma)) ;
h->Draw("BOX") ;
```



*Pulls and errors
have separate
entries for
easy access
and plotting*

A RooMCStudy example

- If the “r” fit option is supplied
the **RooFitResult** output of each fit is be saved

```
mgr.fitResult(10)->Print("v") ;
```

```
RooFitResult: minimized NLL value: 2585.13, estimated distance to minimum: 3.18389e-06
```

Floating Parameter	InitialValue	FinalValue +/-	Error	GblCorr.
mean	0.0000e+00	1.4814e-01 +/-	1.91e-01	0.597596 <none>
sigma	4.0000e+00	4.0619e+00 +/-	1.43e-01	0.597596 <none>

```
mgr.fitResult(10)->correlation("sigma")->Print("v") ;
```

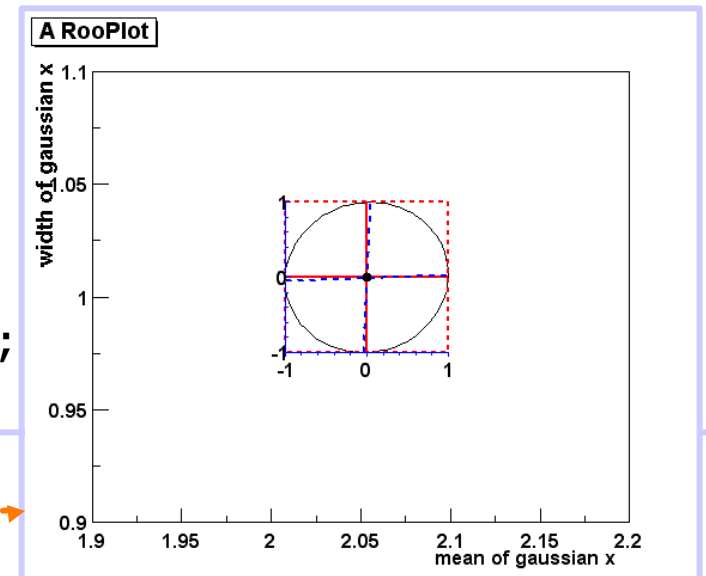
```
RooArgList::C[sigma,*]: (Owning contents)
```

```
1) RooRealVar::C[sigma,mean] : -0.597596 C
```

```
2) RooRealVar::C[sigma,sigma] : 1.0000 C
```

```
RooPlot* frame = new RooPlot(...)
```

```
mgr.fitResult(10)->plotOn(frame,meanx,  
                           sigmax,"ME12VHB") ;
```



Using RooMCStudy for sin2b

- sin2b fit is relatively expensive (~30 minutes)
 - Don't want do 1000 consecutive fits on 1 processor...
 - *Use only generator part*
- Example: generating 1000 toys for goodness-of-fit

// Create manager

```
RooMCStudy mgr(cpmixPdf, cpmixPdf, RooArgSet(dt, mB),  
              "", "", protoData) ;
```

*Prototype data
(with all other observables)*

*Observables to
generate with PDF*

// Generate 1000 ToyMC sets in memory

```
mgr.generate(1000, 0, kTRUE) ;
```

Keep generated datasets in memory

Warning: may be large!

*Write out each dataset
immediately to ASCII file.
Do not retain in memory*

// Generate 1000 ToyMC sets in memory

```
mgr.generate(1000, 0, kFALSE, "output/cpfit_%04d.dat") ;
```

General accept/reject generating caveats

- Monolithic multi-dimensional PDFs have *high startup overhead*
 - Need to find maximum function value empirically
 - *Large number* of samples needed
 - 1D – 1000, 2-D 100,000, 3-D 10,000,000
 - Initial samples will be reused for generation, but usually requests need <10M samples
 - Potential solution:
If more efficient generation technique exists, *implement that method in PDF* and advertise it (see 'writing PDF yourself' section)
- *Pathological* distributions may be *sampled incorrectly*
 - *Narrow peak* may be missed by initial sampling (<1% of phase-space)
 - Otherwise generation is *very inefficient* in nearly all of phase space
 - Solution: generate your dataset in parts
 - Generate peak and non-peak areas separately, append afterwards