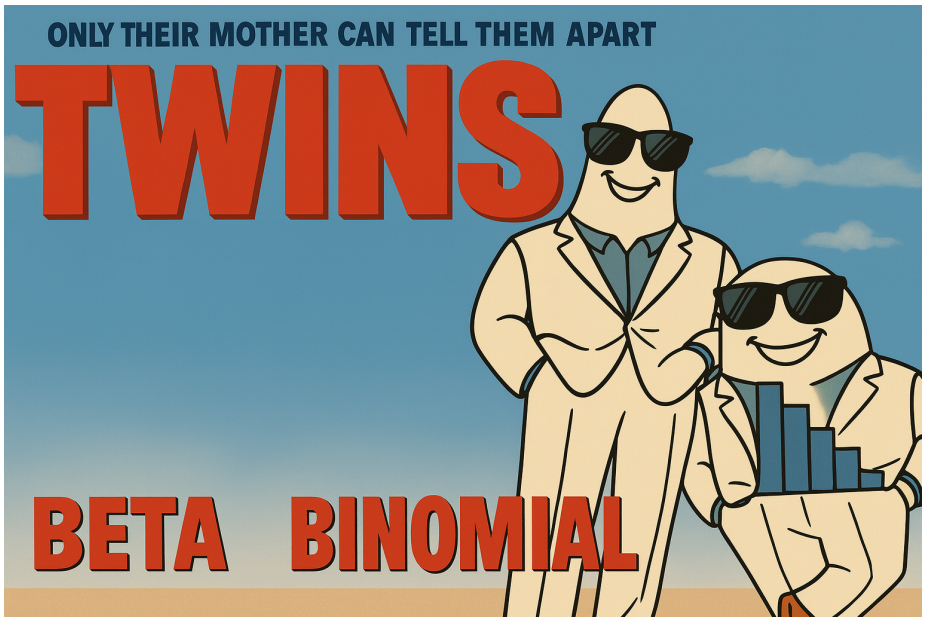
Beta vs Binomial Distribution

Understand the Difference Using Simulations

Russ Zaliznyak <rzaliznyak@gmail.com>

2025-12-09

Table of contents



1 Introduction

In experimentation we often estimate conversion rates or event probabilities. Understanding when to apply a Binomial model versus a Beta model is important for Significance (p-values) and Bayesian (credible intervals) analysis.

Below we present the formal definitions of our distributions, but will later run simulations to build our intuition for the Beta and Binomial Distribution.

2 Formulation

Let's spend a few minutes on the "tough" stuff: a side-by-side comparison of *Binomial Distribution* vs *Beta Distribution*. Both distributions arise from the same underlying relationship — one models outcomes given a probability, and the other models the probability itself given outcomes.

Binomial

$$P(X = k \mid n, p) = \binom{n}{k} p^k (1-p)^{n-k}$$

$$\binom{n}{k} = \frac{n!}{k!(n-k)!}$$

Purpose

Model the probability of observing k successes in n independent Bernoulli trials,
where each trial has success probability p.

Example

Given assumption that $p = 0.50$, what is the probability of generating 525 or more conversions out of 1,000 samples?

Beta

$$f(p \mid \alpha, \beta) = \frac{1}{B(\alpha, \beta)} p^{\alpha-1}(1-p)^{\beta-1},$$

$$B(\alpha, \beta) = \int_0^1 t^{\alpha-1}(1-t)^{\beta-1}\, dt = \frac{\Gamma(\alpha)\Gamma(\beta)}{\Gamma(\alpha+\beta)}.$$

Purpose

Describe the probability of different values of the success parameter p, given successes and failures in an experiment.

Example

Given 525 conversions out of 1,000 samples, what are the values of p that could have generated such a test result?

Use the **Binomial** when assessing how likely your observed data are under a hypothesis; use the **Beta** when estimating the underlying conversion rate.

3 Sim Code

Now we analyze the **same** experiment with *Binomial* and *Beta* distributions.

- The *binomial* will be used to estimate the *likelihood* of our outcome (p-value).
- The *beta* will be used to estimate our *posterior distribution* of conversion rates.

```
import numpy as np
import plotly.graph_objects as go
```

```
def plot_histogram(
    data,
    bins=40,
    title=None,
    color="royalblue",
    opacity=0.7,
    normalize=False,
    show_yaxis=True,
    x_symbol="p",
    show_mean=False,
    mean_line_color="black",
    mean_line_dash="dash",
    is_rate=False,
    highlight_tails=None,  # "left", "right", or "both"
    tail_alpha=0.05,  # proportion per tail (e.g., 0.05 → 5%)
    tail_color="crimson",
):
    """
    Plotly histogram with optional mean line, tail highlighting, and CDF-based hover.
    """

    # Compute histogram and CDF
    hist, edges = np.histogram(
        data,
        bins=bins,
        density=normalize,
    )
    centers = 0.5 * (
        edges[1:] + edges[:-1]
    )
    cdf = np.cumsum(hist)
    cdf = (
        cdf / cdf[-1]
    )  # normalize to 1
    mean_value = np.mean(data)

    # Tail cutoffs
    left_cut = (
        np.quantile(data, tail_alpha)
        if highlight_tails
        in ["left", "both"]
        else None
    )
    right_cut = (
```

```
        np.quantile(
            data, 1 - tail_alpha
        )
        if highlight_tails
        in ["right", "both"]
        else None
    )

    # Assign colors per bar
    colors = np.full_like(
        centers, color, dtype=object
    )
    if highlight_tails:
        if left_cut is not None:
            colors[
                centers <= left_cut
            ] = tail_color
        if right_cut is not None:
            colors[
                centers >= right_cut
            ] = tail_color

    # Hover template
    if is_rate:
        hovertemplate = (
            f"P({x_symbol} < "
            + "%{customdata[0]:.2%})"
            + " = %{customdata[1]:.1%}<extra></extra>"
        )
    else:
        hovertemplate = (
            f"P({x_symbol} < "
            + "%{customdata[0]:.2f})"
            + " = %{customdata[1]:.1%}<extra></extra>"
        )

    # Single bar trace (no overlap)
    fig = go.Figure()
    fig.add_trace(
        go.Bar(
            x=centers,
            y=hist,
            marker_color=colors,
            opacity=opacity,
            customdata=np.column_stack(
```

```
                [centers, cdf]
            ),
            hovertemplate=hovertemplate,
            showlegend=False,
        )
    )

    # Add tail annotations
    annos = []

    # Add mean line
    if show_mean:
        annotation_text = (
            f"mean = {mean_value:.2%}"
            if is_rate
            else f"mean = {mean_value:.2f}"
        )
        fig.add_vline(
            x=mean_value,
            line_width=3,
            line_dash=mean_line_dash,
            line_color=mean_line_color,
            annotation_text=annotation_text,
            annotation_position="top",
        )

    # Layout styling
    fig.update_layout(
        title=title,
        xaxis_title=f"{x_symbol}",
        template="simple_white",
        bargap=0.05,
        height=320,
        yaxis=dict(
            visible=show_yaxis,
            showticklabels=False,
            title="",
        ),
        xaxis=dict(
            tickformat=".0%"
            if is_rate
            else None,
            showline=True,
            showgrid=False,
            zeroline=False,
```

```
        ),
        margin=dict(
            t=30, b=30, l=30, r=30
        ),
    )

    return fig
```

```
import pandas as pd
from IPython.display import display

conversions = 525
trials = 1000
null_rate = 0.50

df = pd.DataFrame([{
    "Trials": f"{trials:,}",
    "Conversions": conversions,
    "Null Hypothesis": f"{null_rate:.1%}"
}])

df = df.round(2)
```

Table 1

Trials	Conversions	Null Hypothesis
1,000	525	50.0%

```
from numpy.random import binomial, seed
from numpy import (
    where,
    mean,
    percentile,
)
import plotly.graph_objects as go

NUMBER_SIMULATIONS = int(5e6)
seed(5)

# Create 5 Million Simulations each with
# n = trials and p = null_rate
control_simulated_experiments = (
    binomial(
        n=trials,
```

```
        p=null_rate,
        size=NUMBER_SIMULATIONS,
    )
)
p_value = mean(
    where(
        control_simulated_experiments
        >= conversions,
        1,
        0,
    )
)
fig = plot_histogram(
    control_simulated_experiments,
    x_symbol="conversions",
    highlight_tails="right",
    tail_alpha=p_value,
)


fig.show()
```

```
Unable to display output for mime type(s): text/html
```

```
Unable to display output for mime type(s): text/html
```

p-value = 0.061

*The **p-value** is the likelihood of seeing our experiment data (or more extreme); assuming the* Null Hypothesis *is true.*

```
# Observed data
from numpy.random import beta

failures = trials - conversions
tail_alpha = 0.025

beta_control_samples = beta(
    conversions,
    failures,
    size=NUMBER_SIMULATIONS,
)

fig = plot_histogram(
    beta_control_samples,
    x_symbol="Possible Conversion Rate",
    is_rate=True,
```

```
    highlight_tails="both",
    tail_alpha=tail_alpha,
    color="crimson",
    tail_color="royalblue",
)

lower_bound = percentile(
    beta_control_samples, tail_alpha * 100
)
upper_bound = percentile(
    beta_control_samples,
    100 - tail_alpha * 100,
)


fig.show()
```

```
Unable to display output for mime type(s): text/html
```

95% Credible Interval: (49.40% , 55.59%)

The **95% credible interval** from the Beta distribution represents where the true rate most likely lies given our data.

4 Replace With Normal

Both distributions can be well approximated with the *Normal Distribution* because of CLT. Note: The Normal approximation breaks down when n is small or when p is near 0 or 1, where the distributions become skewed.

```
from numpy.random import normal
from numpy import where, mean
import plotly.graph_objects as go

# Create 1 Million Simulations each with
# n = trials and p = null_rate
mu = trials * null_rate
sigma = (
    trials * null_rate * (1 - null_rate)
) ** 0.5

control_simulated_experiments = (
    np.random.normal(
        loc=mu,
        scale=sigma,
        size=NUMBER_SIMULATIONS,
```

```
    )
)
p_value = mean(
    where(
        control_simulated_experiments
        >= conversions,
        1,
        0,
    )
)
fig = plot_histogram(
    control_simulated_experiments,
    x_symbol="conversions",
    highlight_tails="right",
    tail_alpha=p_value,
)

fig.show()
```

```
Unable to display output for mime type(s): text/html
```

p-value $= 0.0568$

$$\text{Binomial}(n, p) \approx \mathcal{N}(np,\, np(1-p))$$

```
# Observed data
alpha = conversions
beta_param = failures
tail_alpha = 0.025

# --- Normal approximation parameters ---
mu = alpha / (alpha + beta_param)
sigma = (
    alpha
    * beta_param
    / (
        (alpha + beta_param) ** 2
        * (alpha + beta_param + 1)
    )
) ** 0.5

# Draw samples from the Normal approximation
beta_control_samples = normal(
    loc=mu,
    scale=sigma,
```

```
    size=NUMBER_SIMULATIONS,
)


fig = plot_histogram(
    beta_control_samples,
    x_symbol="Possible Conversion Rate",
    is_rate=True,
    highlight_tails="both",
    tail_alpha=tail_alpha,
    color="crimson",
    tail_color="royalblue",
)


lower_bound = percentile(
    beta_control_samples,
    tail_alpha * 100,
)
upper_bound = percentile(
    beta_control_samples,
    100 - tail_alpha * 100,
)


fig.show()
```

```
Unable to display output for mime type(s): text/html
```

95% Credible Interval: (49.41% , 55.59%)

$$\text{Beta}(\alpha, \beta) \approx \mathcal{N}\left(\mu = \frac{\alpha}{\alpha+\beta},\ \sigma^2 = \frac{\alpha\beta}{(\alpha+\beta)^2(\alpha+\beta+1)}\right).$$

5 Two-Proportion Test

To perform an analogous analysis for the difference of two proportions, we model the difference in `# of conversions` and `delta-to-control` using the difference of our simulations for *treatment* and *control* groups.

5.1 Estimate P-values

```
import pandas as pd
from IPython.display import display
```

```
control_events = 500
treatment_events = 535
delta_conversions = treatment_events - control_events
trials = 1000
null_rate = 0

df = pd.DataFrame([{
    "control_trials": f"{trials:,}",
    "control_events": control_events,
    "treatment_trials": f"{trials:,}",
    "treatment_events": treatment_events,
    "Null Hypothesis": f"{0:.1%}"
}])

df = df.round(2)

display(df.style.hide(axis="index"))
```

Table 2

control_trials	control_events	treatment_trials	treatment_events	Null Hypothesis
1,000	500	1,000	535	0.0%

```
blended_rate = (
    control_events + treatment_events
) / (2 * trials)
control_simulated_experiments = (
    binomial(
        n=trials,
        p=blended_rate,
        size=NUMBER_SIMULATIONS,
    )
)
treatment_simulated_experiments = (
    binomial(
        n=trials,
        p=blended_rate,
        size=NUMBER_SIMULATIONS,
    )
)
delta_simualated_experiments = (
    treatment_simulated_experiments
    - control_simulated_experiments
```

```
)
p_value = mean(
    where(
        delta_simualated_experiments
        >= delta_conversions,
        1,
        0,
    )
)
fig = plot_histogram(
    delta_simualated_experiments,
    x_symbol="Difference of Conversions",
    highlight_tails="right",
    tail_alpha=p_value,
)


fig.show()
```

```
Unable to display output for mime type(s): text/html
```

p-value $= 0.0611$

```
control_se = (
    trials
    * blended_rate
    * (1 - blended_rate)
) ** 0.5
treatment_se = control_se
delta_se = (
    control_se**2 + treatment_se**2
) ** 0.5

delta_simualated_experiments = normal(
    loc=0,
    scale=delta_se,
    size=NUMBER_SIMULATIONS,
)
p_value = mean(
    where(
        delta_simualated_experiments
        >= delta_conversions,
        1,
        0,
    )
)
```

```
fig = plot_histogram(
    delta_simualated_experiments,
    x_symbol="Difference of Conversions",
    highlight_tails="right",
    tail_alpha=p_value,
)


fig.show()
```

```
Unable to display output for mime type(s): text/html
```

p-value $= 0.0586$

5.2 Generate Credible Intervals

```
# Observed data
from numpy.random import beta

control_failures = (
    trials - control_events
)
treatment_failures = (
    trials - treatment_events
)
tail_alpha = 0.025

beta_control_samples = beta(
    control_events,
    control_failures,
    size=NUMBER_SIMULATIONS,
)
beta_treatment_samples = beta(
    treatment_events,
    treatment_failures,
    size=NUMBER_SIMULATIONS,
)
beta_delta_samples = (
    beta_treatment_samples
    - beta_control_samples
)
fig = plot_histogram(
    beta_delta_samples,
    x_symbol="Possible Difference of Conversion Rate",
    is_rate=True,
```

```
    highlight_tails="both",
    tail_alpha=tail_alpha,
    color="crimson",
    tail_color="royalblue",
)

lower_bound = percentile(
    beta_delta_samples, tail_alpha * 100
)
upper_bound = percentile(
    beta_delta_samples,
    100 - tail_alpha * 100,
)


fig.show()
```

```
Unable to display output for mime type(s): text/html
```

95% Credible Interval: (-0.88% , 7.86%)

```
tail_alpha = 0.025

# --- Normal approximation parameters ---
control_mu = control_events / trials
control_sigma = (
    control_events
    * control_failures
    / (
        (
            control_events
            + control_failures
        )
        ** 2
        * (
            control_events
            + control_failures
            + 1
        )
    )
) ** 0.5

treatment_mu = treatment_events / trials
treatment_sigma = (
    treatment_events
    * treatment_failures
```

```
    / (
        (
            treatment_events
            + treatment_failures
        )
        ** 2
        * (
            treatment_events
            + treatment_failures
            + 1
        )
    )
) ** 0.5

delta_mu = treatment_mu - control_mu
delta_se = (
    control_sigma**2
    + treatment_sigma**2
) ** 0.5


# Draw samples from the Normal approximation
beta_delta_samples = normal(
    loc=delta_mu,
    scale=delta_se,
    size=NUMBER_SIMULATIONS,
)


fig = plot_histogram(
    beta_delta_samples,
    x_symbol="Possible Difference of Conversion Rate",
    is_rate=True,
    highlight_tails="both",
    tail_alpha=tail_alpha,
    color="crimson",
    tail_color="royalblue",
)

lower_bound = percentile(
    beta_delta_samples, tail_alpha * 100
)
upper_bound = percentile(
    beta_delta_samples,
    100 - tail_alpha * 100,
```

```
)

fig.show()
```

```
Unable to display output for mime type(s): text/html
```

95% Credible Interval: (-0.88% , 7.88%)

6 Common Pitfalls

1. Using the normal approximation when $np < 5$ or $n(1-p) < 5$ can distort tail probabilities.
2. Confusing p-values (likelihoods of data under H_0) with posterior probabilities about p.
3. Ignoring the $+1$ in Beta$(1, 1)$ priors isn't catastrophic, but slightly understates uncertainty when n is small.

7 Beta Distribution & Priors

The **Beta distribution** naturally supports *updating beliefs* as new data arrive.

$$\text{Prior: Beta}(\alpha_0, \beta_0) \xrightarrow[\text{observe } k,n]{} \text{Posterior: Beta}(\alpha_0 + k,\ \beta_0 + n - k)$$

This property allows the model to evolve over time — today's posterior becomes tomorrow's prior,
making the Beta approach ideal for iterative experiments or streaming data.

8 Key Takeaways

The Binomial distribution quantifies how surprising the observed data are under a fixed p_0, while the Beta distribution estimates which values of p are most plausible given the outcomes.

Under large-sample conditions, both are well-approximated by the Normal distribution, though this breaks down when n is small or p is near 0 or 1.

The Beta model's ability to update priors as new data arrive makes it especially useful for iterative experiments or streaming environments, where today's posterior becomes tomorrow's prior.

9 Future Topics

Request future training sessions: Bayesian Priors, Analyzing Continuous Data, SRM, CUPED, and other AB Testing topics.