```
In [1]: from dsc80_utils import *
```

```
In [2]: from lec08_utils import *
```

Lecture 8 – Imputation

DSC 80, Fall 2025

Agenda 📆

- Review: Missingness mechanisms.
- Identifying missingness mechanisms in data.
  - How do we decide between MCAR and MAR using a permutation test?
  - The Kolmogorov-Smirnov test statistic.
- Imputation.
  - Mean imputation.
  - Probabilistic imputation.

Review: Missingness mechanisms

Flowchart

A good strategy is to assess missingness in the following order.

Missing by design (MD)
Can I determine the missing value exactly by looking at the other columns? 🤔
⬇️

Not missing at random (NMAR)
Is there a good reason why the missingness depends on the values themselves? 🤔
⬇️

Missing at random (MAR)
Do other columns tell me anything about the likelihood that a value is missing? 🤔
⬇️

Missing completely at random (MCAR)
The missingness must not depend on other columns or the values themselves. 😄

Question 🤔

Taken from the Winter 2023 DSC 80 Midterm Exam.

The DataFrame `tv_excl` contains all of the information we have for TV shows that are only available for streaming on a single streaming service.

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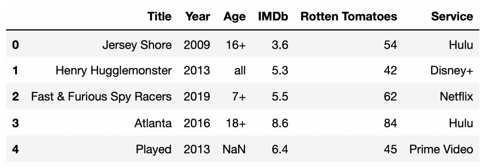


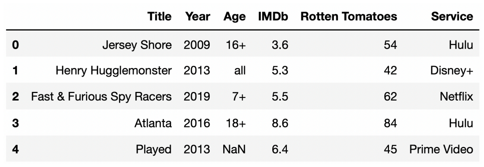
	Title	Year	Age	IMDb	Rotten Tomatoes	Service
0	Jersey Shore	2009	16+	3.6	54	Hulu
1	Henry Hugglemonster	2013	all	5.3	42	Disney+
2	Fast & Furious Spy Racers	2019	7+	5.5	62	Netflix
3	Atlanta	2016	18+	8.6	84	Hulu
4	Played	2013	NaN	6.4	45	Prime Video

Given no other information other than a TV show's `"Title"` and `"IMDb"` rating, what is the most likely missingness mechanism of the `"IMDb"` column?

- A. Missing by design
- B. Not missing at random
- C. Missing at random
- D. Missing completely at random

Question 🤔

Taken from the Winter 2023 DSC 80 Midterm Exam.



	Title	Year	Age	IMDb	Rotten Tomatoes	Service
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3	Atlanta	2016	18+	8.6	84	Hulu
4	Played	2013	NaN	6.4	45	Prime Video

Now, suppose we discover that the median `"Rotten Tomatoes"` rating among TV shows with a missing `"IMDb"` rating is a 13, while the median `"Rotten Tomatoes"` rating among TV shows with a present `"IMDb"` rating is a 52.

Given this information, what is the most likely missingness mechanism of the `"IMDb"` column?

- A. Missing by design
- B. Not missing at random
- C. Missing at random
- D. Missing completely at random

Question 🤔

Suppose Sam collects the blood pressures of 30 people in January. Then, in February, he asks a subset of the people to come back for a second reading (which means that there are missing blood pressures for February). What are the missing mechanisms for the blood pressures in February in the following situations?

1. Sam uses `np.random.choice()` to select 7 individuals from January.
2. Sam asks the individuals who had hypertension (blood pressure > 140) in January to come back in February.
3. Sam asks everyone to come back for a second reading in February, but only records the data for people who had hypertension (blood pressure > 140).

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[illegible]ing missingness mechanisms in data

- If we have ruled out MBD and NMAR, we can often decide between MCAR and MAR with a permutation test.

Example: Heights

- Let's load in Galton's dataset containing the heights of adult children and their parents (which you may have seen in DSC 10).
- The dataset does not contain any missing values – we will **artifically introduce missing values** such that the values are MCAR, for illustration.

In [3]:
```
heights_path = Path('data') / 'midparent.csv'
heights = pd.read_csv(heights_path).rename(columns={'childHeight': 'child'})[['father', 'mothe
heights.head()
```

Out[3]:

	father	mother	gender	child
0	78.5	67.0	male	73.2
1	78.5	67.0	female	69.2
2	78.5	67.0	female	69.0
3	78.5	67.0	female	69.0
4	75.5	66.5	male	73.5

Simulating MCAR data

- We will make `'child'` MCAR by taking a random subset of `heights` and setting the corresponding `'child'` heights to `np.NaN`.
- This is equivalent to flipping a (biased) coin for each row.
  - If heads, we delete the `'child'` height.
- **You will not do this in practice!**

In [4]:
```
np.random.seed(42) # So that we get the same results each time (for lecture).

heights_mcar = heights.copy()
idx = heights_mcar.sample(frac=0.3).index
heights_mcar.loc[idx, 'child'] = np.nan
```

In [5]:
```
heights_mcar.head(10)
```

Out[5]:

	father	mother	gender	child
0	78.5	67.0	male	73.2
1	78.5	67.0	female	69.2
2	78.5	67.0	female	NaN
...	...	...	...	...
7	75.5	66.5	female	NaN
8	75.0	64.0	male	71.0
9	75.0	64.0	female	68.0

10 rows × 4 columns

In [6]:
```
heights_mcar.isna().mean()
```

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Out[6]:
```
father    0.0
mother    0.0
gender    0.0
child     0.3
dtype: float64
```

Verifying that child heights are MCAR in `heights_mcar`

- Each row of `heights_mcar` belongs to one of two **groups**:
  - Group 1: `'child'` is missing.
  - Group 2: `'child'` is not missing.

In [7]:
```python
heights_mcar['child_missing'] = heights_mcar['child'].isna()
heights_mcar.head()
```

Out[7]:

	father	mother	gender	child	child_missing
0	78.5	67.0	male	73.2	False
1	78.5	67.0	female	69.2	False
2	78.5	67.0	female	NaN	True
3	78.5	67.0	female	69.0	False
4	75.5	66.5	male	73.5	False

- We need to look at the distributions of every other column – `'gender'`, `'mother'`, and `'father'` – separately for these two groups, and check to see if they are similar.

In [8]:
```python
gender_dist = (
    heights_mcar
    .assign(child_missing=heights_mcar['child'].isna())
    .pivot_table(index='gender', columns='child_missing', aggfunc='size')
)

# Added just to make the resulting pivot table easier to read.
gender_dist.columns = ['child_missing = False', 'child_missing = True']

gender_dist = gender_dist / gender_dist.sum()
gender_dist
```

Out[8]:

	child_missing = False	child_missing = True
gender		
female	0.49	0.48
male	0.51	0.52

In [9]:
```python
gender_dist.plot(kind='barh', title='Gender by Missingness of Child Height (MCAR Example)', ba
```

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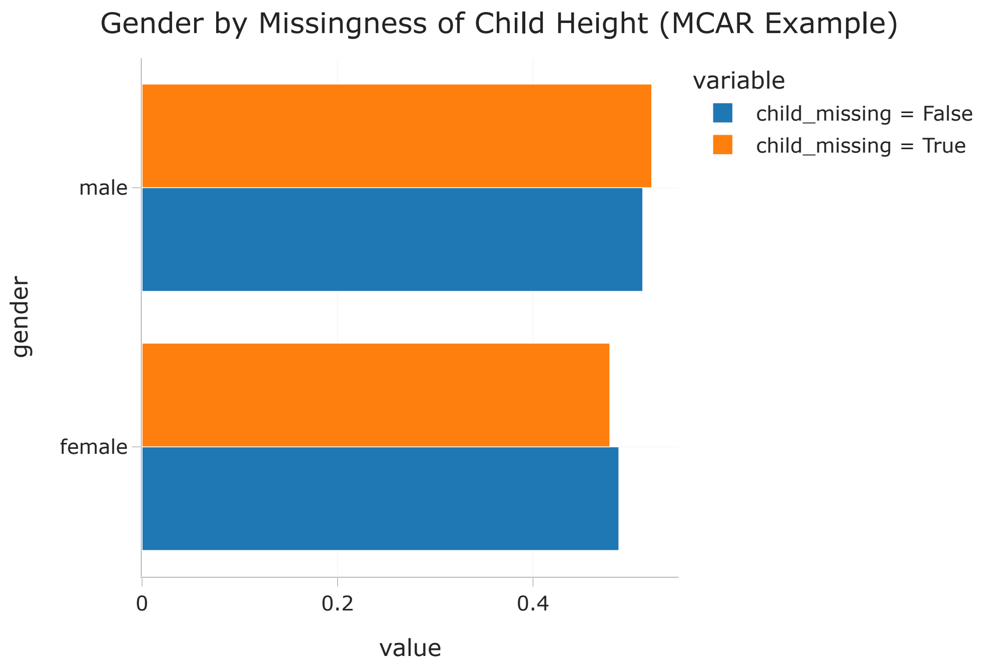
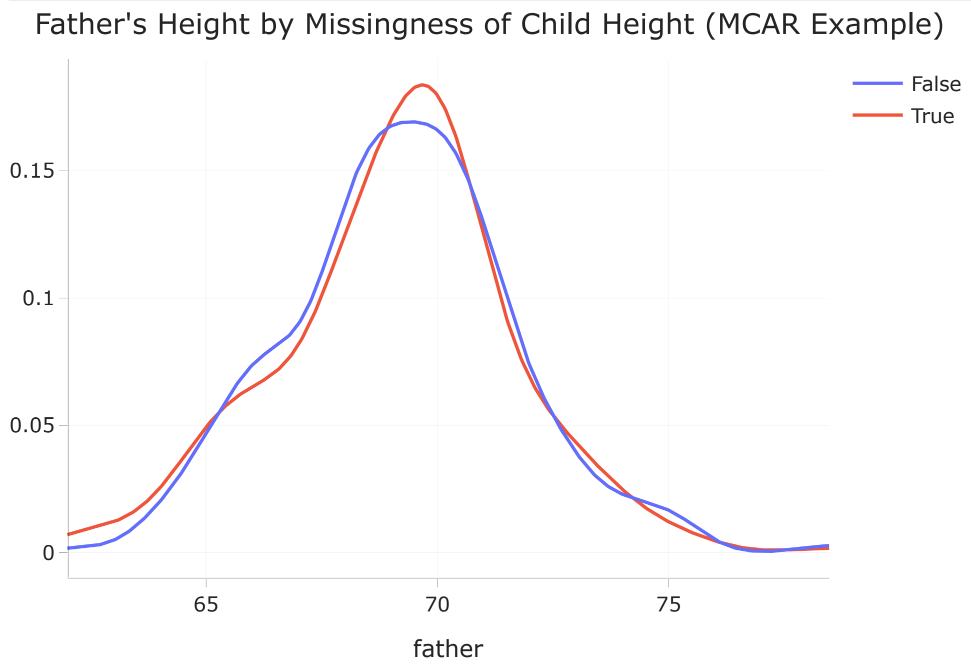


Since `'gender'` is categorical, we're looking at two categorical variables here. The two distributions look similar, but to make formal what we mean by similar, we'd need to run a permutation test.

```
In [10]: create_kde_plotly(heights_mcar, 'child_missing', True, False, 'father',
                           "Father's Height by Missingness of Child Height (MCAR Example)")
```



Since `'father'` s heights are numerical, we're looking at two numerical variables here. The two distributions look similar, but to make formal what we mean by similar, we'd need to run a permutation test.

```
In [11]: create_kde_plotly(heights_mcar, 'child_missing', True, False, 'mother',
                           "Mother's Height by Missingness of Child Height (MCAR Example)")
```

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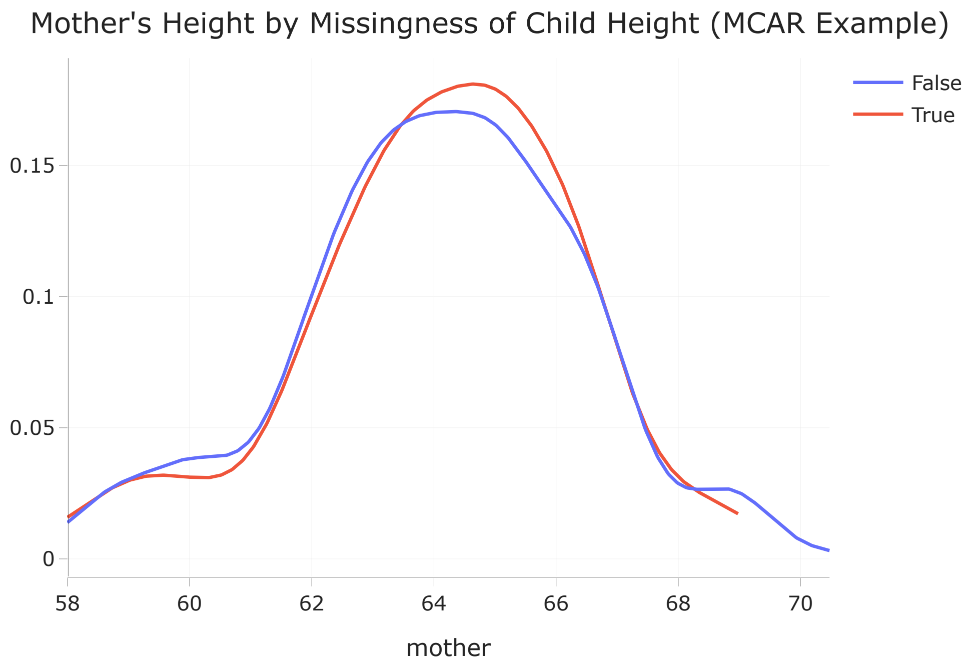

Again, `'mother'`s heights are numerical, we're looking at two numerical variables here. The two distributions look similar, but to make formal what we mean by similar, we'd need to run a permutation test.

Concluding that `'child'` is MCAR

- We need to run three permutation tests – one for each column in `heights_mcar` other than `'child'`.
- For every other column, if we **fail to reject the null** that the distribution of the column when `'child'` is missing is the same as the distribution of the column when `'child'` is not missing, then we can conclude `'child'` is MCAR.
    - In such a case, its missingness is not tied to any other columns.
    - For instance, children with shorter fathers are not any more likely to have missing heights than children with taller fathers.

Simulating MAR data

Now, we will make `'child'` heights MAR by deleting `'child'` heights according to a random procedure that **depends on other columns**.

In [12]:
```python
np.random.seed(42) # So that we get the same results each time (for lecture).

def make_missing(r):
    rand = np.random.uniform() # Random real number between 0 and 1.
    if r['father'] > 72 and rand < 0.5:
        return np.nan
    elif r['gender'] == 'female' and rand < 0.3:
        return np.nan
    else:
        return r['child']

heights_mar = heights.copy()
heights_mar['child'] = heights_mar.apply(make_missing, axis=1)
heights_mar['child_missing'] = heights_mar['child'].isna()
```

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```python
r.head()
```

Out[13]:

	father	mother	gender	child	child_missing
0	78.5	67.0	male	NaN	True
1	78.5	67.0	female	69.2	False
2	78.5	67.0	female	69.0	False
3	78.5	67.0	female	69.0	False
4	75.5	66.5	male	NaN	True

Comparing null and non-null `'child'` distributions for `'gender'`, again

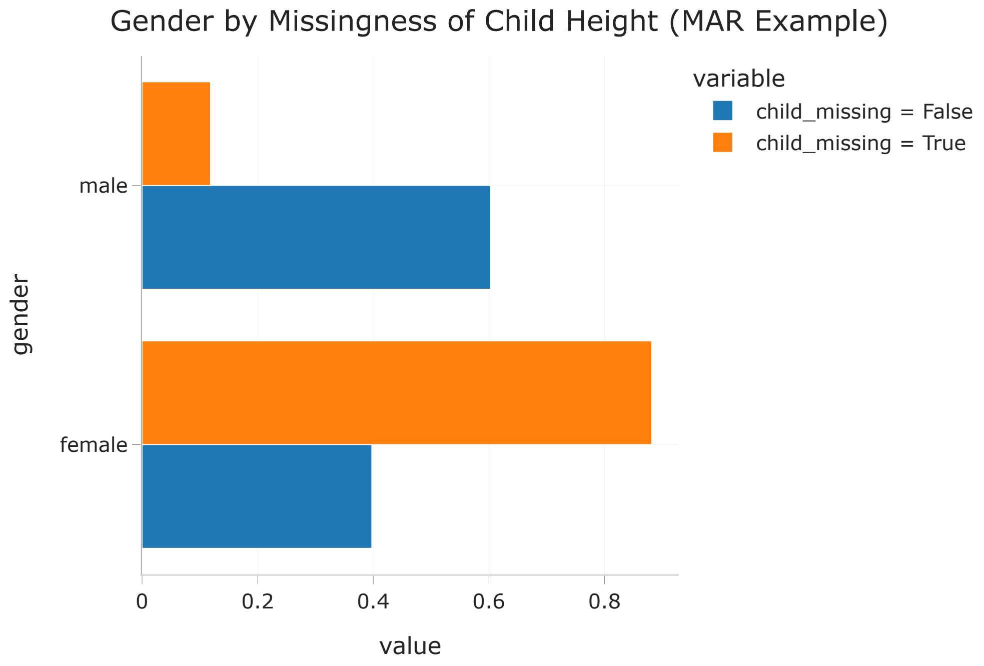
This time, the distribution of `'gender'` in the two groups is very different.

In [14]:
```
gender_dist = (
    heights_mar
    .assign(child_missing=heights_mar['child'].isna())
    .pivot_table(index='gender', columns='child_missing', aggfunc='size')
)

# Added just to make the resulting pivot table easier to read.
gender_dist.columns = ['child_missing = False', 'child_missing = True']

gender_dist = gender_dist / gender_dist.sum()
gender_dist
```

Out[14]:

gender	child_missing = False	child_missing = True
female	0.4	0.88
male	0.6	0.12

In [15]:
```
gender_dist.plot(kind='barh', title='Gender by Missingness of Child Height (MAR Example)', bar
```



Comparing null and non-null `'child'` distributions for `'father'`, again

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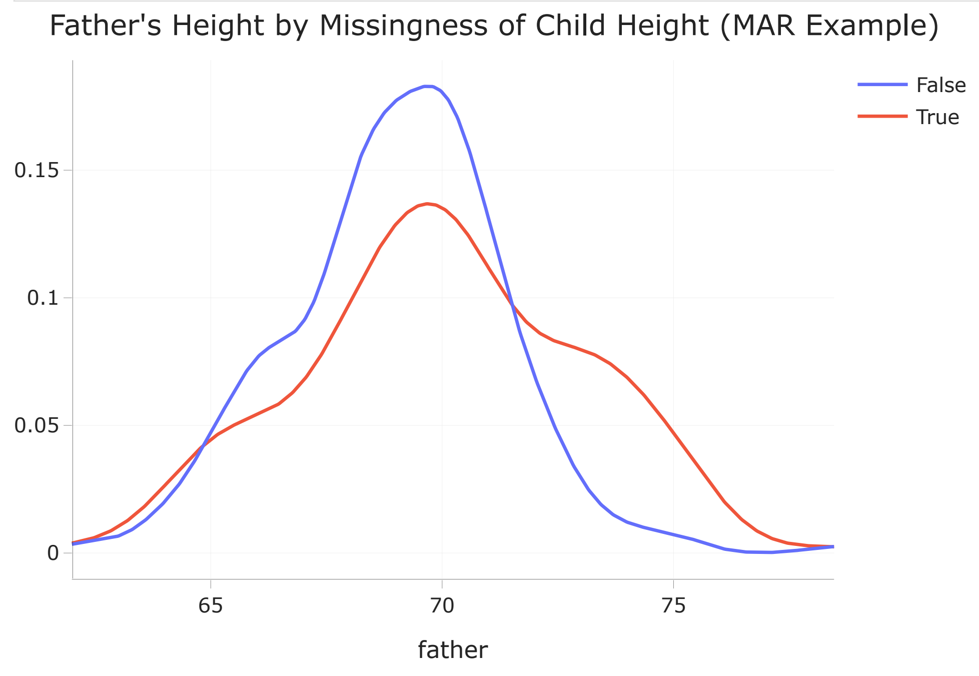
```
In [16]: create_kde_plotly(heights_mar, 'child_missing', True, False, 'father',
                           "Father's Height by Missingness of Child Height (MAR Example)")
```



- The above two distributions look quite different.
  - This is because we artificially created missingness in the dataset in a way that depended on `'father'` and `'gender'`.

- However, their difference in means is small:

```
In [17]: (
             heights_mar
             .groupby('child_missing')
             ['father']
             .mean()
             .diff()
             .iloc[-1]
         )
```

```
Out[17]: np.float64(1.0055466604787853)
```

- If we ran a permutation test with the difference in means as our test statistic, we would fail to reject the null.
  - **Using just the difference in means, it is hard to tell these two distributions apart.**

The Kolmogorov-Smirnov test statistic

Recap: Permutation tests

- Permutation tests help decide whether **two samples look like they were drawn from the same population distribution**.

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- In a permutation test, we simulate data under the null by **shuffling** either group labels or numerical features.
  - In effect, this **randomly assigns individuals to groups**.

- If the two distributions are **numerical**, we've used as our test statistic the **difference in group means or medians**.

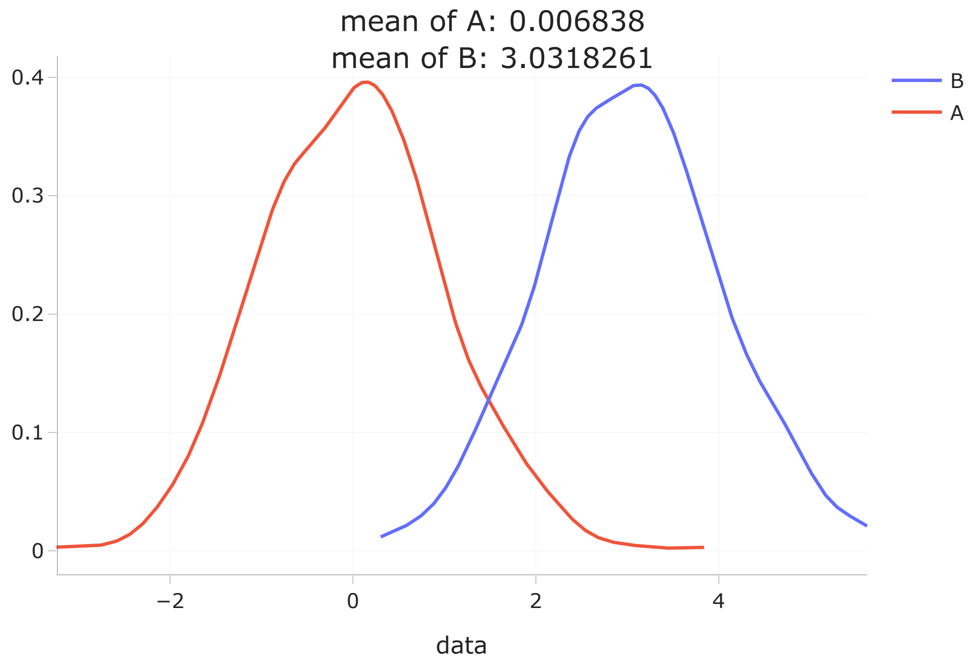
- If the two distributions are **categorical**, we've used as our test statistic the **total variation distance (TVD)**.

Difference in means

The difference in means works well in some cases. Let's look at one such case.

Below, we artificially generate two numerical datasets.

In [18]:
```
np.random.seed(42) # So that we get the same results each time (for lecture).

N = 1000 # Number of samples for each distribution.

# Distribution 'A'.
distr1 = pd.Series(np.random.normal(0, 1, size=N // 2))

# Distribution 'B'.
distr2 = pd.Series(np.random.normal(3, 1, size=N // 2))

data = pd.concat([distr1, distr2], axis=1, keys=['A', 'B']).unstack().reset_index().drop('leve
data = data.rename(columns={'level_0': 'group', 0: 'data'})

meanA, meanB = data.groupby('group')['data'].mean().round(7).tolist()
create_kde_plotly(data, 'group', 'A', 'B', 'data', f'mean of A: {meanA}<br>mean of B: {meanB}'
```



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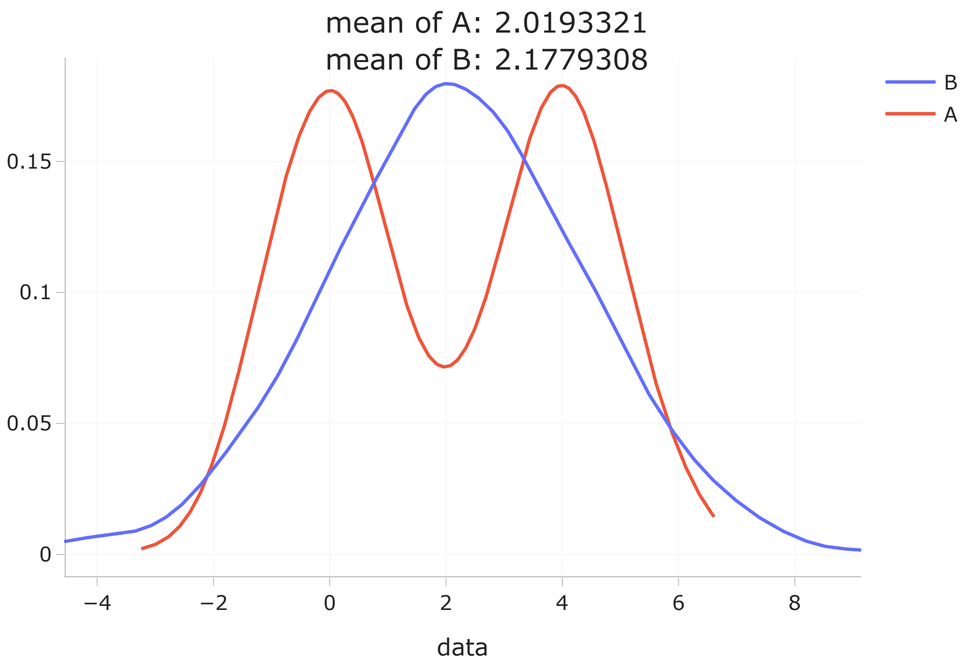
Different distributions with the same mean

Let's generate two distributions that look very different but have the same mean.

In [19]:
```
np.random.seed(42) # So that we get the same results each time (for lecture).

N = 1000 # Number of samples for each distribution.

# Distribution 'A'.
a = pd.Series(np.random.normal(0, 1, size=N//2))
b = pd.Series(np.random.normal(4, 1, size=N//2))
distr1 = pd.concat([a,b], ignore_index=True)

# Distribution 'B'.
distr2 = pd.Series(np.random.normal(distr1.mean(), distr1.std(), size=N))

data = pd.concat([distr1, distr2], axis=1, keys=['A', 'B']).unstack().reset_index().drop('leve
data = data.rename(columns={'level_0': 'group', 0: 'data'})

meanA, meanB = data.groupby('group')['data'].mean().round(7).tolist()
create_kde_plotly(data, 'group', 'A', 'B', 'data', f'mean of A: {meanA}<br>mean of B: {meanB}'
```



In this case, if we use the difference in means as our test statistic in a permutation test, we will fail to reject the null that the two distributions are different.

In [20]:
```
n_repetitions = 500
shuffled = data.copy()

diff_means = []
for _ in range(n_repetitions):

    # Shuffling the values, while keeping the group labels in place.
    shuffled['data'] = np.random.permutation(shuffled['data'])

    # Computing and storing the absolute difference in means.
    diff_mean = shuffled.groupby('group')['data'].mean().diff().abs().iloc[-1]
    diff_means.append(diff_mean)
```

```
       iff = data.groupby('group')['data'].mean().diff().abs().iloc[-1]
fig = px.histogram(pd.DataFrame(diff_means), x=0, nbins=50, histnorm='probability',
```

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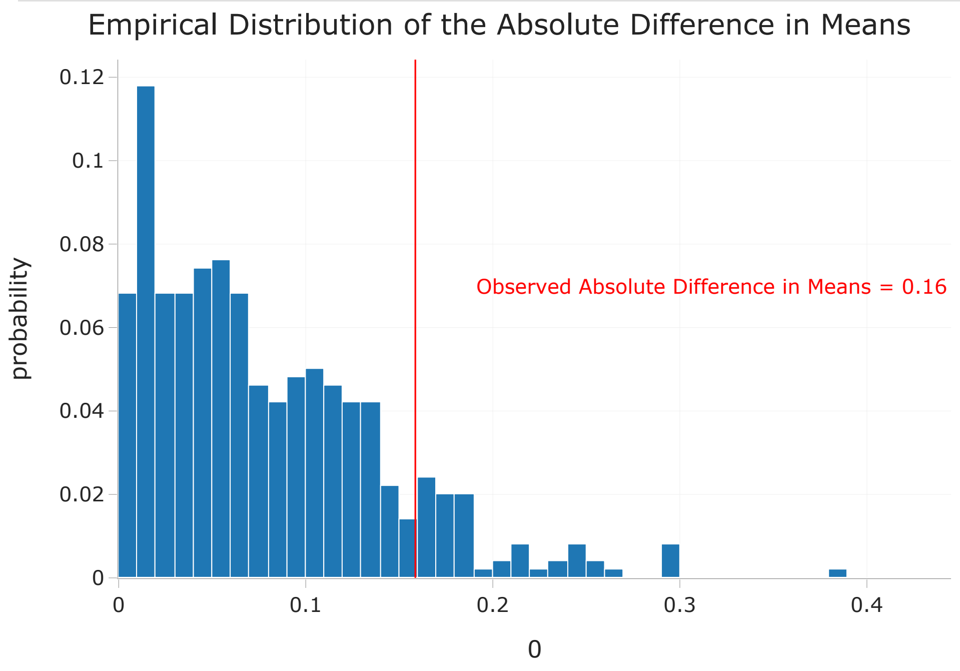
```
                   title='Empirical Distribution of the Absolute Difference in Means')
fig.add_vline(x=observed_diff, line_color='red', line_width=1, opacity=1)
fig.add_annotation(text=f'<span style="color:red">Observed Absolute Difference in Means = {rou
                   x=2 * observed_diff, showarrow=False, y=0.07)
```



In [22]:
```
# The computed p-value is fairly large.
np.mean(np.array(diff_means) >= observed_diff)
```

Out[22]:
```
np.float64(0.108)
```

Telling numerical distributions apart

- The difference in means only works as a test statistic in permutation tests **if the two distributions have similar shapes**.
  - It tests to see if one is a shifted version of the other.

- We need a better test statistic to differentiate between numerical distributions with different shapes.

- In other words, we need a **distance** metric between numerical.
  - The TVD is a distance metric between categorical distributions.

In [23]:
```
create_kde_plotly(data, 'group', 'A', 'B', 'data', f'mean of A: {meanA}<br>mean of B: {meanB}'
```

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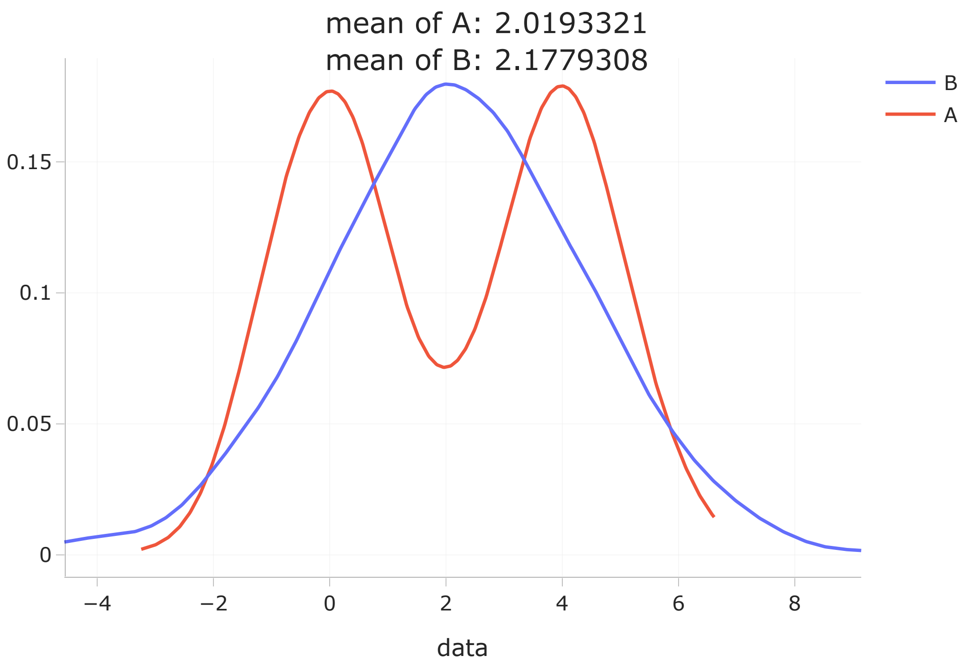
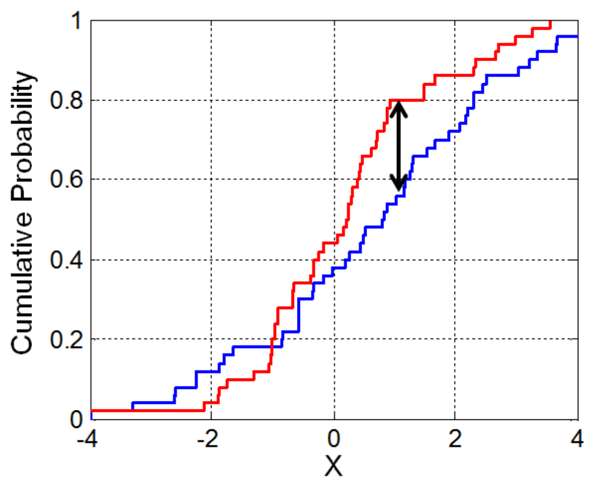


The Kolmogorov-Smirnov test statistic

- The K-S test statistic measures the similarity between two distributions.
- It is defined in terms of the **cumulative distribution function (CDF)** of a given distribution.
    - If $f(x)$ is a distribution, then the CDF $F(x)$ is the proportion of values in distribution $f$ that are less than or equal to $x$.
- The K-S statistic is roughly defined as the **largest difference between two CDFs**.



Aside: Cumulative distribution functions

First, some setup.

```
In [24]: fig1 = create_kde_plotly(data, 'group', 'A', 'B', 'data', f'Distributions of A and B')

         # Think about what this function is doing!
         def create_cdf(group):
             return data.loc[data['group'] == group, 'data'].value_counts(normalize=True).sort_index().

         fig2 = go.Figure()
```

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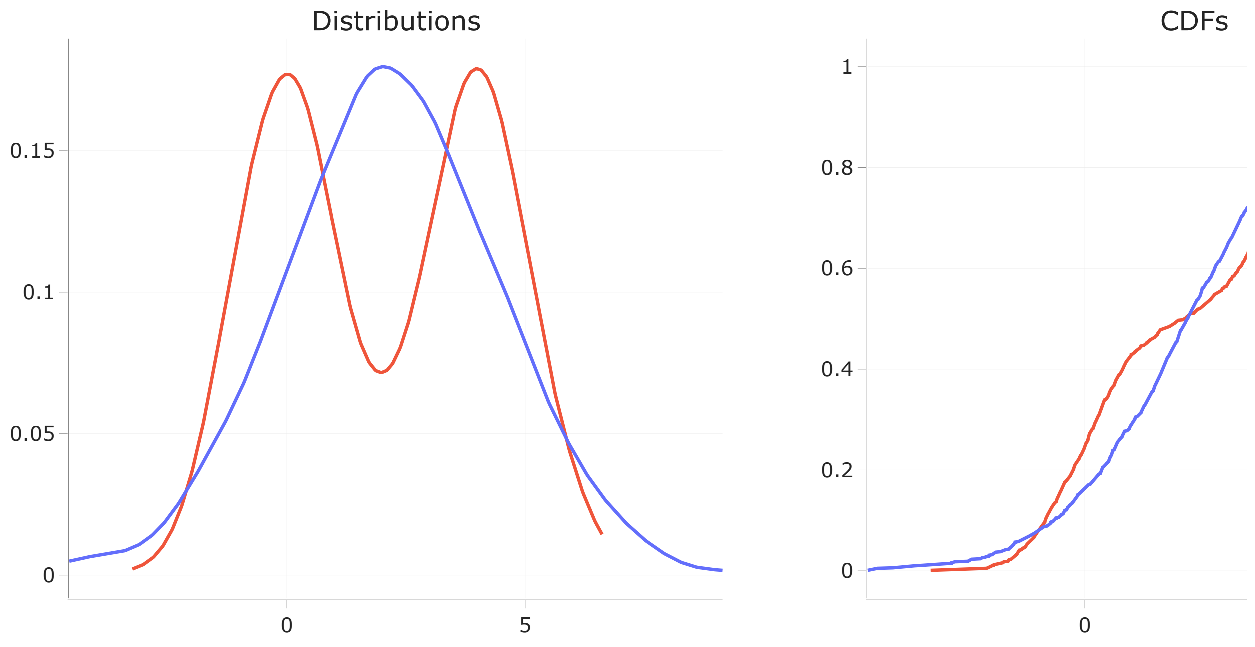
```
fig2.add_trace(
    go.Scatter(x=create_cdf('A').index, y=create_cdf('A'), name='CDF of A')
)

fig2.add_trace(
    go.Scatter(x=create_cdf('B').index, y=create_cdf('B'), name='CDF of B')
)

fig2.update_layout(title='CDFs of A and B')

from plotly.subplots import make_subplots

for i in range(2):
    fig2.data[i]['marker']['color'] = fig1.data[i]['marker']['color']
    fig2.data[i]['showlegend'] = False

fig = make_subplots(rows=1, cols=2, subplot_titles=['Distributions', 'CDFs'])
fig.add_trace(fig1.data[0], row=1, col=1)
fig.add_trace(fig1.data[1], row=1, col=1)
fig.add_trace(fig2.data[0], row=1, col=2)
fig.add_trace(fig2.data[1], row=1, col=2)
fig.update_layout(width=1000, height=400);
```

Aside: Cumulative distribution functions

Let's look at the CDFs of our two synthetic distributions.

```
In [25]: fig
```



The K-S statistic in Python

Fortunately, **we don't need to calculate the K-S statistic ourselves**! Python can do it for us (and you can use this pre-built version in all assignments).

```
In [26]: from scipy.stats import ks_2samp
```

```
In [27]: ks_2samp?
```

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```
Signature:
ks_2samp(
    data1,
    data2,
    alternative='two-sided',
    method='auto',
    *,
    axis=0,
    nan_policy='propagate',
    keepdims=False,
)
Docstring:
Performs the two-sample Kolmogorov-Smirnov test for goodness of fit.

This test compares the underlying continuous distributions F(x) and G(x)
of two independent samples.  See Notes for a description of the available
null and alternative hypotheses.

Parameters
----------
data1, data2 : array_like, 1-Dimensional
    Two arrays of sample observations assumed to be drawn from a continuous
    distribution, sample sizes can be different.
alternative : {'two-sided', 'less', 'greater'}, optional
    Defines the null and alternative hypotheses. Default is 'two-sided'.
    Please see explanations in the Notes below.
method : {'auto', 'exact', 'asymp'}, optional
    Defines the method used for calculating the p-value.
    The following options are available (default is 'auto'):

      * 'auto' : use 'exact' for small size arrays, 'asymp' for large
      * 'exact' : use exact distribution of test statistic
      * 'asymp' : use asymptotic distribution of test statistic
axis : int or None, default: 0
    If an int, the axis of the input along which to compute the statistic.
    The statistic of each axis-slice (e.g. row) of the input will appear in a
    corresponding element of the output.
    If ``None``, the input will be raveled before computing the statistic.
nan_policy : {'propagate', 'omit', 'raise'}
    Defines how to handle input NaNs.

    - ``propagate``: if a NaN is present in the axis slice (e.g. row) along
      which the  statistic is computed, the corresponding entry of the output
      will be NaN.
    - ``omit``: NaNs will be omitted when performing the calculation.
      If insufficient data remains in the axis slice along which the
      statistic is computed, the corresponding entry of the output will be
      NaN.
    - ``raise``: if a NaN is present, a ``ValueError`` will be raised.
keepdims : bool, default: False
    If this is set to True, the axes which are reduced are left
    in the result as dimensions with size one. With this option,
    the result will broadcast correctly against the input array.

Returns
-------
res: KstestResult
    An object containing attributes:

    statistic : float
        KS test statistic.
    pvalue : float
        One-tailed or two-tailed p-value.
    statistic_location : float
        Value from `data1` or `data2` corresponding with the KS statistic;
        i.e., the distance between the empirical distribution functions is
        measured at this observation.
```

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```
    statistic_sign : int
        +1 if the empirical distribution function of `data1` exceeds
        the empirical distribution function of `data2` at
        `statistic_location`, otherwise -1.

See Also
--------

:func:`kstest`, :func:`ks_1samp`, :func:`epps_singleton_2samp`, :func:`anderson_ksamp`
    ..

Notes
-----
There are three options for the null and corresponding alternative
hypothesis that can be selected using the `alternative` parameter.

- `less`: The null hypothesis is that F(x) >= G(x) for all x; the
  alternative is that F(x) < G(x) for at least one x. The statistic
  is the magnitude of the minimum (most negative) difference between the
  empirical distribution functions of the samples.

- `greater`: The null hypothesis is that F(x) <= G(x) for all x; the
  alternative is that F(x) > G(x) for at least one x. The statistic
  is the maximum (most positive) difference between the empirical
  distribution functions of the samples.

- `two-sided`: The null hypothesis is that the two distributions are
  identical, F(x)=G(x) for all x; the alternative is that they are not
  identical. The statistic is the maximum absolute difference between the
  empirical distribution functions of the samples.

Note that the alternative hypotheses describe the *CDFs* of the
underlying distributions, not the observed values of the data. For example,
suppose x1 ~ F and x2 ~ G. If F(x) > G(x) for all x, the values in
x1 tend to be less than those in x2.

If the KS statistic is large, then the p-value will be small, and this may
be taken as evidence against the null hypothesis in favor of the
alternative.

If ``method='exact'``, `ks_2samp` attempts to compute an exact p-value,
that is, the probability under the null hypothesis of obtaining a test
statistic value as extreme as the value computed from the data.
If ``method='asymp'``, the asymptotic Kolmogorov-Smirnov distribution is
used to compute an approximate p-value.
If ``method='auto'``, an exact p-value computation is attempted if both
sample sizes are less than 10000; otherwise, the asymptotic method is used.
In any case, if an exact p-value calculation is attempted and fails, a
warning will be emitted, and the asymptotic p-value will be returned.

The 'two-sided' 'exact' computation computes the complementary probability
and then subtracts from 1.  As such, the minimum probability it can return
is about 1e-16.  While the algorithm itself is exact, numerical
errors may accumulate for large sample sizes.   It is most suited to
situations in which one of the sample sizes is only a few thousand.

We generally follow Hodges' treatment of Drion/Gnedenko/Korolyuk [1]_.

Beginning in SciPy 1.9, ``np.matrix`` inputs (not recommended for new
code) are converted to ``np.ndarray`` before the calculation is performed. In
this case, the output will be a scalar or ``np.ndarray`` of appropriate shape
rather than a 2D ``np.matrix``. Similarly, while masked elements of masked
arrays are ignored, the output will be a scalar or ``np.ndarray`` rather than a
masked array with ``mask=False``.

References
```

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```
.. [1] Hodges, J.L. Jr.,  "The Significance Probability of the Smirnov
       Two-Sample Test," Arkiv fiur Matematik, 3, No. 43 (1958), 469-486.

Examples
--------
Suppose we wish to test the null hypothesis that two samples were drawn
from the same distribution.
We choose a confidence level of 95%; that is, we will reject the null
hypothesis in favor of the alternative if the p-value is less than 0.05.

If the first sample were drawn from a uniform distribution and the second
were drawn from the standard normal, we would expect the null hypothesis
to be rejected.

>>> import numpy as np
>>> from scipy import stats
>>> rng = np.random.default_rng()
>>> sample1 = stats.uniform.rvs(size=100, random_state=rng)
>>> sample2 = stats.norm.rvs(size=110, random_state=rng)
>>> stats.ks_2samp(sample1, sample2)
KstestResult(statistic=0.5454545454545454,
             pvalue=7.37417839555191e-15,
             statistic_location=-0.014071496412861274,
             statistic_sign=-1)

Indeed, the p-value is lower than our threshold of 0.05, so we reject the
null hypothesis in favor of the default "two-sided" alternative: the data
were *not* drawn from the same distribution.

When both samples are drawn from the same distribution, we expect the data
to be consistent with the null hypothesis most of the time.

>>> sample1 = stats.norm.rvs(size=105, random_state=rng)
>>> sample2 = stats.norm.rvs(size=95, random_state=rng)
>>> stats.ks_2samp(sample1, sample2)
KstestResult(statistic=0.10927318295739348,
             pvalue=0.5438289009927495,
             statistic_location=-0.1670157701848795,
             statistic_sign=-1)

As expected, the p-value of 0.54 is not below our threshold of 0.05, so
we cannot reject the null hypothesis.

Suppose, however, that the first sample were drawn from
a normal distribution shifted toward greater values. In this case,
the cumulative density function (CDF) of the underlying distribution tends
to be *less* than the CDF underlying the second sample. Therefore, we would
expect the null hypothesis to be rejected with ``alternative='less'``:

>>> sample1 = stats.norm.rvs(size=105, loc=0.5, random_state=rng)
>>> stats.ks_2samp(sample1, sample2, alternative='less')
KstestResult(statistic=0.4055137844611529,
             pvalue=3.5474563068855554e-08,
             statistic_location=-0.13249370614972575,
             statistic_sign=-1)

and indeed, with p-value smaller than our threshold, we reject the null
hypothesis in favor of the alternative.
File:      ~/workbench/dsc80/.venv/lib/python3.12/site-packages/scipy/stats/_stats_py.py
Type:      function
```

In [28]:
```python
observed_ks = ks_2samp(data.loc[data['group'] == 'A', 'data'], data.loc[data['group'] == 'B',
observed_ks
```

Out[28]:
```
np.float64(0.14)
```

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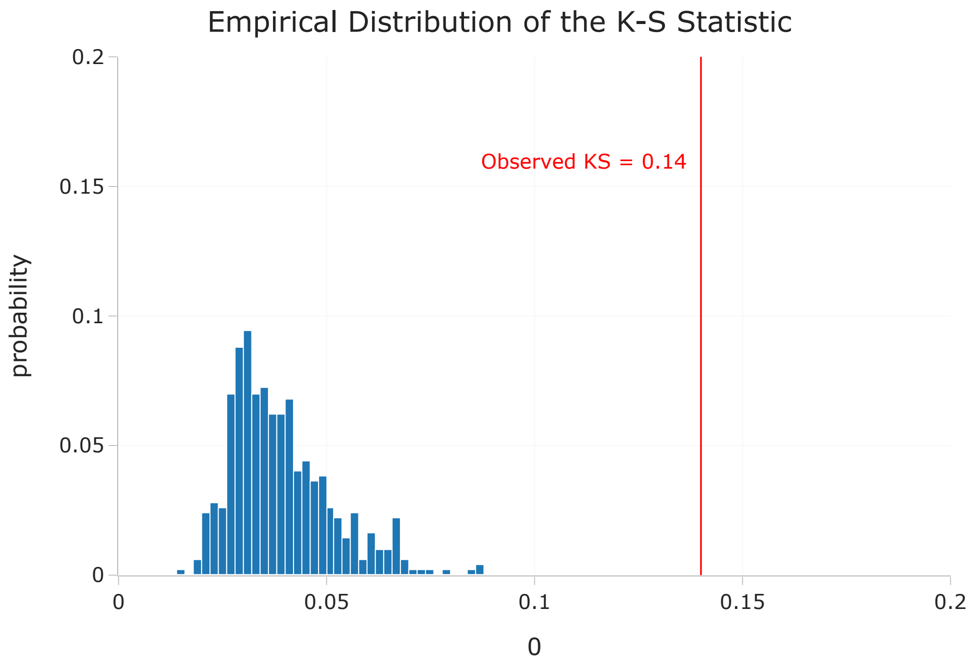
We don't know if this number is big or small. We need to run a permutation test!

In [29]:
```python
n_repetitions = 500
shuffled = data.copy()

ks_stats = []
for _ in range(n_repetitions):

    # Shuffling the data.
    shuffled['data'] = np.random.permutation(shuffled['data'])

    # Computing and storing the K-S statistic.
    groups = shuffled.groupby('group')['data']
    ks_stat = ks_2samp(groups.get_group('A'), groups.get_group('B')).statistic
    ks_stats.append(ks_stat)

ks_stats[:10]
```

Out[29]:
```
[np.float64(0.037),
 np.float64(0.048),
 np.float64(0.04),
 np.float64(0.068),
 np.float64(0.045),
 np.float64(0.04),
 np.float64(0.042),
 np.float64(0.052),
 np.float64(0.019),
 np.float64(0.029)]
```

In [30]:
```python
fig = px.histogram(pd.DataFrame(ks_stats), x=0, nbins=50, histnorm='probability',
                   title='Empirical Distribution of the K-S Statistic')
fig.add_vline(x=observed_ks, line_color='red', line_width=1, opacity=1)
fig.add_annotation(text=f'<span style="color:red">Observed KS = {round(observed_ks, 2)}</span>
                   x=0.8 * observed_ks, showarrow=False, y=0.16)

fig.update_layout(xaxis_range=[0, 0.2])
fig.update_layout(yaxis_range=[0, 0.2])
```



In [31]:
```python
np.mean(np.array(ks_stats) >= observed_ks)
```

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We were able to differentiate between the two distributions using the K-S test statistic!

`ks_2samp`

- `scipy.stats.ks_2samp` actually returns **both** the statistic **and** a p-value.
- The p-value is calculated using the permutation test we just performed!

In [32]:
```
ks_2samp(data.loc[data['group'] == 'A', 'data'], data.loc[data['group'] == 'B', 'data'])
```

Out[32]:
```
KstestResult(statistic=np.float64(0.14), pvalue=np.float64(5.822752148022591e-09), statistic_
location=np.float64(0.9755451271223592), statistic_sign=np.int8(1))
```

Difference in means vs. K-S statistic

- The K-S statistic measures the difference between two numerical distributions.

- It **does not** quantify if one is larger than the other on average, so there are times we still need to use the difference in means.

- Strategy: Always plot the two distributions you are comparing.
  - If the distributions have similar shapes but are centered in different places, use the difference in means (or absolute difference in means).
  - If your alternative hypothesis involves a "direction" (i.e. smoking weights were are on average than non-smoking weights), use the difference in means.
  - If the distributions have different shapes but roughly the same center, and your alternative hypothesis is simply that the two distributions are different, use the K-S statistic.

Back to our Example: Missingness of `'child'` heights on `'father'`'s heights (MAR)

In [33]:
```
heights_mar['child_missing'] = heights_mar['child'].isna()
create_kde_plotly(heights_mar[['child_missing', 'father']], 'child_missing', True, False, 'fat
                      "Father's Height by Missingness of Child Height (MAR example)")
```

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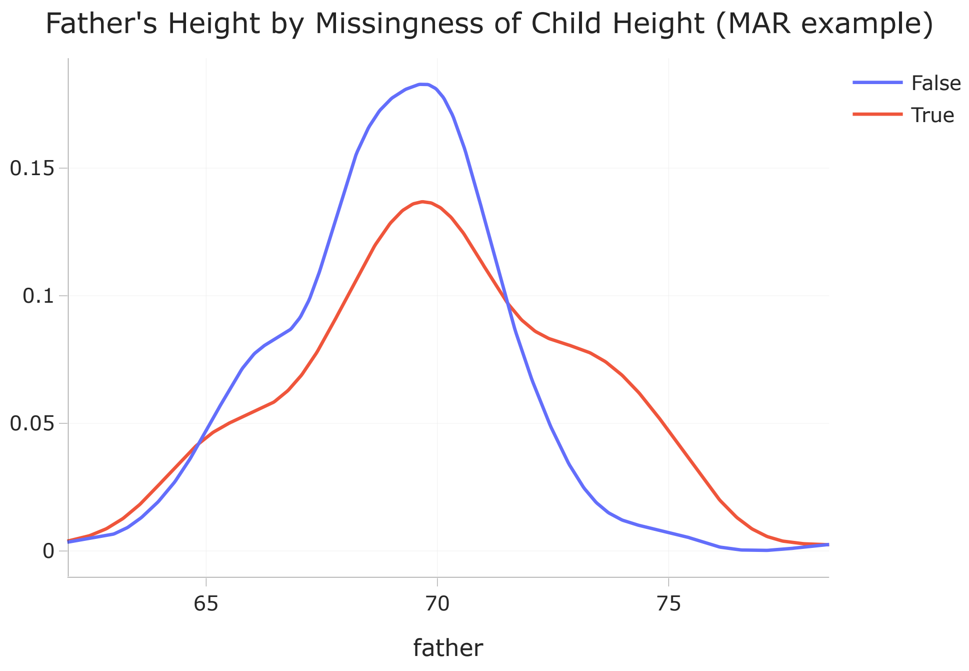

- The above picture shows us that missing `'child'` heights tend to come from taller `'father'`s heights.
- To determine whether the two distributions are significantly different, we must use a permutation test. This time, the difference in means is not a good choice, since the centers are similar but the shapes are different.

Performing the test

In [34]:
```
heights_mar
```

Out[34]:

	father	mother	gender	child	child_missing
0	78.5	67.0	male	NaN	True
1	78.5	67.0	female	69.2	False
2	78.5	67.0	female	69.0	False
...	...	...	...	...	...
931	62.0	66.0	female	61.0	False
932	62.5	63.0	male	66.5	False
933	62.5	63.0	female	57.0	False

934 rows × 5 columns

In [35]:
```
ks_2samp(heights_mar.query('child_missing')['father'], heights_mar.query('not child_missing')[
```

Out[35]:
```
KstestResult(statistic=np.float64(0.20676025834396874), pvalue=np.float64(1.1424922868036869e
-05), statistic_location=np.float64(72.0), statistic_sign=np.int8(-1))
```

The p-value is very small, so we conclude that the child height is MAR, conditional on the father's height.

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Handling missing values

What do we do with missing data?

- Suppose we are interested in a dataset Y.
- We get to **observe** Y_{obs}, while the rest of the dataset, Y_{mis}, is **missing**.
- Issue: Y_{obs} may look quite different than Y.
  - The mean and other measures of central tendency may be different.
  - The variance may be different.
  - The correlations between variables may be different.

Solution 1: Dropping missing values

- If the data are MCAR (missing completely at random), then dropping the missing values entirely doesn't significantly change the data.
  - For instance, the mean of the dataset post-dropping is an unbiased estimate of the true mean.
  - This is because MCAR data is a **random sample** of the full dataset.
  - From DSC 10, we know that random samples tend to resemble the larger populations they are drawn from.

- **If the data are not MCAR, then dropping the missing values will introduce bias.**
  - MCAR is rare!
  - For instance, suppose we asked people "How much do you give to charity?" People who give little are less likely to respond, so the average response is **biased high**.

Listwise deletion

- *Listwise deletion* is the act of dropping entire rows that contain missing values.
- Issue: This can delete perfectly good data in other columns for a given row.
  - Improvement: Drop missing data only when working with the column that contains missing data.

To illustrate, let's generate two datasets with missing `'child'` heights – one in which the heights are MCAR, and one in which they are MAR dependent on `'gender'` only.

In practice, you'll have to run permutation tests to determine the likely missingness mechanism first!

In [36]:
```
np.random.seed(42) # So that we get the same results each time (for lecture).
heights_mcar = make_mcar(heights, 'child', pct=0.5)
heights_mar = make_mar_on_cat(heights, 'child', 'gender', pct=0.5)
```

Listwise deletion

Below, we compute the means and standard deviations of the `'child'` column in all three datasets. Remember, `.mean()` and `.std()` ignore missing values.

In [37]:
```
multiple_describe({
    'Original': heights,
    'MCAR': heights_mcar,
    'MAR': heights_mar
})
```

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Out[37]:

Dataset	Mean	Standard Deviation
Original	66.75	3.58
MCAR	66.64	3.56
MAR	68.52	3.12

Observations:

- The `'child'` mean (and SD) in the MCAR dataset is very close to the true `'child'` mean (and SD).
- The `'child'` mean in the MAR dataset is biased **high**.

Solution 2: Imputation

Imputation is the act of filling in missing data with plausable values. Ideally, imputation:

- is quick and easy to do.
- shouldn't introduce bias into the dataset.

These are hard to do at the same time!

Kinds of imputation

- There are three main types of imputation, two of which we will focus on today:
  - **Imputation with a single value: mean, median, mode.**
  - Imputation with a single value, using a model: regression, kNN.
  - **Probabilistic imputation by drawing from a distribution.**
- Each has upsides and downsides, and **each works differently with different types of missingness**.

Mean imputation

Mean imputation

- Mean imputation is the act of filling in missing values in a column with the mean of the observed values in that column.
- This strategy:
  - 👍 Preserves the mean of the observed data, for all types of missingness.
  - 👎 Decreases the variance of the data, for all types of missingness.
  - 👎 Creates a biased estimate of the true mean when the data are not MCAR.

Example: Mean imputation in the MCAR `heights` dataset

Let's look at two distributions:

- The distribution of the `'child'` column in `heights`, where we have all the data.
- The distribution of the `'child'` column in `heights_mcar`, where some values are MCAR.

In [38]:

```
# Look in util.py to see how multiple_kdes is defined.
multiple_kdes({'Original': heights, 'MCAR, Unfilled': heights_mcar})
```

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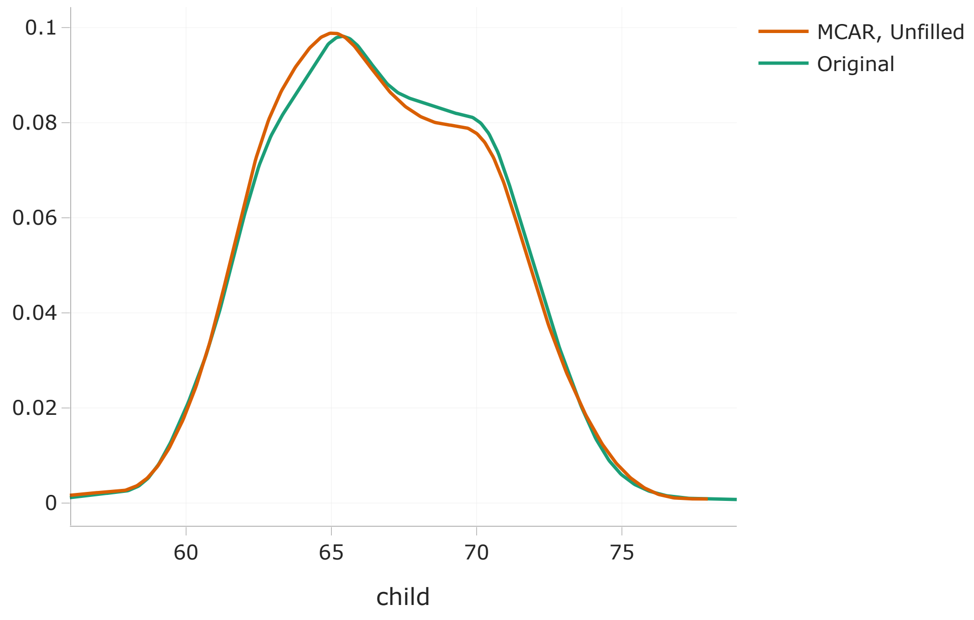

- Since the `'child'` heights are MCAR, the **orange distribution, in which some values are missing**, has roughly the same shape as the **turquoise distribution, which has no missing values**.

Mean imputation of MCAR data

Let's fill in missing values in `heights_mcar['child']` with the mean of the observed `'child'` heights in `heights_mcar['child']`.

In [39]:
```
heights_mcar['child'].head()
```

Out[39]:
```
0    73.2
1    69.2
2     NaN
3     NaN
4    73.5
Name: child, dtype: float64
```

In [40]:
```
heights_mcar_mfilled = heights_mcar.fillna(heights_mcar['child'].mean())
heights_mcar_mfilled['child'].head()
```

Out[40]:
```
0    73.20
1    69.20
2    66.64
3    66.64
4    73.50
Name: child, dtype: float64
```

In [41]:
```
df_map = {'Original': heights, 'MCAR, Unfilled': heights_mcar, 'MCAR, Mean Imputed': heights_m
multiple_describe(df_map)
```

Out[41]:

Dataset	Mean	Standard Deviation
Original	66.75	3.58
MCAR, Unfilled	66.64	3.56
MCAR, Mean Imputed	66.64	2.52

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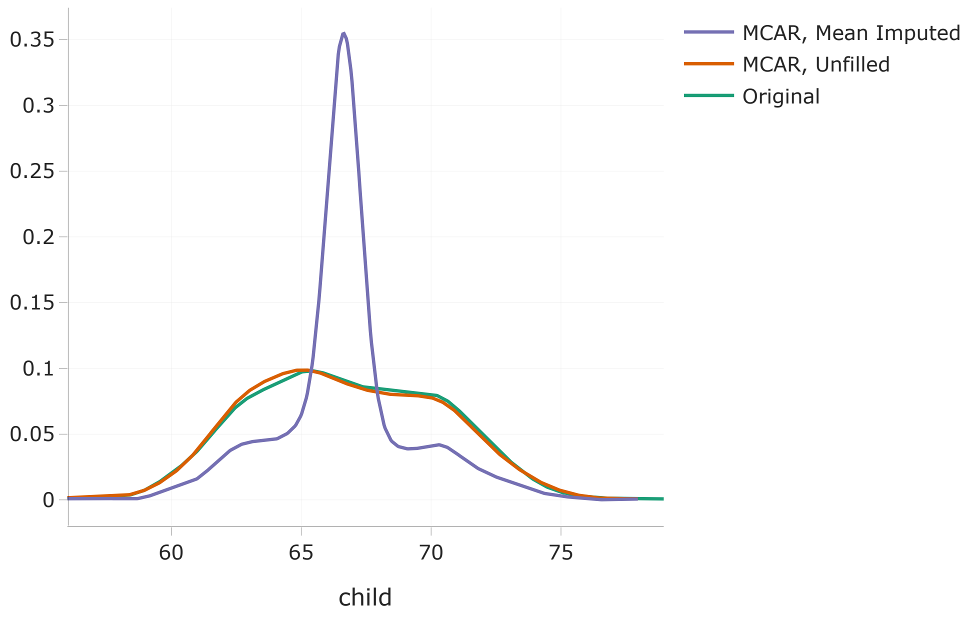
Observations:

- The mean of the imputed dataset is the same as the mean of the subset of heights that aren't missing (which is close to the true mean).
- The standard deviation of the imputed dataset smaller than that of the other two datasets. **Why?**

Mean imputation of MCAR data

Let's visualize all three distributions: the original, the MCAR heights with missing values, and the mean-imputed MCAR heights.

```
In [42]: multiple_kdes(df_map)
```



Takeaway: When data are MCAR and you impute with the mean:

- The mean of the imputed dataset is an **unbiased estimator** of the true mean.
- The variance of the imputed dataset is smaller than the variance of the full dataset.
  - Mean imputation tricks you into thinking your data are more reliable than they are!

Example: Mean imputation in the MAR `heights` dataset

- When data are MAR, mean imputation leads to biased estimates of the mean across groups.
- The bias may be different in different groups.
  - For example: If the missingness depends on gender, then different genders will have differently-biased means.
  - The overall mean will be biased towards one group.
- Again, let's look at two distributions:
  - The distribution of the `'child'` column in `heights`, where we have all the data.
  - The distribution of the `'child'` column in `heights_mar`, where some values are MAR.

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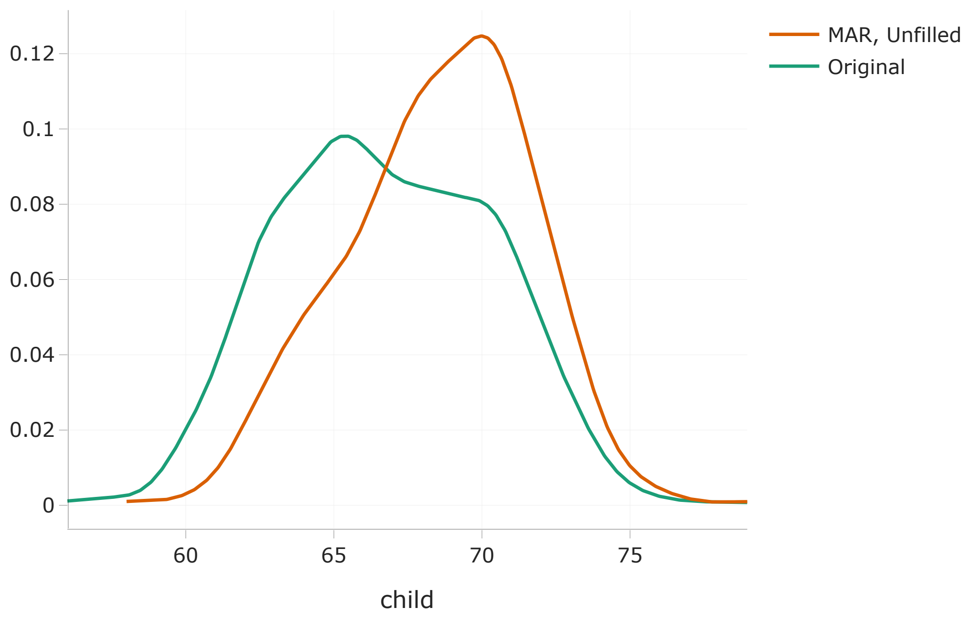
```
In [43]: multiple_kdes({'Original': heights, 'MAR, Unfilled': heights_mar})
```



The distributions are not very similar!

Remember that in reality, you won't get to see the **turquoise distribution, which has no missing values** – instead, you'll try to recreate it, using your sample with missing values.

Mean imputation of MAR data

Let's fill in missing values in `heights_mar['child']` with the mean of the observed `'child'` heights in `heights_mar['child']` and see what happens.

In [44]:
```
heights_mar['child'].head()
```

Out[44]:
```
0    73.2
1    69.2
2     NaN
3     NaN
4    73.5
Name: child, dtype: float64
```

In [45]:
```
heights_mar_mfilled = heights_mar.fillna(heights_mar['child'].mean())
heights_mar_mfilled['child'].head()
```

Out[45]:
```
0    73.20
1    69.20
2    68.52
3    68.52
4    73.50
Name: child, dtype: float64
```

In [46]:
```
df_map = {'Original': heights, 'MAR, Unfilled': heights_mar, 'MAR, Mean Imputed': heights_mar_
multiple_describe(df_map)
```

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Out[46]:

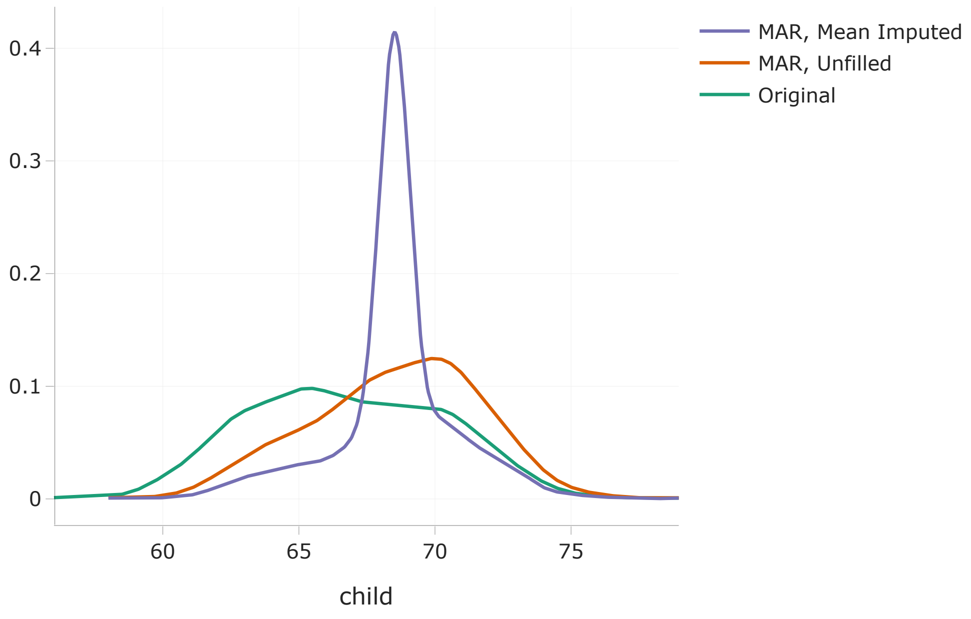
Dataset	Mean	Standard Deviation
Original	66.75	3.58
MAR, Unfilled	68.52	3.12
MAR, Mean Imputed	68.52	2.20

Note that the latter two means are biased **high**.

Mean imputation of MAR data

Let's visualize all three distributions: the original, the MAR heights with missing values, and the mean-imputed MAR heights.

In [47]:
```
multiple_kdes(df_map)
```



Since the sample with MAR values was already biased high, mean imputation kept the sample biased – it did not bring the data **closer to the data generating process**.

With our single mean imputation strategy, the resulting female mean height is biased quite high.

In [48]:
```
pd.concat([
    heights.groupby('gender')['child'].mean().rename('Original'),
    heights_mar.groupby('gender')['child'].mean().rename('MAR, Unfilled'),
    heights_mar_mfilled.groupby('gender')['child'].mean().rename('MAR, Mean Imputed')
], axis=1).T
```

Out[48]:

gender	female	male
Original	64.10	69.23
MAR, Unfilled	64.22	69.28
MAR, Mean Imputed	67.85	69.14

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Within-group (conditional) mean imputation

- **Improvement**: Since MAR data are MCAR within each group, we can perform group-wise mean imputation.
  - In our case, since the missingness of `'child'` is dependent on `'gender'`, we can impute separately for each `'gender'`.
  - For instance, if there is a missing `'child'` height for a `'female'` child, impute their height with the mean observed `'female'` height.
- With this technique, the overall mean remains unbiased, as do the within-group means.
- Like with "single" mean imputation, the variance of the dataset is reduced.

`transform` returns!

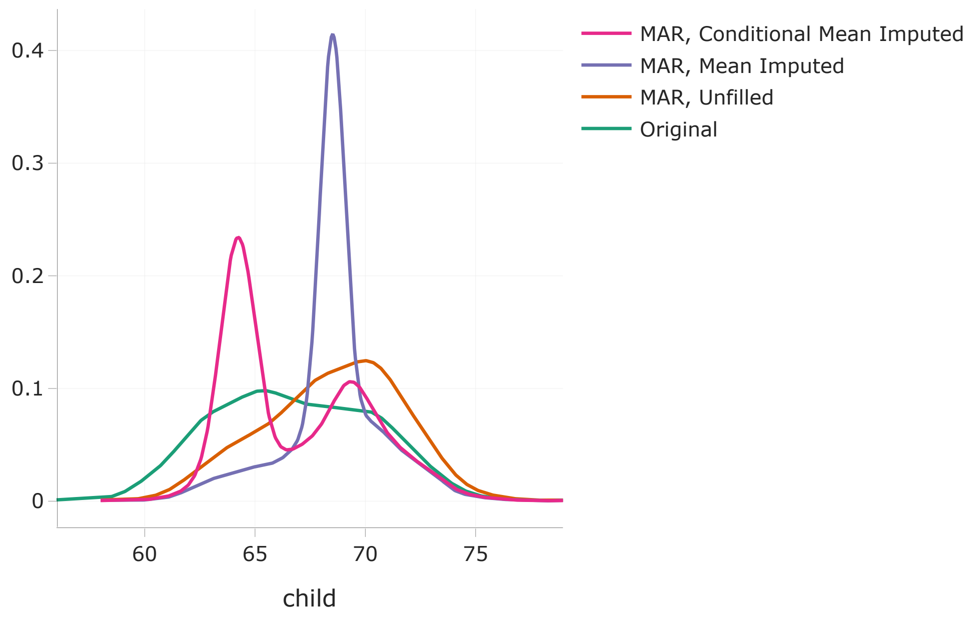
- In MAR data, imputation by the overall mean gives a biased estimate of the mean of each group.
- To obtain an unbiased estimate of the mean within each group, impute using the mean within each group.
- To perform an operation separately to each gender, we `groupby('gender')` and use the `transform` method.

In [49]:
```
def mean_impute(s):
    return s.fillna(s.mean())

heights_mar_cond = heights_mar.groupby('gender')['child'].transform(mean_impute).to_frame()
heights_mar_cond['child'].head()
```

Out[49]:
```
0    73.20
1    69.20
2    64.22
3    64.22
4    73.50
Name: child, dtype: float64
```

In [50]:
```
df_map['MAR, Conditional Mean Imputed'] = heights_mar_cond
multiple_kdes(df_map)
```



The **pink distribution** does a slightly better job of approximating the **turquoise distribution** than the **purple** [Loading [MathJax]/extensions/Safe.js], but not by much.

Conclusion: Imputation with single values

- Imputing missing data in a column with the mean of the column:
  - faithfully reproduces the mean of the observed dataset,
  - reduces the variance, and
  - biases relationships between the column and other columns if the data are not MCAR.
- The same is true with other statistics (e.g. median and mode).

Probabilistic imputation

Imputing missing values using distributions

- So far, each missing value in a column has been filled in with a constant value.
  - This creates "spikes" in the imputed distributions.

- **Idea**: We can **probabilistically** impute missing data from a distribution.
  - We can fill in missing data by drawing from the distribution of the **non-missing** data.
  - There are 5 missing values? Pick 5 values from the data that aren't missing.
  - How? Using `np.random.choice` or `.sample`.

- If the data are MCAR, then sample from the entire column of present values. If the data are MAR on some categorical column, then sample from the present values separately for each category.

Example: Probabilistic imputation in the MAR `heights` dataset

Let's use `transform` to call `prob_impute` separately on each `'gender'`.

In [51]:
```
def prob_impute(s):
    s = s.copy()

    # Step 1: Find the number of missing child heights for that gender.
    num_null = s.isna().sum()

    # Step 2: Sample num_null observed child heights for that gender.
    fill_values = np.random.choice(s.dropna(), num_null)

    # Step 3: Fill in missing values and return ser.
    s[s.isna()] = fill_values
    return s
```

In [52]:
```
heights_mar_pfilled = heights_mar.copy()
heights_mar_pfilled['child'] = (
    heights_mar
    .groupby('gender')
    ['child']
    .transform(prob_impute)
)
heights_mar_pfilled['child'].head()
```

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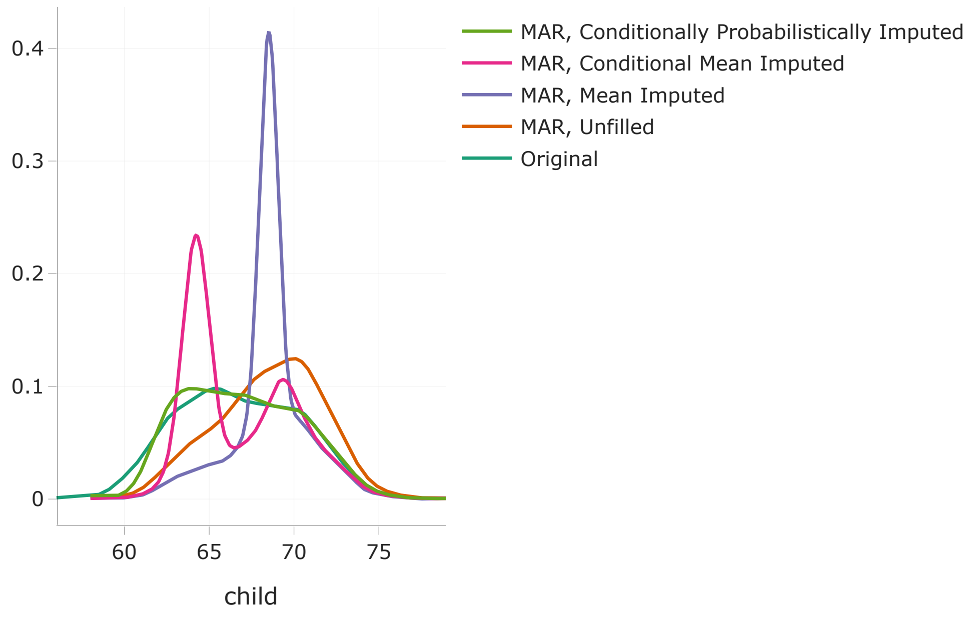
Out[52]:
```
0    73.2
1    69.2
2    62.0
3    62.5
4    73.5
Name: child, dtype: float64
```

In [53]:
```
df_map['MAR, Conditionally Probabilistically Imputed'] = heights_mar_pfilled
multiple_kdes(df_map)
```



The **green distribution (conditional probabilistic imputation)** does the best job of approximating the **turqoise distribution (the full dataset with no missing values)**!

Remember that the graph above is interactive – you can hide/show lines by clicking them in the legend.

Observations

- With this technique, the missing values were filled in with observed values in the dataset.
- If a value was never observed in the dataset, it will never be used to fill in a missing value.
    - For instance, if the observed heights were 68, 69, and 69.5 inches, we will never fill a missing value with 68.5 inches even though it's a perfectly reasonable height.
- Solution? Create a histogram (with `np.histogram`) to bin the data, then sample from the histogram.
    - See Lab 5, Question 6.

Randomness

- Unlike mean imputation, probabilistic imputation is **random** – each time you run the cell in which imputation is performed, the results could be different.
- If we're interested in estimating some population **parameter** given our (incomplete) sample, it's best not to rely on just a single random imputation.
- **Multiple imputation**: Generate multiple imputed datasets and aggregate the results!

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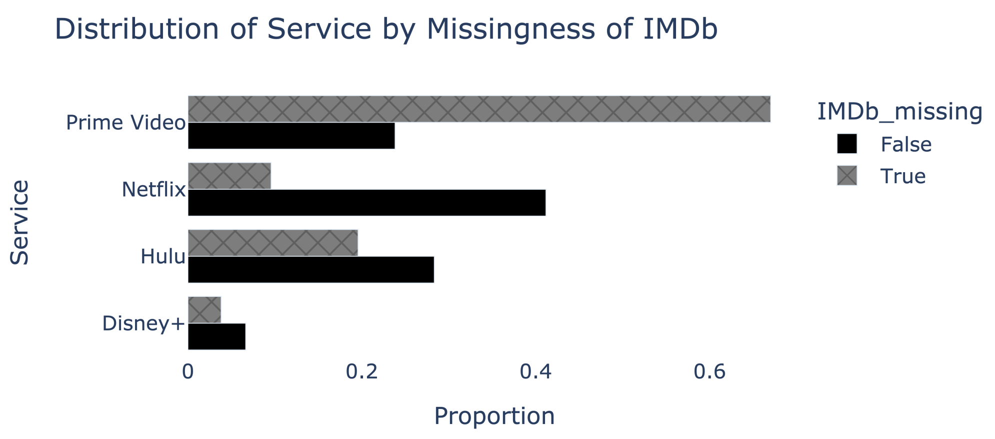
- Similar to bootstrapping.

Question 🤔

Taken from the Winter 2023 DSC 80 Midterm Exam.

To determine whether the missingness of `"IMDb"` depends on `"Service"`, we produce the following plot.



We'd like to fill in missing "IMDb" values in the fastest, most efficient way possible, such that the mean of the imputed "IMDb" column is as close to the true mean of the "IMDb" column in nature as possible. Which imputation technique should we use?

A. Unconditional mean imputation

B. Mean imputation, conditional on "Service"

C. Unconditional probabilistic imputation

D. Probabilistic imputation, conditional on "Service"

Summary, next time

Summary of imputation techniques

- Listwise deletion.
- Mean imputation.
- Group-wise (conditional) mean imputation.
- Probabilistic imputation.
- Multiple imputation.

Summary: Listwise deletion

- Procedure: `df = df.dropna()`.
- If data are MCAR, listwise deletion doesn't change most summary statistics (mean, median, SD) of the data.

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y: Mean imputation

- Procedure: `df[col] = df[col].fillna(df[col].mean())`.
- If data are MCAR, the resulting mean is an unbiased estimate of the true mean, but the variance is too low.
- Analogue for categorical data: imputation with the mode.

Summary: Conditional mean imputation

- Procedure: for a column `c1`, conditional on a second categorical column

`c2`:

```
means = df.groupby('c2').mean().to_dict()
imputed = df['c1'].apply(lambda x: means[x] if np.isnan(x) else x)
```

- If data are MAR, the resulting mean is an unbiased estimate of the true mean, but the variance is too low.
- This increases correlations between the columns.
- If the column with missing values were dependent on *more than one* column, we can use linear regression to predict the missing value.

Summary: Probabilistic imputation

- Procedure: draw from the distribution of **observed data** to fill in missing values.
- If data are MCAR, the resulting mean and variance are unbiased estimates of the true mean and variance.
- Extending to the MAR case: draw from **conditional empirical distributions**.
  - If data are conditional on a single categorical column `c2`, apply the MCAR procedure to the groups of `df.groupby(c2)`.

Summary: Multiple imputation

- Procedure:
  - Apply probabilistic imputation multiple times, resulting in m imputed datasets.
  - Compute statistics separately on the m imputed datasets (e.g. compute the mean or correlation coefficient).
  - Plot the distribution of these statistics and create confidence intervals.
- If a column is missing conditional on multiple columns, your "multiple imputations" should include probabilistic imputations for each!

Next time

- Introduction to HTTP.
- Making requests.

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