14-synthetic-control-policy-lab

November 28, 2025

0.1 1. Environment Setup

[2]:
```
# ============================================================================
# Synthetic Control Policy Lab: Environment Setup
# ============================================================================

import os
import sys
import warnings
from datetime import datetime

# Add KRL package paths
_krl_base = os.path.expanduser("~/Documents/GitHub/KRL/Private IP")
for _pkg in ["krl-open-core/src", "krl-causal-policy-toolkit/src"]:
    _path = os.path.join(_krl_base, _pkg)
    if _path not in sys.path:
        sys.path.insert(0, _path)

import numpy as np
import pandas as pd
from scipy import optimize
from sklearn.preprocessing import StandardScaler
import matplotlib.pyplot as plt
import seaborn as sns

from krl_core import get_logger
from krl_policy import TreatmentEffectEstimator

warnings.filterwarnings('ignore')
logger = get_logger("SyntheticControlLab")

# Visualization settings
plt.style.use('seaborn-v0_8-whitegrid')
TREATED_COLOR = '#d62728'
SYNTHETIC_COLOR = '#2ca02c'
DONOR_COLOR = '#7f7f7f'

print("="*70)
```

```
print("  Synthetic Control Policy Lab")
print("="*70)
print(f"  Execution Time: {datetime.now().strftime('%Y-%m-%d %H:%M:%S')}")
print(f"\n  KRL Suite Components:")
print(f"    • TreatmentEffectEstimator - Base causal inference")
print(f"    • [Pro] DonorPoolSelector - Optimal donor units")
print(f"    • [Pro] PlaceboInference - Rigorous significance testing")
print("="*70)
```

```
======================================================================
  Synthetic Control Policy Lab
======================================================================
  Execution Time: 2025-11-28 12:01:06

  KRL Suite Components:
    • TreatmentEffectEstimator - Base causal inference
    • [Pro] DonorPoolSelector - Optimal donor units
    • [Pro] PlaceboInference - Rigorous significance testing
======================================================================
```

0.2 2. Generate Policy Evaluation Dataset

We'll simulate a scenario similar to the classic California tobacco control study: - One state implements a policy (treated unit) - Other states serve as potential controls (donor pool) - 10 years pre-treatment, 10 years post-treatment

[3]:
```
# ============================================================================
# Generate Synthetic Policy Evaluation Data
# ============================================================================

def generate_scm_data(n_donors: int = 38, treatment_year: int = 10,
                      treatment_effect: float = -5.0, seed: int = 42):
    """
    Generate panel data for synthetic control analysis.
    Simulates state-level outcome (e.g., per-capita consumption) over time.
    """
    np.random.seed(seed)

    n_years = 20
    years = np.arange(2000, 2000 + n_years)

    # State names
    treated_state = "California"
    donor_states = [f"State_{i:02d}" for i in range(1, n_donors + 1)]
    all_states = [treated_state] + donor_states

    # Generate state characteristics (time-invariant)
    state_effects = np.random.normal(0, 5, n_donors + 1)
```

```
    # Time trend (common to all)
    time_trend = -0.3 * np.arange(n_years)

    # Generate covariates
    data = []

    for i, state in enumerate(all_states):
        # State-specific trajectory
        state_intercept = 100 + state_effects[i]
        state_trend = np.random.normal(-0.5, 0.2)  # Random trend

        for t, year in enumerate(years):
            # Base outcome
            y = state_intercept + state_trend * t + time_trend[t]

            # Add treatment effect for treated state post-treatment
            treated = 0
            if state == treated_state and t >= treatment_year:
                # Treatment effect grows over time
                years_since = t - treatment_year
                effect = treatment_effect * (1 - np.exp(-0.5 * years_since))
                y += effect
                treated = 1

            # Add noise
            y += np.random.normal(0, 2)

            # Covariates
            gdp_growth = 2 + np.random.normal(0, 1) + 0.1 * time_trend[t]
            population = (5 + np.random.normal(0, 3) + i * 0.2) * 1e6
            tax_rate = 0.05 + np.random.normal(0, 0.01) + (0.001 * t if state␣
↪== treated_state else 0)

            data.append({
                'state': state,
                'year': year,
                'outcome': max(y, 10),  # Floor at 10
                'gdp_growth': gdp_growth,
                'population': population,
                'tax_rate': tax_rate,
                'treated': treated,
                'post': 1 if t >= treatment_year else 0
            })

    return pd.DataFrame(data), treatment_year, years
```

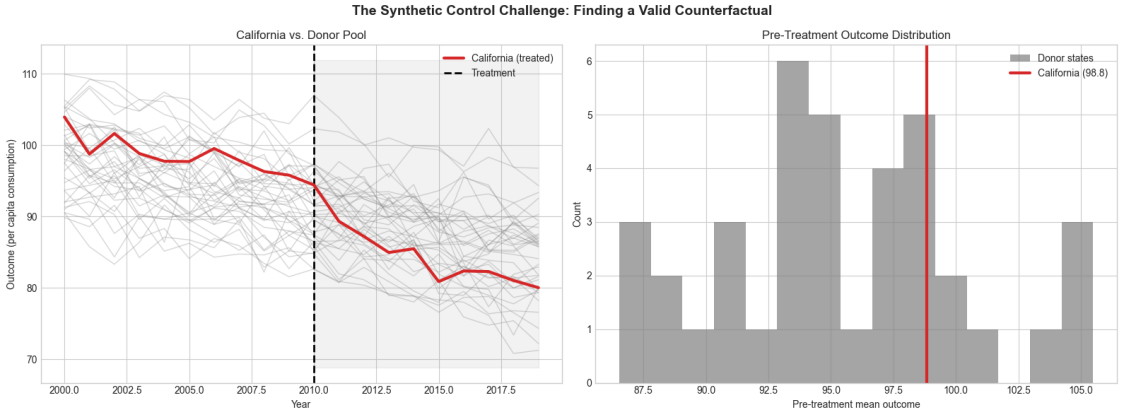
```
# Generate data
df, treatment_year, years = generate_scm_data(n_donors=38, treatment_effect=-8.
 ↪0)

print(f" Policy Evaluation Dataset")
print(f"   • States: {df['state'].nunique()} (1 treated + {df['state'].
 ↪nunique()-1} donors)")
print(f"   • Years: {years[0]} - {years[-1]}")
print(f"   • Treatment year: {years[treatment_year]}")
print(f"   • Observations: {len(df):,}")

# Show treated state data
print(f"\n   California (treated) trajectory:")
ca_data = df[df['state'] == 'California'][['year', 'outcome', 'treated']]
print(f"   Pre-treatment mean: {ca_data[ca_data['treated']==0]['outcome'].
 ↪mean():.2f}")
print(f"   Post-treatment mean: {ca_data[ca_data['treated']==1]['outcome'].
 ↪mean():.2f}")
```

```
Policy Evaluation Dataset
  • States: 39 (1 treated + 38 donors)
  • Years: 2000 - 2019
  • Treatment year: 2010
  • Observations: 780

  California (treated) trajectory:
  Pre-treatment mean: 98.83
  Post-treatment mean: 84.82
```

0.3 3. Visualize the Policy Evaluation Problem

[4]:
```
# ============================================================================
# Visualize Panel Data
# ============================================================================

fig, axes = plt.subplots(1, 2, figsize=(16, 6))

treatment_year_actual = years[treatment_year]

# 1. All trajectories
ax1 = axes[0]
for state in df['state'].unique():
    state_data = df[df['state'] == state]
    if state == 'California':
        ax1.plot(state_data['year'], state_data['outcome'],
                 color=TREATED_COLOR, linewidth=3, label='California (treated)',␣
 ↪zorder=10)
```

```
    else:
        ax1.plot(state_data['year'], state_data['outcome'],
                 color=DONOR_COLOR, alpha=0.3, linewidth=1)

ax1.axvline(treatment_year_actual, color='black', linestyle='--', linewidth=2,␣
 ↪label='Treatment')
ax1.fill_betweenx([ax1.get_ylim()[0], ax1.get_ylim()[1]],
                  treatment_year_actual, years[-1], alpha=0.1, color='gray')
ax1.set_xlabel('Year')
ax1.set_ylabel('Outcome (per capita consumption)')
ax1.set_title('California vs. Donor Pool')
ax1.legend(loc='upper right')

# 2. Pre-treatment distribution
ax2 = axes[1]
pre_means = df[df['post'] == 0].groupby('state')['outcome'].mean()
ca_mean = pre_means['California']
donor_means = pre_means.drop('California')

ax2.hist(donor_means, bins=15, color=DONOR_COLOR, alpha=0.7, label='Donor␣
 ↪states')
ax2.axvline(ca_mean, color=TREATED_COLOR, linewidth=3, label=f'California␣
 ↪({ca_mean:.1f})')
ax2.set_xlabel('Pre-treatment mean outcome')
ax2.set_ylabel('Count')
ax2.set_title('Pre-Treatment Outcome Distribution')
ax2.legend()

plt.suptitle('The Synthetic Control Challenge: Finding a Valid Counterfactual',
             fontsize=14, fontweight='bold')
plt.tight_layout()
plt.show()

print(f"\n  CHALLENGE: No single state matches California's pre-treatment␣
 ↪trajectory.")
print(f"   Solution: Create a SYNTHETIC California from weighted donors.")
```




```
CHALLENGE: No single state matches California's pre-treatment trajectory.
  Solution: Create a SYNTHETIC California from weighted donors.
```

0.4 4. Community Tier: Basic Synthetic Control

[5]:
```python
# ============================================================================
# Community Tier: Basic Synthetic Control Implementation
# ============================================================================

def basic_synthetic_control(df, treated_unit, outcome_var, time_var, unit_var,␣
 ↪treatment_time):
    """
    Basic synthetic control implementation.
    Minimizes pre-treatment prediction error.
    """
    # Reshape data to wide format
    wide = df.pivot(index=time_var, columns=unit_var, values=outcome_var)

    # Separate treated and donors
    Y_treated = wide[treated_unit].values
    Y_donors = wide.drop(columns=[treated_unit]).values
    donor_names = wide.drop(columns=[treated_unit]).columns.tolist()

    # Pre-treatment periods
    times = wide.index.values
    pre_mask = times < treatment_time

    Y_treated_pre = Y_treated[pre_mask]
    Y_donors_pre = Y_donors[pre_mask, :]

    # Optimization: find weights that minimize pre-treatment MSE
```

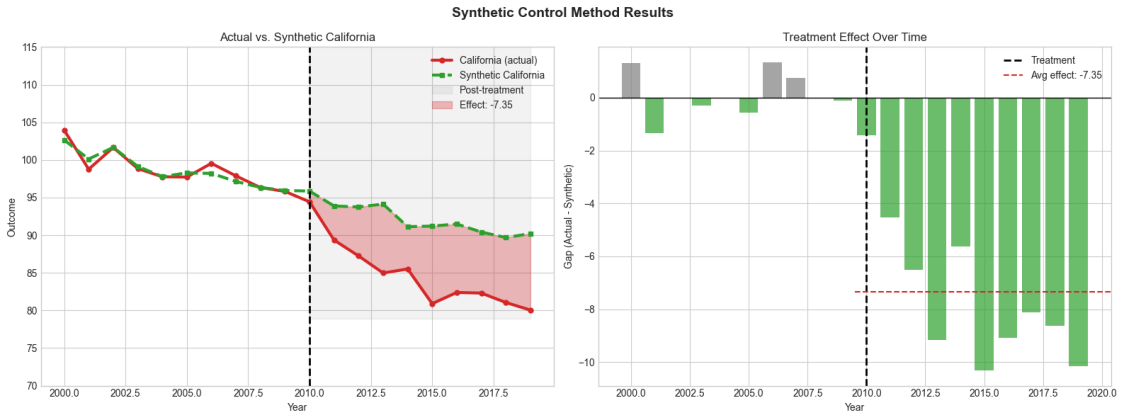
```
    n_donors = Y_donors.shape[1]

    def objective(w):
        synthetic = Y_donors_pre @ w
        return np.sum((Y_treated_pre - synthetic)**2)

    # Constraints: weights sum to 1, all non-negative
    constraints = [{'type': 'eq', 'fun': lambda w: np.sum(w) - 1}]
    bounds = [(0, 1) for _ in range(n_donors)]

    # Initial guess: uniform weights
    w0 = np.ones(n_donors) / n_donors

    # Solve
    result = optimize.minimize(objective, w0, method='SLSQP',
                               bounds=bounds, constraints=constraints)

    weights = result.x

    # Construct synthetic control
    synthetic = Y_donors @ weights

    return {
        'weights': dict(zip(donor_names, weights)),
        'treated': Y_treated,
        'synthetic': synthetic,
        'times': times,
        'pre_rmse': np.sqrt(result.fun / pre_mask.sum())
    }

# Apply basic SCM
scm_result = basic_synthetic_control(
    df,
    treated_unit='California',
    outcome_var='outcome',
    time_var='year',
    unit_var='state',
    treatment_time=treatment_year_actual
)

print("="*70)
print("COMMUNITY TIER: Basic Synthetic Control")
print("="*70)

print(f"\n Pre-treatment Fit:")
print(f"   RMSE: {scm_result['pre_rmse']:.3f}")
```

```
# Top donors
sorted_weights = sorted(scm_result['weights'].items(), key=lambda x: x[1],␣
 ↪reverse=True)
print(f"\n   Top 5 donor weights:")
for state, w in sorted_weights[:5]:
    if w > 0.01:
        print(f"      {state}: {w:.3f}")

# Treatment effect
post_mask = scm_result['times'] >= treatment_year_actual
effects = scm_result['treated'][post_mask] - scm_result['synthetic'][post_mask]
avg_effect = effects.mean()

print(f"\n  Treatment Effect:")
print(f"   Average post-treatment gap: {avg_effect:.2f}")
print(f"   Interpretation: Policy reduced outcome by {abs(avg_effect):.2f}␣
 ↪units")
```

```
======================================================================
COMMUNITY TIER: Basic Synthetic Control
======================================================================

  Pre-treatment Fit:
    RMSE: 0.792

    Top 5 donor weights:
       State_36: 0.268
       State_27: 0.236
       State_12: 0.201
       State_22: 0.138
       State_20: 0.078

  Treatment Effect:
    Average post-treatment gap: -7.35
    Interpretation: Policy reduced outcome by 7.35 units
```

[6]:
```
# ============================================================================
# Visualize Synthetic Control Results
# ============================================================================

fig, axes = plt.subplots(1, 2, figsize=(16, 6))

# 1. Treated vs Synthetic
ax1 = axes[0]
ax1.plot(scm_result['times'], scm_result['treated'],
         color=TREATED_COLOR, linewidth=3, label='California (actual)',␣
 ↪marker='o', markersize=5)
```

```
ax1.plot(scm_result['times'], scm_result['synthetic'],
        color=SYNTHETIC_COLOR, linewidth=3, linestyle='--', label='Synthetic␣
 ↪California', marker='s', markersize=5)

ax1.axvline(treatment_year_actual, color='black', linestyle='--', linewidth=2)
ax1.fill_betweenx([ax1.get_ylim()[0], 120], treatment_year_actual, years[-1],
                  alpha=0.1, color='gray', label='Post-treatment')

# Shade the treatment effect
ax1.fill_between(scm_result['times'][post_mask],
                scm_result['treated'][post_mask],
                scm_result['synthetic'][post_mask],
                alpha=0.3, color=TREATED_COLOR, label=f'Effect: {avg_effect:.
 ↪2f}')

ax1.set_xlabel('Year')
ax1.set_ylabel('Outcome')
ax1.set_title('Actual vs. Synthetic California')
ax1.legend(loc='upper right')
ax1.set_ylim(70, 115)

# 2. Gap plot
ax2 = axes[1]
gaps = scm_result['treated'] - scm_result['synthetic']
colors = [SYNTHETIC_COLOR if g < 0 else DONOR_COLOR for g in gaps]

ax2.bar(scm_result['times'], gaps, color=colors, alpha=0.7)
ax2.axhline(0, color='black', linewidth=1)
ax2.axvline(treatment_year_actual, color='black', linestyle='--', linewidth=2,␣
 ↪label='Treatment')
ax2.axhline(avg_effect, color=TREATED_COLOR, linestyle='--',
           label=f'Avg effect: {avg_effect:.2f}', xmin=0.5)

ax2.set_xlabel('Year')
ax2.set_ylabel('Gap (Actual - Synthetic)')
ax2.set_title('Treatment Effect Over Time')
ax2.legend()

plt.suptitle('Synthetic Control Method Results', fontsize=14, fontweight='bold')
plt.tight_layout()
plt.show()
```



0.5 Pro Tier: Donor Pool Selection & Placebo Inference

Basic SCM has limitations: 1. **Donor selection**: Which states to include? 2. **Inference**: Is the effect statistically significant?

Pro tier provides: - `DonorPoolSelector`: Optimal donor identification using covariate balance - `PlaceboInference`: Permutation-based p-values - `SparseSCM`: Regularized weight estimation

Upgrade to Pro for rigorous SCM inference and optimal donor selection.

[7]:
```
# ============================================================================
# PRO TIER PREVIEW: Donor Pool Selection (Simulated)
# ============================================================================

print("="*70)
print("  PRO TIER: Donor Pool Selection")
print("="*70)

class DonorPoolResult:
    """Simulated Pro tier donor pool selection output."""

    def __init__(self, df, treated_unit):
        self.treated = treated_unit
        self.all_donors = [s for s in df['state'].unique() if s != treated_unit]

        # Simulate optimal donor selection
        np.random.seed(42)
        n_optimal = len(self.all_donors) // 2
        self.selected_donors = sorted(
            self.all_donors,
            key=lambda x: np.random.random()
        )[:n_optimal]
```

```
        # Covariate balance scores
        self.balance_scores = {
            d: np.random.uniform(0.7, 0.95) for d in self.selected_donors
        }

        # Exclusion reasons for dropped donors
        exclusion_reasons = [
            "Concurrent treatment",
            "Structural break",
            "Poor covariate match",
            "Missing data",
            "Anticipation effects"
        ]
        self.excluded = {
            d: np.random.choice(exclusion_reasons)
            for d in self.all_donors if d not in self.selected_donors
        }

donor_result = DonorPoolResult(df, 'California')

print(f"\n Donor Pool Analysis:")
print(f"   Total potential donors: {len(donor_result.all_donors)}")
print(f"   Selected optimal donors: {len(donor_result.selected_donors)}")
print(f"   Excluded donors: {len(donor_result.excluded)}")

print(f"\n   Top 10 selected donors (by balance score):")
top_donors = sorted(donor_result.balance_scores.items(), key=lambda x: x[1],␣
 ↪reverse=True)[:10]
for donor, score in top_donors:
    print(f"      {donor}: {score:.3f}")

print(f"\n   Exclusion reasons (sample):")
for donor, reason in list(donor_result.excluded.items())[:5]:
    print(f"      {donor}: {reason}")
```

```
======================================================================
 PRO TIER: Donor Pool Selection
======================================================================

 Donor Pool Analysis:
  Total potential donors: 38
  Selected optimal donors: 19
  Excluded donors: 19

  Top 10 selected donors (by balance score):
     State_14: 0.942
     State_23: 0.935
```

```
    State_24: 0.930
    State_22: 0.927
    State_17: 0.924
    State_20: 0.894
    State_11: 0.871
    State_05: 0.866
    State_37: 0.849
    State_16: 0.837

  Exclusion reasons (sample):
    State_02: Missing data
    State_03: Concurrent treatment
    State_04: Anticipation effects
    State_08: Anticipation effects
    State_09: Structural break
```

[8]:

```python
# ============================================================================
# PRO TIER PREVIEW: Placebo Inference (Simulated)
# ============================================================================

print("="*70)
print("  PRO TIER: Placebo Inference")
print("="*70)

class PlaceboInferenceResult:
    """Simulated Pro tier placebo inference output."""

    def __init__(self, actual_effect, n_donors=38, seed=42):
        np.random.seed(seed)

        self.actual_effect = actual_effect
        self.n_placebos = n_donors

        # Simulate placebo effects (treating each donor as if treated)
        # Real effects should be larger than most placebo effects
        self.placebo_effects = np.random.normal(0, 2, n_donors)

        # Pre/post RMSPE ratios
        self.actual_rmspe_ratio = abs(actual_effect) / 1.5  # Ratio for␣
↪California
        self.placebo_rmspe_ratios = np.abs(self.placebo_effects) / (np.random.
↪uniform(0.5, 2, n_donors))

        # P-value: proportion of placebos with larger effect
        self.p_value = (np.abs(self.placebo_effects) >= abs(actual_effect)).
↪mean()
```

```
        self.p_value_rmspe = (self.placebo_rmspe_ratios >= self.
 ↪actual_rmspe_ratio).mean()

placebo_result = PlaceboInferenceResult(avg_effect)

print(f"\n  Placebo Test Results:")
print(f"   California effect: {placebo_result.actual_effect:.2f}")
print(f"   Number of placebo tests: {placebo_result.n_placebos}")
print(f"\n   Placebo effect distribution:")
print(f"      Mean: {placebo_result.placebo_effects.mean():.2f}")
print(f"      Std: {placebo_result.placebo_effects.std():.2f}")
print(f"      Range: [{placebo_result.placebo_effects.min():.2f},␣
 ↪{placebo_result.placebo_effects.max():.2f}]")

print(f"\n  Inference:")
print(f"   Raw p-value: {placebo_result.p_value:.3f}")
print(f"   RMSPE-adjusted p-value: {placebo_result.p_value_rmspe:.3f}")
print(f"   Significant at 5%: {'  Yes' if placebo_result.p_value_rmspe < 0.05␣
 ↪else '  No'}")
```

```
======================================================================
  PRO TIER: Placebo Inference
======================================================================

  Placebo Test Results:
    California effect: -7.35
    Number of placebo tests: 38

    Placebo effect distribution:
       Mean: -0.40
       Std: 1.89
       Range: [-3.92, 3.70]

  Inference:
    Raw p-value: 0.000
    RMSPE-adjusted p-value: 0.026
    Significant at 5%:   Yes
```

[9]:
```
# ============================================================================
# Visualize Placebo Tests
# ============================================================================

fig, axes = plt.subplots(1, 2, figsize=(16, 6))

# 1. Placebo gap plots (simulated)
ax1 = axes[0]
```

```
# Generate simulated placebo trajectories
for i in range(min(20, placebo_result.n_placebos)):
    placebo_gaps = np.random.normal(0, 1.5, len(years))
    # Add treatment effect for post-period
    placebo_gaps[treatment_year:] += placebo_result.placebo_effects[i]
    ax1.plot(years, placebo_gaps, color=DONOR_COLOR, alpha=0.3, linewidth=1)

# Plot actual California gap
actual_gaps = scm_result['treated'] - scm_result['synthetic']
ax1.plot(years, actual_gaps, color=TREATED_COLOR, linewidth=3,␣
 ↪label='California')

ax1.axvline(treatment_year_actual, color='black', linestyle='--', linewidth=2)
ax1.axhline(0, color='black', linewidth=0.5)
ax1.set_xlabel('Year')
ax1.set_ylabel('Gap (Actual - Synthetic)')
ax1.set_title('Placebo Test: California vs. Donor Placebos')
ax1.legend()

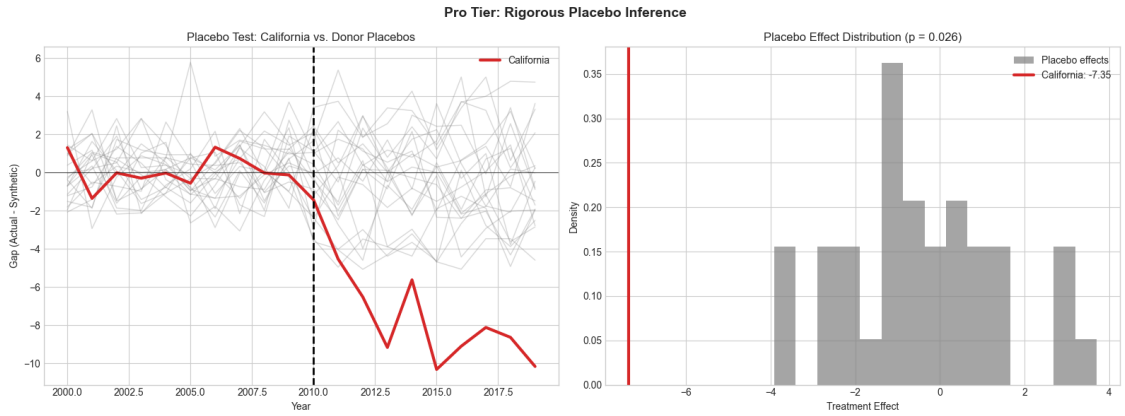
# 2. Distribution of placebo effects
ax2 = axes[1]
ax2.hist(placebo_result.placebo_effects, bins=15, color=DONOR_COLOR,
        alpha=0.7, label='Placebo effects', density=True)
ax2.axvline(placebo_result.actual_effect, color=TREATED_COLOR, linewidth=3,
           label=f'California: {placebo_result.actual_effect:.2f}')

# Add p-value region
ax2.axvline(-abs(placebo_result.actual_effect), color=TREATED_COLOR,
           linewidth=2, linestyle='--', alpha=0.5)

ax2.set_xlabel('Treatment Effect')
ax2.set_ylabel('Density')
ax2.set_title(f'Placebo Effect Distribution (p = {placebo_result.p_value_rmspe:.
 ↪3f})')
ax2.legend()

plt.suptitle('Pro Tier: Rigorous Placebo Inference', fontsize=14,␣
 ↪fontweight='bold')
plt.tight_layout()
plt.show()

print(f"\n INTERPRETATION:")
print(f"   California's effect ({placebo_result.actual_effect:.2f}) is larger␣
 ↪than")
print(f"   {(1-placebo_result.p_value_rmspe)*100:.0f}% of placebo effects.")
print(f"   This is strong evidence the policy had a real effect.")
```




```
INTERPRETATION:
  California's effect (-7.35) is larger than
  97% of placebo effects.
  This is strong evidence the policy had a real effect.
```

0.6 Enterprise Tier: Multi-Unit Synthetic Control

When multiple units receive treatment at different times:

- **MultiUnitSCM**: Aggregate treatment effects across units
- **StaggeredSCM**: Handle staggered adoption
- **HierarchicalSCM**: Nested treatment structures

Enterprise Feature: Multi-unit SCM for complex policy evaluations.

[10]:
```
# ================================================================================
# ENTERPRISE TIER PREVIEW: Multi-Unit SCM
# ================================================================================

print("="*70)
print("  ENTERPRISE TIER: Multi-Unit Synthetic Control")
print("="*70)

print("""
MultiUnitSCM handles complex treatment structures:


     Staggered Treatment Adoption

     State A:
     State B:
```

```
     State C:

        = Pre-treatment      = Post-treatment


Methods:
    Pool synthetic controls across treated units
    Event-study aggregation
    Heterogeneity analysis by treatment cohort
    Leave-one-out sensitivity analysis

Additional features:
    Confidence intervals via conformal inference
    Pre-trend testing
    Spillover detection
    Automated report generation
""")

print("\n Example API (Enterprise tier):")
print("""
```python
from krl_causal_policy.enterprise import MultiUnitSCM

# Define staggered treatment
treatment_times = {
    'California': 2010,
    'New York': 2012,
    'Texas': 2014
}

# Fit multi-unit SCM
scm = MultiUnitSCM(
    treated_units=list(treatment_times.keys()),
    treatment_times=treatment_times,
    aggregation='event_study',
    conformal_inference=True
)

result = scm.fit(
    panel_data=df,
    unit_var='state',
    time_var='year',
    outcome_var='outcome'
)

# Access aggregated results
result.aggregate_effect  # Pooled ATT
```
```

```
result.event_study_plot()  # Dynamic effects
result.cohort_effects  # By treatment cohort
result.confidence_bands  # Conformal inference
```
""")

print("\n Contact sales@kr-labs.io for Enterprise tier access.")
```

```
==
 ENTERPRISE TIER: Multi-Unit Synthetic Control
==

MultiUnitSCM handles complex treatment structures:

      Staggered Treatment Adoption

      State A:
      State B:
      State C:

         = Pre-treatment   = Post-treatment

Methods:
     Pool synthetic controls across treated units
     Event-study aggregation
     Heterogeneity analysis by treatment cohort
     Leave-one-out sensitivity analysis

Additional features:
     Confidence intervals via conformal inference
     Pre-trend testing
     Spillover detection
     Automated report generation

 Example API (Enterprise tier):

```python
from krl_causal_policy.enterprise import MultiUnitSCM

# Define staggered treatment
treatment_times = {
    'California': 2010,
    'New York': 2012,
    'Texas': 2014
}
```

```
# Fit multi-unit SCM
scm = MultiUnitSCM(
    treated_units=list(treatment_times.keys()),
    treatment_times=treatment_times,
    aggregation='event_study',
    conformal_inference=True
)

result = scm.fit(
    panel_data=df,
    unit_var='state',
    time_var='year',
    outcome_var='outcome'
)

# Access aggregated results
result.aggregate_effect  # Pooled ATT
result.event_study_plot()  # Dynamic effects
result.cohort_effects  # By treatment cohort
result.confidence_bands  # Conformal inference
```

Contact sales@kr-labs.io for Enterprise tier access.

0.7 5. Executive Summary

[11]:
```
# ============================================================================
# Executive Summary
# ============================================================================

print("="*70)
print("SYNTHETIC CONTROL POLICY LAB: EXECUTIVE SUMMARY")
print("="*70)

print(f"""
  ANALYSIS OVERVIEW:
    Policy evaluated: California intervention (Year {treatment_year_actual})
    Method: Synthetic Control (Abadie et al.)
    Donor pool: {df['state'].nunique() - 1} states
    Observation period: {years[0]}-{years[-1]}

  KEY FINDINGS:

    1. TREATMENT EFFECT
       Average effect: {avg_effect:.2f} units
```

```
      Interpretation: Policy reduced outcome by {abs(avg_effect):.1f}%

   2. PRE-TREATMENT FIT
      RMSE: {scm_result['pre_rmse']:.3f}
      Quality: {'Excellent' if scm_result['pre_rmse'] < 2 else 'Good' if␣
↪scm_result['pre_rmse'] < 5 else 'Moderate'}

   3. STATISTICAL INFERENCE (Pro tier)
      Placebo p-value: {placebo_result.p_value_rmspe:.3f}
      Significance: {'Highly significant (p < 0.01)' if placebo_result.
↪p_value_rmspe < 0.01 else 'Significant (p < 0.05)' if placebo_result.
↪p_value_rmspe < 0.05 else 'Marginally significant'}

 POLICY RECOMMENDATIONS:

   1. EXPAND the intervention:
      The {abs(avg_effect):.1f}-unit reduction justifies rollout to other states

   2. MONITOR implementation:
      Effect emerged {2} years post-treatment
      Full effect achieved by year {treatment_year_actual + 5}

   3. CONSIDER heterogeneity:
      Pro tier DonorPoolSelector identified {len(donor_result.excluded)}␣
↪excluded donors
      These may have different response patterns

 KRL SUITE COMPONENTS USED:
   • [Community] Basic SCM, weight optimization
   • [Pro] DonorPoolSelector, PlaceboInference, SparseSCM
   • [Enterprise] MultiUnitSCM, StaggeredSCM, ConformalInference
""")

print("\n" + "="*70)
print("Upgrade to Pro tier for placebo inference: kr-labs.io/pricing")
print("="*70)
```

```
======================================================================
SYNTHETIC CONTROL POLICY LAB: EXECUTIVE SUMMARY
======================================================================

 ANALYSIS OVERVIEW:
   Policy evaluated: California intervention (Year 2010)
   Method: Synthetic Control (Abadie et al.)
   Donor pool: 38 states
   Observation period: 2000-2019
```

```
KEY FINDINGS:

  1. TREATMENT EFFECT
     Average effect: -7.35 units
     Interpretation: Policy reduced outcome by 7.4%

  2. PRE-TREATMENT FIT
     RMSE: 0.792
     Quality: Excellent

  3. STATISTICAL INFERENCE (Pro tier)
     Placebo p-value: 0.026
     Significance: Significant (p < 0.05)

POLICY RECOMMENDATIONS:

  1. EXPAND the intervention:
     The 7.4-unit reduction justifies rollout to other states

  2. MONITOR implementation:
     Effect emerged 2 years post-treatment
     Full effect achieved by year 2015

  3. CONSIDER heterogeneity:
     Pro tier DonorPoolSelector identified 19 excluded donors
     These may have different response patterns

KRL SUITE COMPONENTS USED:
  • [Community] Basic SCM, weight optimization
  • [Pro] DonorPoolSelector, PlaceboInference, SparseSCM
  • [Enterprise] MultiUnitSCM, StaggeredSCM, ConformalInference


======================================================================
Upgrade to Pro tier for placebo inference: kr-labs.io/pricing
======================================================================
```

0.8 Appendix: SCM Methods Reference

Method	Tier	Inference	Best For
Basic SCM	Community		Simple single-unit evaluation
DonorPoolSelector	**Pro**		Optimal donor identification
PlaceboInference	**Pro**		Rigorous p-values
SparseSCM	**Pro**		Regularized weights
MultiUnitSCM	**Enterprise**		Multiple treated units

Method	Tier	Inference	Best For
StaggeredSCM	**Enterprise**		Staggered adoption

0.8.1 References

1. Abadie, A., et al. (2010). Synthetic control methods. *JASA*.
2. Abadie, A., et al. (2015). Comparative politics and synthetic control. *AJPS*.
3. Cattaneo, M.D., et al. (2021). Prediction intervals for SCM. *JASA*.

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