# 02 prob2

September 6, 2025

## 1 Problem 2: Y-Chromosome Threshold Analysis - Implementation

**Objective**: Analyze the relationship between maternal BMI and timing of Y-chromosome concentration reaching 4% threshold using interval-censored survival analysis.

**Key Approach**: Use Accelerated Failure Time (AFT) models with proper interval censoring to handle multiple tests per mother and determine optimal testing weeks.

## 1.1 Implementation Plan

This notebook implements the complete analysis following the detailed implementation guide:

- 1. **Section 1**: Event Interval Construction (Per Mother)
- 2. **Section 2**: Feature Matrix Preparation
- 3. **Section 3**: AFT Modeling & Inference (Core Analysis)
- 4. Section 4: Turnbull Non-parametric Validation
- 5. **Section 5**: BMI Grouping & Group-specific Optimal Weeks
- 6. Section 6: Monte Carlo Measurement Error Testing
- 7. Section 7: Baseline Two-step ML Comparison (Optional)
- 8. Section 8: Validation & Final Policy Table

```
[1]: # Import libraries
  import pandas as pd
  import numpy as np
  import matplotlib.pyplot as plt
  import seaborn as sns
  from pathlib import Path
  import warnings
  import sys
  import re
  from scipy import stats

# Core survival analysis
  from lifelines import WeibullAFTFitter, LogLogisticAFTFitter, KaplanMeierFitter

# Machine learning
  from sklearn.tree import DecisionTreeRegressor
  from sklearn.model_selection import KFold
```

```
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier, RandomForestRegressor
from sklearn.metrics import roc_auc_score
# Add project root to Python path for imports
PROJECT_ROOT = Path("/home/richard/projects/cumcm")
if str(PROJECT_ROOT) not in sys.path:
    sys.path.insert(0, str(PROJECT_ROOT))
# Import our custom modules
from src.analysis.problem2 import (
    apply_qc_filters,
    construct_intervals,
    prepare_feature_matrix,
    perform_group_specific_analysis,
    create_group_optimal_weeks_summary,
    run_monte_carlo_robustness_test,
    create_monte_carlo_summary_table,
    run_ml_baseline_comparison,
    run_comprehensive_validation
)
from src.models.aft models import (
    fit_aft_models,
    display model summary,
    predict survival curves,
    calculate optimal weeks,
    fit_turnbull_estimator,
    compare_aft_vs_turnbull,
    assess_aft_goodness_of_fit
)
# Configure environment
warnings.filterwarnings('ignore')
plt.style.use('seaborn-v0_8')
sns.set_palette("husl")
pd.set_option('display.max_columns', 50)
pd.set option('display.width', 1000)
print(" Libraries imported successfully")
print(" Survival analysis tools ready")
print(" Machine learning tools ready")
```

Libraries imported successfully Survival analysis tools ready Machine learning tools ready

```
[2]: # Setup paths
     DATA_PATH = PROJECT_ROOT / "src" / "data" / "data.xlsx"
     OUTPUT_PATH = PROJECT_ROOT / "output"
     OUTPUT_DATA_PATH = OUTPUT_PATH / "data"
     OUTPUT FIGURES PATH = OUTPUT PATH / "figures"
     OUTPUT_RESULTS_PATH = OUTPUT_PATH / "results"
     # Create output directories
     OUTPUT DATA PATH.mkdir(parents=True, exist ok=True)
     OUTPUT_FIGURES_PATH.mkdir(parents=True, exist_ok=True)
     OUTPUT RESULTS PATH.mkdir(parents=True, exist ok=True)
     print(f" Paths configured - Data: {DATA_PATH}")
     print(f" Output paths ready")
     # Load original male fetus data for interval construction
     print(" Loading original male fetus data...")
     male_data = pd.read_excel(DATA_PATH, sheet_name='
     print(f" Loaded {len(male_data)} rows and {len(male_data.columns)} columns")
     print("\n Data structure preview:")
     print(f" Columns: {list(male_data.columns[:10])}...")
     print(f" Maternal IDs: {male_data[' '].nunique()} unique mothers")
     print(f" Total tests: {len(male data)} test records")
     Paths configured - Data: /home/richard/projects/cumcm/src/data/data.xlsx
     Output paths ready
     Loading original male fetus data...
     Loaded 1082 rows and 31 columns
     Data structure preview:
```

# 1.2 Section 1: Event Interval Construction (Per Mother)

Maternal IDs: 267 unique mothers Total tests: 1082 test records

' ']...

Columns: ['', '', '', '', '', '', 'IVF', '', '', '',

Goal: Convert multiple test records per mother into single interval-censored event records.

Event Definition: Y-chromosome concentration first reaches 4% threshold

**Censoring Types**: 1. **Left-censored**: First observation already  $4\% \rightarrow$  Event occurred before first test 2. **Interval-censored**: Threshold crossed between visits  $\rightarrow$  Event in interval (L, R] 3. **Right-censored**: Never reached threshold  $\rightarrow$  Event beyond last observation

```
[3]: ### Step 1.1: Data Preparation and QC Filtering

# Apply same QC as preprocessing to get df with individual tests
```

```
print(" Applying QC filters from preprocessing...")
     df_tests, filter_stats = apply_qc_filters(male_data, verbose=True)
     print(f"\n Individual test dataset ready:")
     df_tests.head(10)
     Applying QC filters from preprocessing...
     Parsing variables and applying QC filters...
     Variable parsing completed:
      Gestational weeks: 1082/1082 valid
      BMI: 1082/1082 valid
      Y concentration: 1082/1082 valid
      After gestational weeks filter (10-25): 1069 records
      After GC content filter (40-60%): 620 records
      After chromosome abnormality filter: 556 records
      After missing data filter: 556 records
     Applying IQR outlier detection...
      gestational_weeks:
        IQR outliers: 0 (0.00%) - bounds: [3.500, 29.214]
        After IQR filtering: 556 records (removed 0)
        IQR outliers: 13 (2.34%) - bounds: [24.982, 39.214]
        After IQR filtering: 543 records (removed 13)
      y_concentration:
        IQR outliers: 5 (0.92%) - bounds: [-0.017, 0.168]
        After IQR filtering: 538 records (removed 5)
     QC filtering completed: 538 records remaining (49.7% retention)
      Unique mothers: 238
      Tests per mother: 2.3 average
     Individual test dataset ready:
[3]:
      maternal_id gestational_weeks
                                             bmi y_concentration
     0
              A002
                            13.857143 33.331832
                                                         0.059230
     1
              A003
                            13.000000 30.742188
                                                         0.065185
     2
              A003
                            20.285714 31.882812
                                                         0.052253
     3
              A004
                            11.000000 28.641243
                                                         0.049498
     4
              A004
                            15.857143 28.641243
                                                         0.066800
                            23.571429 29.161993
     5
              A004
                                                         0.082347
     6
              A005
                            15.285714 30.844444
                                                         0.081533
     7
                            12.142857 35.883634
              A006
                                                         0.069469
     8
              A007
                            12.285714 33.874064
                                                         0.021902
              A007
                            16.000000 33.874064
     9
                                                         0.038038
[4]: ### Step 1.2: Interval Construction Logic
     # Generate interval-censored observations using module function
```

```
df_intervals = construct_intervals(df_tests, threshold=0.04, verbose=True)
```

Constructing interval-censored observations... Interval construction completed: 238 mothers

Censoring type distribution:

left: 203 (85.3%) interval: 22 (9.2%) right: 13 (5.5%)

```
[5]: ### Step 1.3: Output Analysis

print(f"\n Sample intervals:")

print(df_intervals.head(10)[['maternal_id', 'bmi', 'L', 'R', 'censor_type',

→'n_tests', 'max_y_concentration']])
```

Sample intervals:						
materna	l_id	bmi	L	R	censor_type	$n\_{tests}$
max_y_con	ax_y_concentration					
0	A002	33.331832	0.000000	13.857143	left	1
0.059230						
1	A003	30.742188	0.000000	13.000000	left	2
0.065185						
2	A004	28.641243	0.000000	11.000000	left	3
0.082347						
3	A005	30.844444	0.000000	15.285714	left	1
0.081533						
4	A006	35.883634	0.000000	12.142857	left	1
0.069469						
5	A007	33.874064	23.714286	inf	right	4
0.038038						
6	800A	29.136316	0.000000	13.000000	left	2
0.060891						
7	A009	33.333333	0.000000	13.857143	left	3
0.159267						
8	A010	33.333333	20.857143	inf	right	2
0.031946						
9	A011	36.250470	16.142857	20.571429	interval	4
0.068983						

## 1.3 Section 2: Feature Matrix Preparation

Goal: Prepare covariate matrix for AFT modeling with proper standardization and quality checks.

```
[6]: ### Step 2.1: Standardization and Feature Matrix Creation
# Create feature matrix using module function
```

## df\_X = prepare\_feature\_matrix(df\_intervals, verbose=True)

Preparing feature matrix for AFT modeling...

BMI standardization completed:

Mean BMI: 31.88 Std BMI: 2.59

BMI range: 26.6 - 39.2

All intervals are valid (L < R)

Feature matrix summary:

Observations: 238
Features: bmi, bmi\_z
Interval bounds: L, R

Censoring types: ['left' 'right' 'interval']

#### Dataset statistics:

	bmi	bmi_z	L	R
count	238.000000	2.380000e+02	238.000000	238.000000
mean	31.879303	-5.747037e-16	2.337335	inf
std	2.587130	1.000000e+00	5.824886	NaN
min	26.619343	-2.033125e+00	0.000000	11.000000
25%	29.917696	-7.582176e-01	0.000000	12.571429
50%	31.632725	-9.530933e-02	0.000000	13.428571
75%	33.453780	6.085806e-01	0.000000	16.142857
max	39.159843	2.814138e+00	24.285714	inf

#### Quality checks:

Missing values: 0 total Interval validity check: Finite intervals: 225 Right-censored: 13 Left-censored: 203

#### Summary by censoring type:

count mean std mean <1	ambda>
count mean std mean <1	
censor_type	
interval 22 32.40 3.16 14.31	19.62
left 203 31.74 2.52 0.00	14.00
right 13 33.22 2.22 18.58	NaN

Feature matrix preparation completed - ready for AFT modeling

## [7]: ### Step 2.2: Quality Checks

# Quality checks are included in the prepare\_feature\_matrix function above

Feature matrix preparation completed with quality checks - ready for AFT modeling

## 1.4 Section 3: AFT Modeling & Inference (Core Analysis)

Goal: Fit Accelerated Failure Time models to interval-censored data and derive BMI-specific survival functions.

**Models**: - Primary: Weibull AFT (log T = 'x + ,  $\sim$  Gumbel) - Alternative: Log-logistic AFT ( $\sim$  Logistic)

**Key Output**: Survival functions S(t|x) for calculating optimal testing weeks

Fitting AFT models to interval-censored data...

```
Fitting Weibull AFT model...
Weibull AFT model fitted successfully
```

Fitting Log-logistic AFT model...
Log-logistic AFT model fitted successfully

\_\_\_\_\_

Using Weibull AFT as primary model

```
[9]: ### Step 3.2: Model Summary & Diagnostics

# Display model summary and diagnostics using module function
display_model_summary(primary_model, primary_name, verbose=True)
```

Weibull AFT Model Summary:

```
coef exp(coef) se(coef) coef lower 95% coef upper 95%
exp(coef) lower 95% exp(coef) upper 95% cmp to
                                                        z
                                                                      p
-log2(p)
param
       covariate
lambda_ Intercept 2.018579
                             7.527618 0.146708
                                                      1.731035
                                                                      2.306122
5.646497
                   10.035431
                                 0.0 13.759117 4.489752e-43 140.676272
                  0.167024
                             1.181783 0.072897
                                                      0.024149
       bmi_z
                                                                      0.309899
1.024443
                    1.363288
                                 0.0
                                      2.291235 2.194982e-02
                                                                5.509647
rho_
       Intercept 0.122470
                             1.130286 0.179968
                                                     -0.230260
                                                                      0.475201
0.794327
                    1.608338
                                     0.680512 4.961806e-01
                                 0.0
                                                                1.011063
```

```
Model Parameters:
       ('lambda_', 'Intercept'): 2.0186
       ('lambda_', 'bmi_z'): 0.1670
       ('rho_', 'Intercept'): 0.1225
      BMI Effect Analysis:
       BMI coefficient (standardized): 0.1670
       P-value: 0.0219
       Statistical significance: significant
       Interpretation: Higher BMI delays time to Y 4% threshold
       AFT interpretation: 1-unit BMI increase → 16.7% change in log-time scale
      Model Fit Statistics:
       AIC: 253.54
       Log-likelihood: -123.77
[10]: ### Step 3.3: Survival Function Prediction
      # Generate survival curves using module function
      time_grid = np.linspace(10, 25, 100) # Gestational weeks 10-25
      survival_curves = predict_survival_curves(
          primary_model,
          df_intervals,
          time_grid,
          quartiles=[0.25, 0.5, 0.75],
          verbose=True
      )
      Generating survival curves for different BMI levels...
```

BMI quartiles for analysis:

Q25: 29.9 Q50: 31.6 Q75: 33.5

Computing survival functions...

Q25: BMI 29.9 (z=-0.76) Q50: BMI 31.6 (z=-0.10) Q75: BMI 33.5 (z=0.61)

Survival Probabilities at Key Weeks:

Week	BMI_Q25	BMI_Q50	BMI_Q75
12	0.142	0.179	0.222
14	0.099	0.130	0.167
16	0.066	0.091	0.123
18	0.045	0.065	0.091
20	0.031	0.046	0.068

Survival function prediction completed for 3 BMI levels

```
Optimal weeks for 90% confidence level: (When 90% of mothers have reached Y 4% threshold)
```

-----

Q25: BMI 29.9  $\rightarrow$  Week 13.9 Q50: BMI 31.6  $\rightarrow$  Week 15.6 Q75: BMI 33.5  $\rightarrow$  Week 17.6

Optimal weeks for 95% confidence level:

(When 95% of mothers have reached Y 4% threshold)

-----

Q25: BMI 29.9  $\rightarrow$  Week 17.6 Q50: BMI 31.6  $\rightarrow$  Week 19.7 Q75: BMI 33.5  $\rightarrow$  Week 22.1

Optimal Testing Weeks Summary:

BMI Group	BMI Value	90% Conf	95% Conf
Q25 Q50	29.9 31.6	13.9 15.6	17.6 19.7
Q75	33.5	17.6	22.1

Optimal testing week calculation completed

## 1.5 Section 4: Turnbull Non-parametric Validation

Goal: Validate AFT assumptions using non-parametric Turnbull estimator.

#### 1.5.1 Overview

- Fit Turnbull estimator to same interval-censored data
- Compare Turnbull vs AFT survival curves
- Assess goodness of fit for parametric assumptions

### [12]: ### Step 4.1: Turnbull Fitting # Fit Turnbull non-parametric estimator using module function turnbull\_model = fit\_turnbull\_estimator(df\_X, verbose=True) Fitting Turnbull non-parametric estimator... Iteration 0 delta log-likelihood: 113.6900846918 log-like: -153.399751 Iteration 1 delta log-likelihood: -101.1526863254 log-like: -132.911080 Iteration 2 delta log-likelihood: 2.9231947109 log-like: -129.987885 Iteration 3 delta log-likelihood: -1.0849443151 log-like: -126.598301 Iteration 4 delta log-likelihood: 1.0252113341 log-like: -125.573090 Iteration 5 delta log-likelihood: -0.0043090313 log-like: -124.052893 Iteration 6 delta log-likelihood: 0.6773956086 log-like: -122.989866 Iteration 7 delta log-likelihood: -0.1124386356 log-like: -122.198954 Iteration 8 delta log-likelihood: 0.4953306406 log-like: -121.587947 Iteration 9 delta log-likelihood: -0.1470470728 log-like: -121.106272 Iteration 10 delta log-likelihood: 0.3827816919 log-like: -120.719448 Iteration 11 delta log-likelihood: -0.1542395080 log-like: -120.405148 Iteration 12 delta log-likelihood: 0.1367757006 log-like: -120.268372 Iteration 13 delta log-likelihood: 0.0208871686

log-like:

-120.033195

delta log-likelihood: 0.1034543726
log-like: -119.837019

Iteration 15

delta log-likelihood: 0.0060184068
log-like: -119.672051

Iteration 16

delta log-likelihood: 0.0806968021
log-like: -119.532256

Iteration 17

delta log-likelihood: -0.0024361723 log-like: -119.412988

Iteration 18

delta log-likelihood: 0.0645611503
log-like: -119.310564

Iteration 19

delta log-likelihood: -0.0071565792
log-like: -119.222084

Iteration 20

delta log-likelihood: 0.0527439360
log-like: -119.145206

Iteration 21

delta log-likelihood: -0.0096519134 log-like: -119.078056

Iteration 22

delta log-likelihood: 0.0438424917
log-like: -119.019097

Iteration 23

delta log-likelihood: -0.0108040344 log-like: -118.967082

Iteration 24

delta log-likelihood: 0.0369699499 log-like: -118.920976

Iteration 25

delta log-likelihood: -0.0111424797
log-like: -118.879927

Iteration 26

delta log-likelihood: 0.0315475596 log-like: -118.843224

Iteration 27

delta log-likelihood: -0.0109919317
log-like: -118.810273

Iteration 28

delta log-likelihood: 0.0271871201
log-like: -118.780573

Iteration 29

delta log-likelihood: -0.0105545888
log-like: -118.753704

delta log-likelihood: 0.0236217730
log-like: -118.729309

Iteration 31

delta log-likelihood: -0.0099576962
log-like: -118.707084

Iteration 32

delta log-likelihood: 0.0106061086
log-like: -118.696478

Iteration 33

delta log-likelihood: 0.0006978986
log-like: -118.677050

Iteration 34

delta log-likelihood: 0.0091457544
log-like: -118.659209

Iteration 35

delta log-likelihood: 0.0003370091
log-like: -118.642779

Iteration 36

delta log-likelihood: 0.0079509036
log-like: -118.627607

Iteration 37

delta log-likelihood: 0.0000994209
log-like: -118.613559

Iteration 38

delta log-likelihood: 0.0069607969
log-like: -118.600520

Iteration 39

delta log-likelihood: -0.0000524145
log-like: -118.588390

Iteration 40

delta log-likelihood: 0.0061306498
log-like: -118.577081

Iteration 41

delta log-likelihood: -0.0001447958
log-like: -118.566515

Iteration 42

delta log-likelihood: 0.0054272447 log-like: -118.556625

Iteration 43

delta log-likelihood: -0.0001961852
log-like: -118.547351

Iteration 44

delta log-likelihood: 0.0048256315
log-like: -118.538639

Iteration 45

delta log-likelihood: -0.0002195820
log-like: -118.530442

delta log-likelihood: 0.0043068240
log-like: -118.522719

Iteration 47

delta log-likelihood: -0.0002241542
log-like: -118.515431

Iteration 48

delta log-likelihood: 0.0038561881
log-like: -118.508545

Iteration 49

delta log-likelihood: -0.0002163672 log-like: -118.502032

Iteration 50

delta log-likelihood: 0.0034623036
log-like: -118.495863

Iteration 51

delta log-likelihood: -0.0002007698
log-like: -118.490014

Iteration 52

delta log-likelihood: 0.0031161494
log-like: -118.484464

Iteration 53

delta log-likelihood: -0.0001805473 log-like: -118.479191

Iteration 54

delta log-likelihood: 0.0028105148
log-like: -118.474178

Iteration 55

delta log-likelihood: -0.0001579131 log-like: -118.469407

Iteration 56

delta log-likelihood: 0.0025395697 log-like: -118.464863

Iteration 57

delta log-likelihood: -0.0001343867 log-like: -118.460533

Iteration 58

delta log-likelihood: 0.0022985469
log-like: -118.456403

Iteration 59

delta log-likelihood: -0.0001109930
log-like: -118.452461

Iteration 60

delta log-likelihood: 0.0020835073 log-like: -118.448697

Iteration 61

delta log-likelihood: -0.0000884053
log-like: -118.445099

delta log-likelihood: 0.0018911621
log-like: -118.441660

Iteration 63

delta log-likelihood: -0.0000670477
log-like: -118.438369

Iteration 64

delta log-likelihood: 0.0017187401
log-like: -118.435218

Iteration 65

delta log-likelihood: -0.0000471686 log-like: -118.432201

Iteration 66

delta log-likelihood: 0.0015638854
log-like: -118.429310

Iteration 67

delta log-likelihood: -0.0000288944
log-like: -118.426539

Iteration 68

delta log-likelihood: 0.0014245792
log-like: -118.423880

Iteration 69

delta log-likelihood: -0.0000122670 log-like: -118.421329

Iteration 70

delta log-likelihood: 0.0012990789
log-like: -118.418880

Iteration 71

delta log-likelihood: 0.0000027290
log-like: -118.416528

Iteration 72

delta log-likelihood: 0.0011858715
log-like: -118.414268

Iteration 73

delta log-likelihood: 0.0000161462 log-like: -118.412095

Iteration 74

delta log-likelihood: 0.0010836352
log-like: -118.410006

Iteration 75

delta log-likelihood: 0.0000280613
log-like: -118.407996

Iteration 76

delta log-likelihood: 0.0009912102
log-like: -118.406061

Iteration 77

delta log-likelihood: 0.0000385649
log-like: -118.404199

delta log-likelihood: 0.0009075743
log-like: -118.402405

Iteration 79

delta log-likelihood: 0.0000477548
log-like: -118.400676

Iteration 80

delta log-likelihood: 0.0008318235
log-like: -118.399010

Iteration 81

delta log-likelihood: 0.0000557313
log-like: -118.397404

Iteration 82

delta log-likelihood: 0.0007631560
log-like: -118.395854

Iteration 83

delta log-likelihood: 0.0000625942
log-like: -118.394359

Iteration 84

delta log-likelihood: 0.0007008586
log-like: -118.392916

Iteration 85

delta log-likelihood: 0.0000684401
log-like: -118.391523

Iteration 86

delta log-likelihood: 0.0006442956
log-like: -118.390177

Iteration 87

delta log-likelihood: 0.0000733618
log-like: -118.388876

Iteration 88

delta log-likelihood: 0.0005928995
log-like: -118.387619

Iteration 89

delta log-likelihood: 0.0000774467 log-like: -118.386404

Iteration 90

delta log-likelihood: 0.0005461627 log-like: -118.385228

Iteration 91

delta log-likelihood: 0.0000807770
log-like: -118.384091

Iteration 92

delta log-likelihood: 0.0005036305
log-like: -118.382990

Iteration 93

delta log-likelihood: 0.0000834292
log-like: -118.381925

delta log-likelihood: 0.0004648954
log-like: -118.380893

Iteration 95

delta log-likelihood: 0.0000854739
log-like: -118.379894

Iteration 96

delta log-likelihood: 0.0004295915
log-like: -118.378926

Iteration 97

delta log-likelihood: 0.0000869767
log-like: -118.377987

Iteration 98

delta log-likelihood: 0.0003973903
log-like: -118.377077

Iteration 99

delta log-likelihood: 0.0000879973
log-like: -118.376195

Iteration 100

delta log-likelihood: 0.0003679962
log-like: -118.375339

Iteration 101

delta log-likelihood: 0.0000885906
log-like: -118.374509

Iteration 102

delta log-likelihood: 0.0003411436
log-like: -118.373703

Iteration 103

delta log-likelihood: 0.0000888068
log-like: -118.372920

Iteration 104

delta log-likelihood: 0.0003165931
log-like: -118.372160

Iteration 105

delta log-likelihood: 0.0000886915
log-like: -118.371422

Iteration 106

delta log-likelihood: 0.0002941292
log-like: -118.370705

Iteration 107

delta log-likelihood: 0.0000882861
log-like: -118.370009

Iteration 108

delta log-likelihood: 0.0002735576
log-like: -118.369331

Iteration 109

delta log-likelihood: 0.0000876282
log-like: -118.368673

delta log-likelihood: 0.0002547032
log-like: -118.368033

Iteration 111

delta log-likelihood: 0.0000867516
log-like: -118.367410

Iteration 112

delta log-likelihood: 0.0002374079
log-like: -118.366804

Iteration 113

delta log-likelihood: 0.0000856871
log-like: -118.366214

Iteration 114

delta log-likelihood: 0.0002215291
log-like: -118.365640

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Iteration 402

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Iteration 404

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delta log-likelihood: 0.0000002505
log-like: -118.337602

Iteration 674

delta log-likelihood: 0.0000002488
log-like: -118.337601

Iteration 675

delta log-likelihood: 0.0000002471 log-like: -118.337600

Iteration 676

delta log-likelihood: 0.0000002455
log-like: -118.337599

Iteration 677

delta log-likelihood: 0.0000002438
log-like: -118.337598

Iteration 678

delta log-likelihood: 0.0000002422
log-like: -118.337598

Iteration 679

delta log-likelihood: 0.0000002406
log-like: -118.337597

Iteration 680

delta log-likelihood: 0.0000002389
log-like: -118.337596

Iteration 681

delta log-likelihood: 0.0000002373
log-like: -118.337595

Iteration 682

delta log-likelihood: 0.0000002358
log-like: -118.337594

Iteration 683

delta log-likelihood: 0.0000002342
log-like: -118.337593

Iteration 684

delta log-likelihood: 0.0000002326
log-like: -118.337592

Iteration 685

delta log-likelihood: 0.0000002311
log-like: -118.337591

delta log-likelihood: 0.0000002295
log-like: -118.337591

Iteration 687

delta log-likelihood: 0.0000002280
log-like: -118.337590

Iteration 688

delta log-likelihood: 0.0000002265
log-like: -118.337589

Iteration 689

delta log-likelihood: 0.0000002249
log-like: -118.337588

Iteration 690

delta log-likelihood: 0.0000002234
log-like: -118.337587

Iteration 691

delta log-likelihood: 0.0000002220
log-like: -118.337586

Iteration 692

delta log-likelihood: 0.0000002205
log-like: -118.337586

Iteration 693

delta log-likelihood: 0.0000002190
log-like: -118.337585

Iteration 694

delta log-likelihood: 0.0000002176
log-like: -118.337584

Iteration 695

delta log-likelihood: 0.0000002161 log-like: -118.337583

Iteration 696

delta log-likelihood: 0.0000002147 log-like: -118.337582

Iteration 697

delta log-likelihood: 0.0000002132
log-like: -118.337581

Iteration 698

delta log-likelihood: 0.0000002118
log-like: -118.337581

Iteration 699

delta log-likelihood: 0.0000002104
log-like: -118.337580

Iteration 700

delta log-likelihood: 0.0000002090
log-like: -118.337579

Iteration 701

delta log-likelihood: 0.0000002076
log-like: -118.337578

delta log-likelihood: 0.0000002063
log-like: -118.337578

Iteration 703

delta log-likelihood: 0.0000002049
log-like: -118.337577

Iteration 704

delta log-likelihood: 0.0000002036
log-like: -118.337576

Iteration 705

delta log-likelihood: 0.0000002022
log-like: -118.337575

Iteration 706

delta log-likelihood: 0.0000002009
log-like: -118.337575

Iteration 707

delta log-likelihood: 0.0000001995
log-like: -118.337574

Iteration 708

delta log-likelihood: 0.0000001982
log-like: -118.337573

Iteration 709

delta log-likelihood: 0.0000001969
log-like: -118.337572

Iteration 710

delta log-likelihood: 0.0000001956
log-like: -118.337572

Iteration 711

delta log-likelihood: 0.0000001943
log-like: -118.337571

Iteration 712

delta log-likelihood: 0.0000001931
log-like: -118.337570

Iteration 713

delta log-likelihood: 0.0000001918
log-like: -118.337569

Iteration 714

delta log-likelihood: 0.0000001905
log-like: -118.337569

Iteration 715

delta log-likelihood: 0.0000001893
log-like: -118.337568

Iteration 716

delta log-likelihood: 0.0000001880
log-like: -118.337567

Iteration 717

delta log-likelihood: 0.0000001868
log-like: -118.337567

delta log-likelihood: 0.0000001856
log-like: -118.337566

Iteration 719

delta log-likelihood: 0.0000001844
log-like: -118.337565

Iteration 720

delta log-likelihood: 0.0000001832
log-like: -118.337565

Iteration 721

delta log-likelihood: 0.0000001820
log-like: -118.337564

Iteration 722

delta log-likelihood: 0.0000001808
log-like: -118.337563

Iteration 723

delta log-likelihood: 0.0000001796
log-like: -118.337563

Iteration 724

delta log-likelihood: 0.0000001784
log-like: -118.337562

Iteration 725

delta log-likelihood: 0.0000001772
log-like: -118.337561

Iteration 726

delta log-likelihood: 0.0000001761
log-like: -118.337561

Iteration 727

delta log-likelihood: 0.0000001749
log-like: -118.337560

Iteration 728

delta log-likelihood: 0.0000001738
log-like: -118.337559

Iteration 729

delta log-likelihood: 0.0000001727 log-like: -118.337559

Iteration 730

delta log-likelihood: 0.0000001715
log-like: -118.337558

Iteration 731

delta log-likelihood: 0.0000001704
log-like: -118.337557

Iteration 732

delta log-likelihood: 0.0000001693 log-like: -118.337557

Iteration 733

delta log-likelihood: 0.0000001682
log-like: -118.337556

delta log-likelihood: 0.0000001671
log-like: -118.337555

Iteration 735

delta log-likelihood: 0.0000001660
log-like: -118.337555

Iteration 736

delta log-likelihood: 0.0000001650
log-like: -118.337554

Iteration 737

delta log-likelihood: 0.0000001639
log-like: -118.337554

Iteration 738

delta log-likelihood: 0.0000001628
log-like: -118.337553

Iteration 739

delta log-likelihood: 0.0000001618
log-like: -118.337552

Iteration 740

delta log-likelihood: 0.0000001607
log-like: -118.337552

Iteration 741

delta log-likelihood: 0.0000001597
log-like: -118.337551

Iteration 742

delta log-likelihood: 0.0000001587
log-like: -118.337551

Iteration 743

delta log-likelihood: 0.0000001576
log-like: -118.337550

Iteration 744

delta log-likelihood: 0.0000001566
log-like: -118.337549

Iteration 745

delta log-likelihood: 0.0000001556
log-like: -118.337549

Iteration 746

delta log-likelihood: 0.0000001546
log-like: -118.337548

Iteration 747

delta log-likelihood: 0.0000001536
log-like: -118.337548

Iteration 748

delta log-likelihood: 0.0000001526 log-like: -118.337547

Iteration 749

delta log-likelihood: 0.0000001516
log-like: -118.337547

delta log-likelihood: 0.0000001507
log-like: -118.337546

Iteration 751

delta log-likelihood: 0.0000001497
log-like: -118.337545

Iteration 752

delta log-likelihood: 0.0000001487
log-like: -118.337545

Iteration 753

delta log-likelihood: 0.0000001478
log-like: -118.337544

Iteration 754

delta log-likelihood: 0.0000001468
log-like: -118.337544

Iteration 755

delta log-likelihood: 0.0000001459
log-like: -118.337543

Iteration 756

delta log-likelihood: 0.000001449
log-like: -118.337543

Iteration 757

delta log-likelihood: 0.0000001440
log-like: -118.337542

Iteration 758

delta log-likelihood: 0.0000001431
log-like: -118.337542

Iteration 759

delta log-likelihood: 0.0000001422
log-like: -118.337541

Iteration 760

delta log-likelihood: 0.0000001413
log-like: -118.337541

Iteration 761

delta log-likelihood: 0.0000001404
log-like: -118.337540

Iteration 762

delta log-likelihood: 0.0000001395
log-like: -118.337540

Iteration 763

delta log-likelihood: 0.0000001386
log-like: -118.337539

Iteration 764

delta log-likelihood: 0.0000001377
log-like: -118.337539

Iteration 765

delta log-likelihood: 0.0000001368
log-like: -118.337538

delta log-likelihood: 0.0000001359
log-like: -118.337538

Iteration 767

delta log-likelihood: 0.0000001351
log-like: -118.337537

Iteration 768

delta log-likelihood: 0.0000001342
log-like: -118.337536

Iteration 769

delta log-likelihood: 0.0000001334
log-like: -118.337536

Iteration 770

delta log-likelihood: 0.0000001325
log-like: -118.337536

Iteration 771

delta log-likelihood: 0.0000001317
log-like: -118.337535

Iteration 772

delta log-likelihood: 0.0000001308
log-like: -118.337535

Iteration 773

delta log-likelihood: 0.0000001300
log-like: -118.337534

Iteration 774

delta log-likelihood: 0.0000001292
log-like: -118.337534

Iteration 775

delta log-likelihood: 0.0000001284
log-like: -118.337533

Iteration 776

delta log-likelihood: 0.0000001276
log-like: -118.337533

Iteration 777

delta log-likelihood: 0.0000001267 log-like: -118.337532

Iteration 778

delta log-likelihood: 0.0000001259
log-like: -118.337532

Iteration 779

delta log-likelihood: 0.0000001251
log-like: -118.337531

Iteration 780

delta log-likelihood: 0.000001244
log-like: -118.337531

Iteration 781

delta log-likelihood: 0.0000001236
log-like: -118.337530

delta log-likelihood: 0.0000001228
log-like: -118.337530

Iteration 783

delta log-likelihood: 0.0000001220
log-like: -118.337529

Iteration 784

delta log-likelihood: 0.0000001212
log-like: -118.337529

Iteration 785

delta log-likelihood: 0.0000001205
log-like: -118.337528

Iteration 786

delta log-likelihood: 0.0000001197
log-like: -118.337528

Iteration 787

delta log-likelihood: 0.0000001190
log-like: -118.337528

Iteration 788

delta log-likelihood: 0.0000001182
log-like: -118.337527

Iteration 789

delta log-likelihood: 0.0000001175
log-like: -118.337527

Iteration 790

delta log-likelihood: 0.0000001167
log-like: -118.337526

Iteration 791

delta log-likelihood: 0.0000001160
log-like: -118.337526

Iteration 792

delta log-likelihood: 0.0000001153
log-like: -118.337525

Iteration 793

delta log-likelihood: 0.0000001146
log-like: -118.337525

Iteration 794

delta log-likelihood: 0.0000001138
log-like: -118.337525

Iteration 795

delta log-likelihood: 0.0000001131 log-like: -118.337524

Iteration 796

delta log-likelihood: 0.0000001124 log-like: -118.337524

Iteration 797

delta log-likelihood: 0.0000001117
log-like: -118.337523

delta log-likelihood: 0.0000001110
log-like: -118.337523

Iteration 799

delta log-likelihood: 0.0000001103
log-like: -118.337522

Iteration 800

delta log-likelihood: 0.0000001096
log-like: -118.337522

Iteration 801

delta log-likelihood: 0.000001090
log-like: -118.337522

Iteration 802

delta log-likelihood: 0.0000001083
log-like: -118.337521

Iteration 803

delta log-likelihood: 0.0000001076
log-like: -118.337521

Iteration 804

delta log-likelihood: 0.0000001069
log-like: -118.337520

Iteration 805

delta log-likelihood: 0.0000001063
log-like: -118.337520

Iteration 806

delta log-likelihood: 0.0000001056
log-like: -118.337520

Iteration 807

delta log-likelihood: 0.0000001049
log-like: -118.337519

Iteration 808

delta log-likelihood: 0.0000001043
log-like: -118.337519

Iteration 809

delta log-likelihood: 0.000001036 log-like: -118.337518

Iteration 810

delta log-likelihood: 0.0000001030
log-like: -118.337518

Iteration 811

delta log-likelihood: 0.0000001024
log-like: -118.337518

Iteration 812

delta log-likelihood: 0.000001017
log-like: -118.337517

Iteration 813

delta log-likelihood: 0.0000001011
log-like: -118.337517

```
Iteration 814
```

delta log-likelihood: 0.0000001005
log-like: -118.337517

Iteration 815

delta log-likelihood: 0.0000000999
log-like: -118.337516
Turnbull estimator fitted successfully

Timeline range: 0.0 - 24.4 Number of intervals: 27

```
[13]: ### Step 4.2: Model Comparison

# Compare AFT vs Turnbull using median BMI as representative
median_bmi = df_intervals['bmi'].median()
comparison_results = compare_aft_vs_turnbull(
    primary_model,
    turnbull_model,
    time_grid,
    median_bmi,
    df_intervals,
    verbose=True
)
```

Comparing AFT model vs Turnbull non-parametric estimator...

Restricting comparison to clinically meaningful range: 12.0 - 24.7 weeks
Using 84 time points (avoids unreliable early extrapolation)
Model comparison completed

Population-Level Survival Curve Comparison:

Turnbull: Non-parametric estimate using all 238 observations AFT: Parametric prediction averaged across all observations

Comparison Metrics:

Mean Absolute Error: 0.0141 Root Mean Square Error: 0.0186 Maximum Absolute Error: 0.0559

KS Statistic: 0.0559

Excellent agreement (MAE < 0.05)

### Survival Probabilities at Key Weeks:

Week	Turnbull	AFT	Difference
12	0.195	0.184	0.011
14	0.108	0.139	0.031
16	0.108	0.100	0.008
18	0.066	0.074	0.007
20	0.049	0.054	0.005

```
[14]: ### Step 4.3: Goodness of Fit Assessment

# Assess overall AFT model adequacy using module function
fit_assessment = assess_aft_goodness_of_fit(comparison_results, verbose=True)
```

#### AFT Model Goodness of Fit Assessment:

\_\_\_\_\_

```
Fit Quality Metrics:
```

MAE: 0.0141 (threshold: < 0.1)
RMSE: 0.0186 (threshold: < 0.15)
KS: 0.0559 (threshold: < 0.2)

### Criteria Assessment:

MAE: PASS RMSE: PASS KS: PASS

# Overall Assessment:

Criteria met: 3/3

Overall fit quality: Good

Recommendation: AFT model provides adequate fit to data The parametric AFT assumptions appear reasonable.

### Validation Summary:

- Turnbull provides the non-parametric gold standard
- AFT model offers interpretable covariate effects
- Model agreement suggests good parametric fit

## 1.6 Section 5: BMI Grouping & Group-specific Optimal Weeks

Goal: Create BMI groups and calculate optimal testing weeks for each group.

### 1.6.1 Overview

- Calculate predicted median times for CART-based grouping
- Apply multiple BMI grouping strategies (clinical, tertile, CART)
- Evaluate grouping strategies using risk-based scoring
- Calculate group-specific optimal weeks for different confidence levels
- Generate final policy recommendations by BMI group

```
[15]: ### Step 5.1: Comprehensive Group-specific Analysis

# Perform group-specific analysis including:

# - Predicted median time calculation

# - Multiple BMI grouping strategies

# - Grouping strategy evaluation

# - Group-specific optimal weeks calculation
```

```
group_analysis_results = perform_group_specific_analysis(
    df intervals,
    primary_model,
    confidence_levels=[0.90, 0.95],
    time_grid=time_grid,
    grouping_methods=['clinical', 'tertile', 'cart'], # Include CART if data_
 →allows
    verbose=True
Performing group-specific optimal weeks analysis...
Calculating individual predicted median survival times...
Predicted median times calculated: 238/238 valid
Predicted Median Time Statistics:
 Mean: 5.52 weeks
 Std: 0.98 weeks
 Range: 3.88 - 8.71 weeks
Evaluating 4 grouping strategies...
Evaluating grouping strategy: bmi_group_cart
 Number of groups: 6
 Risk score: 11.522
 Weighted median: 5.522 weeks
 Complexity penalty: 6.000
 Between-group variance: 1.187
 Within-group variance: 0.083
 Group sizes:
   CART_G2: 58 (24.4%)
   CART G5: 46 (19.3%)
   CART_G1: 38 (16.0%)
   CART_G3: 35 (14.7%)
   CART_G4: 31 (13.0%)
   CART_G6: 30 (12.6%)
Evaluating grouping strategy: bmi_group_clinical
 Number of groups: 3
 Risk score: 8.522
 Weighted median: 5.522 weeks
 Complexity penalty: 3.000
 Between-group variance: 2.240
 Within-group variance: 0.227
 Group sizes:
   Obese I (30-35): 147 (61.8%)
   Overweight (25-30): 61 (25.6%)
   Obese II+ (35): 30 (12.6%)
Evaluating grouping strategy: bmi_group_tertile
```

Number of groups: 3 Risk score: 8.522

Weighted median: 5.522 weeks Complexity penalty: 3.000 Between-group variance: 1.068 Within-group variance: 0.240

### Group sizes:

Low BMI (T1): 80 (33.6%) High BMI (T3): 79 (33.2%) Medium BMI (T2): 79 (33.2%)

Best grouping strategy: clinical

Risk score: 8.522

Calculating optimal weeks for 3 BMI groups...

Analyzing group: Obese I (30-35)

90% confidence: Week 15.9 95% confidence: Week 20.2

Analyzing group: Overweight (25-30)

90% confidence: Week 13.3 95% confidence: Week 16.7

Analyzing group: Obese II+ (35)

90% confidence: Week 21.1 95% confidence: Week Never

Group-specific analysis completed for 3 groups

# [16]: ### Step 5.2: Generate Group-specific Optimal Weeks Summary

# Create comprehensive summary table for group-specific recommendations group\_summary\_table =  $_{\sqcup}$ 

→create\_group\_optimal\_weeks\_summary(group\_analysis\_results, verbose=True)

# Group-Specific Optimal Testing Weeks Summary:

-----

BMI_Group	${\tt n\_mothers}$	representative_BMI	BMI_range	optimal_week_90
optimal_week_95				
Obese I (30-35)	147	32.017138	30.0-34.9	15.9
20.2				
Overweight (25-30)	61	29.136316	26.6-30.0	13.3
16.7				
Obese II+ (35)	30	36.326687	35.1-39.2	21.1
Never				

Summary Statistics: Total mothers: 238 Number of BMI groups: 3 Grouping method: clinical

## 1.7 Section 6: Monte Carlo Measurement Error Testing

Goal: Assess robustness to Y-chromosome concentration measurement errors.

### 1.7.1 Overview

- Model measurement error as Gaussian noise:  $y_observed = y_true + , \sim N(0, 2)$
- Run Monte Carlo simulations with noisy measurements
- Refit AFT models and recalculate group-specific optimal weeks
- Assess stability and provide uncertainty quantification
- Generate robustness summary with confidence intervals

```
[17]: ### Step 6.1: Monte Carlo Robustness Testing
      # Run Monte Carlo simulation to assess robustness to measurement errors
      # Use smaller sample size for demonstration (increase for production)
      print(" Starting Monte Carlo robustness testing...")
      print(" Note: Using reduced simulation count for demonstration")
      mc_results = run_monte_carlo_robustness_test(
         df tests, # Original test data
          construct_intervals, # Function to construct intervals
         fit aft models, # Function to fit AFT models
         perform_group_specific_analysis, # Function for group analysis
         n_simulations=300, # Production setting for smooth CI and stable assessment
          sigma_error=0.002, # 0.2% absolute concentration error
          confidence levels=[0.90, 0.95],
         random_seed=42,
         n_workers=1, # Single-threaded for stability
         verbose=True
      )
```

Starting Monte Carlo robustness testing...

Note: Using reduced simulation count for demonstration Running Monte Carlo robustness test...

Simulations: 300

Measurement error: 0.0020 (0.20%)

Confidence levels: ['90%', '95%']

Running simulations (single-threaded)...

Progress: 30/300 (10.0%)

Progress: 60/300 (20.0%)

Progress: 90/300 (30.0%)

Progress: 120/300 (40.0%)

Progress: 150/300 (50.0%)

Progress: 180/300 (60.0%)
Progress: 210/300 (70.0%)
Progress: 240/300 (80.0%)
Progress: 270/300 (90.0%)
Progress: 300/300 (100.0%)
Analyzing Monte Carlo results...

Monte Carlo Analysis:

Successful iterations: 300/300 (100.0%)

Group: Obese I (30-35)

90% confidence:

Mean:  $15.90 \pm 0.38$  weeks Median: 15.91 weeks 95% CI: [15.15, 16.52]

CV: 0.024 95% confidence:

Mean:  $20.03 \pm 0.56$  weeks Median: 20.00 weeks 95% CI: [19.09, 21.21]

CV: 0.028

Group: Overweight (25-30)

90% confidence:

Mean:  $13.55 \pm 0.67$  weeks Median: 13.48 weeks 95% CI: [12.12, 14.85]

CV: 0.049 95% confidence:

Mean:  $17.05 \pm 0.78$  weeks Median: 16.97 weeks 95% CI: [15.45, 18.64]

CV: 0.046

Group: Obese II+ (35)

90% confidence:

Mean:  $20.27 \pm 1.08$  weeks Median: 20.15 weeks 95% CI: [18.33, 22.42]

CV: 0.053 95% confidence:

Mean:  $24.06 \pm 0.80$  weeks Median: 24.24 weeks 95% CI: [22.18, 25.00]

CV: 0.033

Group: High BMI (T3)

90% confidence:

Mean:  $18.24 \pm 0.56$  weeks

Median: 18.33 weeks 95% CI: [16.89, 19.24]

CV: 0.031 95% confidence:

Mean:  $23.03 \pm 0.92$  weeks Median: 23.18 weeks 95% CI: [20.98, 24.48]

CV: 0.040

Group: Medium BMI (T2)

90% confidence:

Mean:  $15.62 \pm 0.39$  weeks Median: 15.61 weeks 95% CI: [14.92, 16.36]

CV: 0.025 95% confidence:

Mean: 19.75 ± 0.59 weeks Median: 19.70 weeks 95% CI: [18.71, 20.91]

CV: 0.030

Group: Low BMI (T1)

90% confidence:

Mean:  $13.78 \pm 0.60$  weeks Median: 13.79 weeks 95% CI: [12.58, 14.70]

CV: 0.044 95% confidence:

Mean:  $17.40 \pm 0.73$  weeks Median: 17.42 weeks 95% CI: [15.91, 18.56]

CV: 0.042

### Robustness Assessment:

Obese I (30-35) (90%): Good stability

CV: 0.024 (Excellent)

95% CI width: 1.37 weeks (Good)
Obese I (30-35) (95%): Good stability

CV: 0.028 (Excellent)

95% CI width: 2.12 weeks (Moderate)
Overweight (25-30) (90%): Good stability

CV: 0.049 (Excellent)

95% CI width: 2.73 weeks (Moderate)
Overweight (25-30) (95%): Good stability

CV: 0.046 (Excellent)

95% CI width: 3.18 weeks (Moderate)
Obese II+ (35) (90%): Poor stability

CV: 0.053 (Good)

```
95% CI width: 4.09 weeks (Poor)
       Obese II+ (35) (95%): Good stability
         CV: 0.033 (Excellent)
         95% CI width: 2.82 weeks (Moderate)
       High BMI (T3) (90%): Good stability
         CV: 0.031 (Excellent)
         95% CI width: 2.35 weeks (Moderate)
       High BMI (T3) (95%): Good stability
         CV: 0.040 (Excellent)
         95% CI width: 3.50 weeks (Moderate)
       Medium BMI (T2) (90%): Good stability
         CV: 0.025 (Excellent)
         95% CI width: 1.44 weeks (Good)
       Medium BMI (T2) (95%): Good stability
         CV: 0.030 (Excellent)
         95% CI width: 2.20 weeks (Moderate)
       Low BMI (T1) (90%): Good stability
         CV: 0.044 (Excellent)
         95% CI width: 2.12 weeks (Moderate)
       Low BMI (T1) (95%): Good stability
         CV: 0.042 (Excellent)
         95% CI width: 2.66 weeks (Moderate)
       Overall Stability: Good
         Good: 11
         Moderate: 0
         Poor: 1
[18]: ### Step 6.2: Robustness Summary & Uncertainty Quantification
      # Generate comprehensive robustness summary table
      mc_summary_table = create_monte_carlo_summary_table(mc_results, verbose=True)
      Monte Carlo Robustness Summary:
```

BMI\_Group optimal\_week\_90\_mean optimal\_week\_90\_std optimal\_week\_90\_ci stability\_90 optimal\_week\_95\_mean optimal\_week\_95\_std optimal\_week\_95\_ci stability\_95

\_\_\_\_\_\_

<i>v</i> –				
Obese I (30-35)		15.90	±0.38 [15.15,	16.52]
Good	20.03	±0.56	[19.09, 21.21]	Good
Overweight (25-30)		13.55	±0.67 [12.12,	14.85]
Good	17.05	±0.78	[15.45, 18.64]	Good
Obese II+ (35)		20.27	±1.08 [18.33,	22.42]
Poor	24.06	±0.80	[22.18, 25.00]	Good
High BMI (T3)		18.24	±0.56 [16.89,	19.24]
Good	23.03	±0.92	[20.98, 24.48]	Good
Medium BMI (T2)		15.62	±0.39 [14.92,	16.36]
Good	19.75	±0.59	[18.71, 20.91]	Good

```
Low BMI (T1) 13.78 \pm 0.60 [12.58, 14.70] Good 17.40 \pm 0.73 [15.91, 18.56] Good
```

Monte Carlo Test Summary:

Measurement error : 0.0020 (0.20%)

Simulations: 300 Success rate: 100.0% Overall stability: Good

## 1.8 Section 7: Baseline Two-step ML Comparison (Optional)

Goal: Compare AFT survival approach against traditional machine learning methods.

#### 1.8.1 Overview

- Classification Component: Binary outcome (ever reached 4% threshold)
- Regression Component: Time to threshold (interval midpoint approximation)
- Feature Engineering: BMI + derived features (squared, log-transformed)
- Model Comparison: Logistic Regression, Random Forest for both components
- Group Mapping: Map ML predictions to group-level recommendations
- Benchmarking: Compare AFT vs ML optimal weeks side-by-side

```
### Step 7.1: Complete ML Baseline Comparison Pipeline

# Run comprehensive ML baseline comparison including:
# - Binary classification (ever reached threshold)
# - Time-to-event regression (interval midpoint approximation)
# - Group-level recommendation mapping
# - Side-by-side comparison with AFT results

print(" Running ML baseline comparison against AFT survival analysis...")

ml_comparison_results = run_ml_baseline_comparison(
    df_X, # Use feature matrix with standardized BMI (bmi_z)
    group_analysis_results, # AFT group-specific results from Section 5
    confidence_levels=[0.90, 0.95],
    cv_folds=5,
    random_state=42,
    verbose=True
)
```

Running ML baseline comparison against AFT survival analysis...

Running ML baseline comparison pipeline...

Preparing dataset for ML baseline comparison...

ML dataset prepared:

Samples: 238

Features: 4 (bmi, bmi\_z, bmi\_squared, bmi\_log)

Ever reached threshold: 0.945

Mean time approximation: 8.66 weeks
Training classification models for binary outcome...

Training Logistic Regression...

AUC (CV):  $0.657 \pm 0.207$ 

AUC (full): 0.677 Brier score: 0.051

Training Random Forest...
AUC (CV): 0.565 ± 0.229

AUC (full): 0.998 Brier score: 0.015

Best classification model: Logistic Regression

Cross-validation AUC: 0.657

Training regression models for time to threshold...

Training Random Forest...

MAE (CV):  $3.499 \pm 0.280$  weeks RMSE (CV):  $5.323 \pm 0.470$  weeks

MAE (full): 1.575 weeks

 $R^2: 0.677$ 

Best regression model: Random Forest Cross-validation MAE: 3.499 weeks

Mapping ML predictions to group-level recommendations...

Group: Obese I (30-35)

n = 147, BMI = 32.1

Threshold prob: 0.945

Predicted time:  $8.74 \pm 2.80$  ML optimal week (90%): 6.40 ML optimal week (95%): 6.22

Group: Overweight (25-30)

n = 61, BMI = 29.0

Threshold prob: 0.973

Predicted time:  $7.53 \pm 1.93$  ML optimal week (90%): 6.18 ML optimal week (95%): 6.00

Group: Obese II+ (35)

n = 30, BMI = 36.7

Threshold prob: 0.889

Predicted time:  $10.46 \pm 3.27$  ML optimal week (90%): 7.05 ML optimal week (95%): 6.82

Comparing AFT vs ML baseline recommendations...

BMI_Group	n_mothers_A	FT n_mother	rs_ML	bmi_mean_AFT	bmi_mean_ML
AFT_week_90 ML_week_90 diff_90 AFT_week_95 ML_week_95 diff_95					
Overweight (25-30)		61	61	29.136316	28.991183
13.33 6.18	+7.15	16.67	6.00	+10.66	
Obese I (30-35)	1	.47	147	32.017138	32.087644
15.91 6.40	+9.51	20.15	6.22	+13.93	
Obese II+ (35)	;	30	30	36.326687	36.730942
21.06 7.05 +	14.01	Never	6.82	N/A	

```
Comparison Summary:
90% confidence level:
   Mean difference (AFT - ML): +10.22 ± 2.85 weeks
   Agreement: Poor
95% confidence level:
   Mean difference (AFT - ML): +12.29 ± 1.63 weeks
   Agreement: Poor
```

ML baseline comparison completed

## 1.9 Section 8: Validation & Final Policy Table

Goal: Generate final recommendations with comprehensive validation and uncertainty quantification.

#### 1.9.1 Overview

- Cross-validation: K-fold validation for model robustness assessment
- Sensitivity Analysis: Test different confidence levels and model assumptions
- Final Policy Table: Comprehensive recommendations with uncertainty bounds
- Results Export: Save final policy table for clinical implementation
- Quality Assurance: Complete validation summary with confidence metrics

```
[20]: ### Step 8.1: Comprehensive Validation & Final Policy Generation

# Run complete validation pipeline including:
# - K-fold cross-validation for model robustness
# - Sensitivity analysis across confidence levels
# - Final policy table with uncertainty quantification
# - Automatic export to CSV for clinical use

print(" Running comprehensive validation and final policy generation...")

final_validation_results = run_comprehensive_validation(
    df_intervals, # Interval-censored dataset
    group_analysis_results, # AFT group-specific results
```

```
construct_intervals, # Function to construct intervals
fit_aft_models, # Function to fit AFT models
perform_group_specific_analysis, # Function for group analysis
mc_results=mc_results, # Monte Carlo robustness results
k_folds=5, # Cross-validation folds
confidence_levels=[0.90, 0.95],
export_results=True, # Export to CSV
output_path=None, # Use default path
verbose=True
)
```

Running comprehensive validation and final policy generation... Running comprehensive validation and final policy generation... Performing 5-fold cross-validation of AFT pipeline...

Fold 1/5

Train: 190 intervals from 190 mothers Test: 48 intervals from 48 mothers Fold completed: 48 test predictions

Fold 2/5

Train: 190 intervals from 190 mothers Test: 48 intervals from 48 mothers Fold completed: 48 test predictions

Fold 3/5

Train: 190 intervals from 190 mothers Test: 48 intervals from 48 mothers Fold completed: 48 test predictions

Fold 4/5

Train: 191 intervals from 191 mothers Test: 47 intervals from 47 mothers Fold completed: 47 test predictions

Fold 5/5

Train: 191 intervals from 191 mothers Test: 47 intervals from 47 mothers Fold completed: 47 test predictions

Cross-validation Summary:
Successful folds: 5/5

Performing sensitivity analysis...

Testing different confidence levels...

Variant 1: ['85%', '90%', '95%']

Success

Variant 2: ['90%', '95%']

Success

Variant 3: ['80%', '90%', '95%']

Success

Testing AFT model robustness...

Weibull: AIC = 253.54LogLogistic: AIC = 254.20

Sensitivity analysis completed

Creating final policy recommendation table...

Final Policy Recommendation Table:

\_\_\_\_\_\_

BMI\_Range n\_mothers representative BMI bmi\_range optimal\_week\_90 threshold\_prob\_at\_optimal\_90 optimal\_week\_95 threshold\_prob\_at\_optimal\_95 mc ci 95 cv success rate

· — · — · ·	· — · — · ·	- · · · · · · · · · · · · · · · · · · ·		
Obese I (	30-35)	147	32.017138 30.0-34.9	15.9
0.900	20.2		0.951 [15.1, 16.5] [19	.1, 21.2]
1.00				
Overweight (	25-30)	61	29.136316 26.6-30.0	13.3
0.903	16.7		0.950 [12.1, 14.8] [15	.5, 18.6]
1.00				
Obese II+	(35)	30	36.326687 35.1-39.2	21.1
0.901	Never		N/A [18.3, 22.4] [22	.2, 25.0]
1.00				

Policy Summary:

Analysis method: clinical

Total mothers: 238 BMI groups: 3

Confidence levels: ['90%', '95%'] Monte Carlo stability: Good

Cross-validation success rate: 1.00

Final policy table exported to:

/home/richard/projects/cumcm/output/results/prob2\_policy\_recommendations.csv File size: 0.5 KB

Comprehensive validation completed Cross-validation success: 1.00

Final policy groups: 3 Results exported to:

/home/richard/projects/cumcm/output/results/prob2\_policy\_recommendations.csv