Healthcare Costs Prediction Using Bayesian Linear Regression

A Comparison with Frequentist Models

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01 Introduction





Abstract/Overview

- This project compares Bayesian and Frequentist linear regression models for predicting healthcare costs.
- The analysis uses the Medical Cost Personal Dataset, which includes demographic and medical variables.
- The Bayesian model incorporates priors, nonlinear terms, and interactions,
 producing credible intervals for interpretation.
- Goal: To evaluate each model's predictive performance and ability to handle uncertainty.

Introduction & Motivation

- Accurate healthcare cost prediction supports budgeting, insurance planning, and policy decisions.
- Traditional (frequentist) models provide point estimates but lack uncertainty quantification.
- Bayesian methods offer full posterior inference, flexible modeling, and clearer interpretation.
- Research Question: Can Bayesian regression provide comparable prediction performance while offering better uncertainty estimates and interpretability?

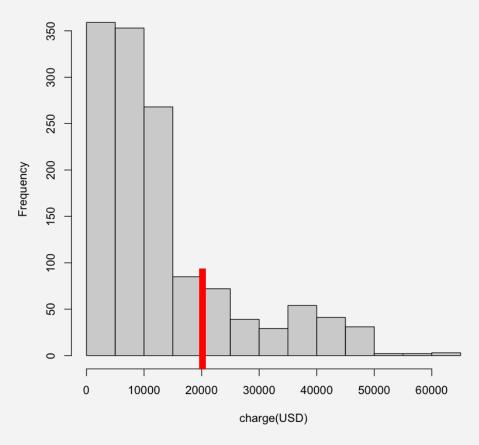
Dataset

- Dataset: Medical Cost Personal Dataset (Kaggle)
- Sample size: 1338 individuals
- Variables(7): age, sex, bmi, children, smoker, region, charges
- target variable : charges (Individual medical costs billed by health insurance)
- no missing values

18-64 age	f/m sex	15-53 bmi	0-5 children	yes/no smoker	4(US) region	Next slide charges	<u>!</u>
<int></int>	<chr></chr>	<dbl></dbl>	<int></int>	<chr></chr>	<chr></chr>	<dbl></dbl>	
19	female	35.150	0	no	northwest	2134.901	
62	female	38.095	2	no	northeast	15230.324	
46	female	28.900	2	no	southwest	8823.279	
18	female	33.880	0	no	southeast	11482.635	
18	male	34.430	0	no	southeast	1137.470	

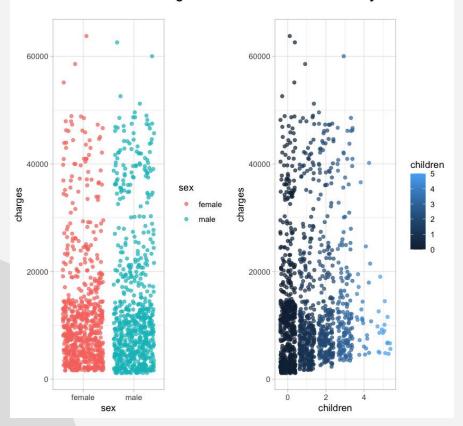
Exploratory Data Analysis (EDA)

Histogram of charge



Most charges in this group are below \$20,000, and high-cost outliers are rare.

Correlation between Charges and Sex / Children covered by insurance

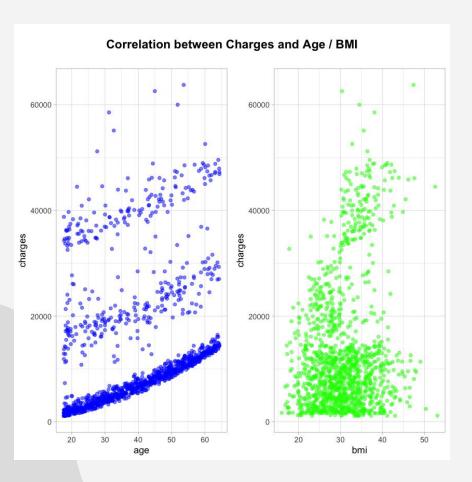


[Charges and Sex]

- Overall, there is no significant difference in the distribution of charges between males and females.
- This suggests that sex may not be a strong standalone predictor of healthcare costs in this dataset,
- → Therefore, it was **excluded from the final model**.

[Charges and Children]

- Charges for insurance with 4-5 children covered seems to go down.
- In general, the number of children alone still shows limited predictive power.

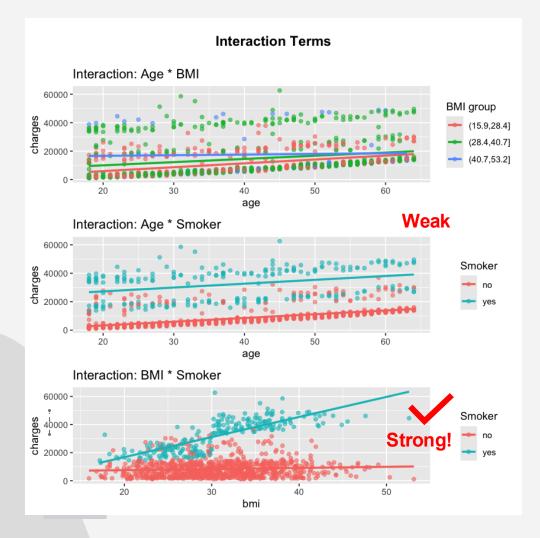


[Charges and Age]

- clear positive correlation between age and medical charges. As people get older, their medical expenses tend to increase.
- Furthermore, the layered appearance of data points suggests that age may interact with other variables, such as smoking status or BMI, influencing medical charges in a more complex way.

[Charges and BMI]

- Unlike age, the correlation here is weaker and more scattered.
 While there is a slight upward trend, particularly among individuals with higher BMI (above 35), the association is not consistent.
- This suggests that BMI alone is not a strong predictor of medical charges, and its effect may depend on interactions with other variables such as age or smoking status.



[Age * BMI] & [Age * Smoker]

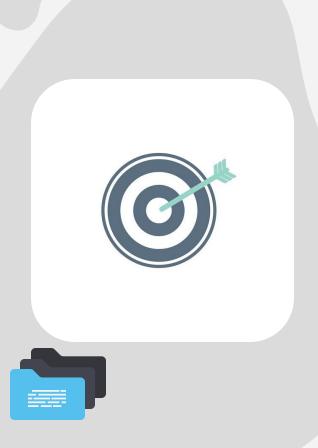
There is a slight upward trend between variables, but the interaction effect remains relatively weak.

→ Given the weak effects, these interactions were excluded from the final model.

[BMI * Smoker]

This interaction is **much stronger**. For smokers, charges increase sharply with higher BMI, while for non-smokers, the pattern remains flat.

→ Thus, only BMI × Smoker was included as an interaction term in the final Bayesian model.





02 Methodology

Frequentist Model

charges $\sim age + age^2 + bmi \times smoker + children + region$

```
Call:
lm(formula = formula_1, data = df_train)

Residuals:
    Min         1Q         Median         3Q         Max
-14279.0   -1881.0   -1309.2    -444.7         30232.7
```

- Nonlinear term: age² to capture acceleration in healthcare costs with age.
- Key interactions: BMI × smoker
- Significant predictors include age, children, smoker, and bmi × smoker

```
Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)
                -1789.022 943.214 -1.897 0.05814 .
age
                  259.782
                             10.645 24.404 < 2e-16 ***
bmi
                    5.269
                             28.458 0.185 0.85316
smokeryes
               -19955.662
                           1847.198 -10.803 < 2e-16 ***
children
                            123.203 4.089 4.67e-05 ***
                 503.729
regionnorthwest
                 -672.383
                            421.652 -1.595 0.11109
regionsoutheast -1159.931
                            426.484 -2.720 0.00664 **
regionsouthwest -1165.246
                            426.087 -2.735 0.00635 **
bmi:smokeryes
                 1429.994
                             58.874 24.289 < 2e-16 ***
```

Residual standard error: 4834 on 1061 degrees of freedom Multiple R-squared: 0.8409, Adjusted R-squared: 0.8397 F-statistic: 701.1 on 8 and 1061 DF, p-value: < 2.2e-16

Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

Bayesian Model

Variable Processing

```
df <- df %>%
 mutate(
    smoker = ifelse(smoker == "yes", 1, 0),
                                            → converted to binary (1 = "yes", 0 = "no")
    sex = as.integer(factor(sex)) - 1,
    region = as.integer(factor(region)), # 1\sim4 \rightarrow converted to integer index(1-4)
    charges = charges / 10000,
                                         # scale down \rightarrow scaled down by 10,000 to improve model stability
    bmi = (bmi - mean(bmi)) / sd(bmi),
    age = (age - mean(age)) / sd(age)
                                       \rightarrow age and bmi standardized (mean = 0, sd = 1) for better convergence
dat_list <- list(</pre>
  charges = df$charges,
  age = df 
  age2 = df age^2,
  bmi = df$bmi,
  smoker = df$smoker,
  region = df$region,
  children = df$children
```

Model Fitting

```
charges \sim Normal(\mu, \sigma)
\mu = a[region]
+ b_A \cdot age
+ b_{A2} \cdot age^2
+ b_B \cdot bmi
+ b_S \cdot smoker
+ b_I \cdot bmi \cdot smoker
+ b_C \cdot children
a[region] \sim Normal(a_{bar}, \sigma_{region})
```

- Fit using rethinking R package with HMC(Hamiltonian Monte Carlo)
- Nonlinear term: age² to capture acceleration in healthcare costs with age.
- **Key interactions**: BMI × smoker
- Group-level intercepts for region, using partial pooling through hierarchical priors to capture individual and group-level effects.
- ightarrow This allows the model to generalize better while capturing important structure in the data.

Priors

```
a[region] \sim Normal(a_{bar}, \sigma_{region})
       a_{\rm bar} \sim {\rm Normal}(0,1)
         b_A \sim \text{Normal}(0,1)
        b_{A2} \sim \text{Normal}(0, 0.5)
         b_B \sim \text{Normal}(0,1)
         b_S \sim \text{Normal}(0,1)
          b_I \sim \text{Normal}(0,2)
         b_C \sim \text{Normal}(0,1)
   \sigma_{\rm region} \sim \text{Exponential}(1)
           \sigma \sim \text{Student-t}(3,0,2)
```

- Normal priors used for all coefficients (centered at 0).
- Narrower prior for age² to regularize nonlinear effect.
- Wider prior for bmi × smoker to allow stronger interaction.
- Each region gets its own intercept a[region], drawn from a common distribution
- → It allows partial pooling and better generalization.
- Student-t prior on σ to improve robustness against outliers.

Posterior summary

Effective sample size

	mean	sd	5.5%	94.5%	rhat	ess_bulk
	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>
a[1]	0.754815804	0.037101148	0.69524852	0.81319317	1.0010766	3405.729
a[2]	0.704751033	0.035125848	0.64867023	0.76120848	1.0015224	3356.370
a[3]	0.655461571	0.035061227	0.59918968	0.71162514	1.0006304	3223.618
a[4]	0.653460423	0.035336899	0.59675505	0.70965157	1.0012693	3228.597
a_bar	0.687475746	0.071921111	0.58915328	0.78082251	1.0013757	2766.301
bA	0.366438888	0.012979543	0.34544085	0.38730460	1.0001156	7316.193
bA2	0.074006091	0.016113620	0.04838000	0.09979718	1.0010022	3386.566
bB	0.009912174	0.015423978	-0.01484373	0.03410852	1.0010531	5486.035
bS	2.377448367	0.032956742	2.32380000	2.42885000	0.9999566	7257.481
bl	0.875087819	0.031414759	0.82490155	0.92494169	1.0012652	6103.980
bC	0.067317408	0.011645894	0.04831901	0.08566258	1.0006048	3932.715
sigma_region	0.099450858	0.095837541	0.02703233	0.24677113	1.0012941	2502.534
sigma	0.481895559	0.009435628	0.46686184	0.49730700	1.0003315	7616.260

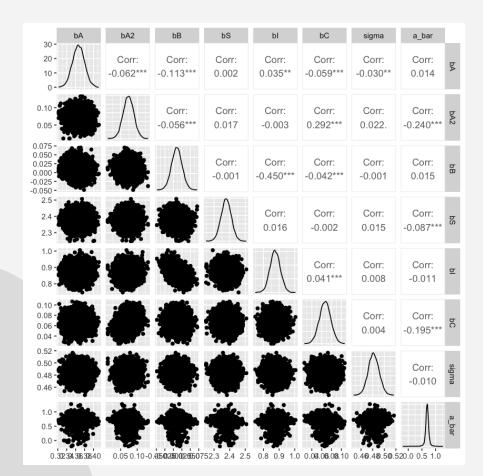
The Strongest effects

Rhat ≈ 1.00 Ess bulk > 1000 for all

→ good convergence and effective sampling

- → Being a smoker increases expected charges
- → Charges increase more steeply with BMI for smokers

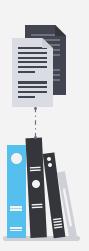
Posterior distribution



- Posterior samples of parameters are shown with pairwise correlations.
- Most parameters have weak correlations (near zero), suggesting low collinearity.
- Distributions look approximately normal.



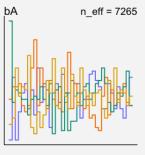
03 RESULT

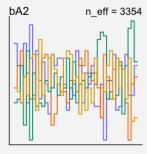


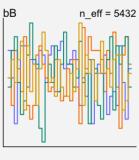
Result

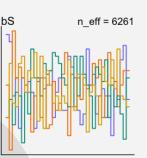
- The model was fit using 8000 samples with 4 chains,
 each running for 4000 iterations.
- → This provides robust posterior samples for each parameter.
- Each chain converged quickly, with total runtimes between 14–23 seconds.

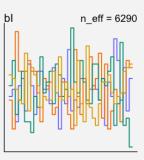
Trankplot

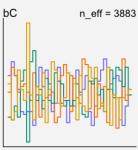




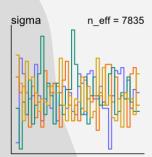


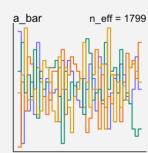




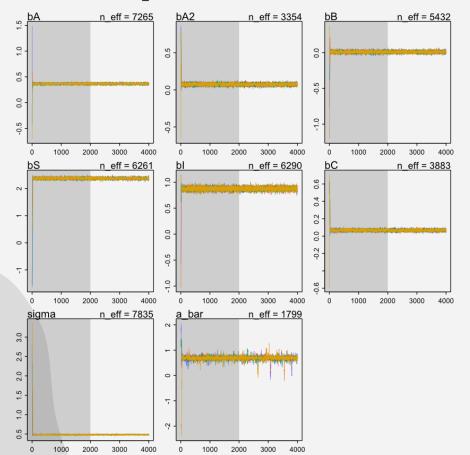


- Visualizes the ranks of parameter draws across chains.
- All chains are well mixed, no major divergences observed.





Traceplot



- All chains mix well with no signs of divergence or drift.
- Burn-in (warmup) phase is shaded gray.
- The results suggest **convergence is satisfactory** and posteriors are reliable for interpretation.

Frequent vs Bayesian

```
        Model
        RMSE
        MAE
        R2
        WAIC

        1
        Frequentist Linear Regression 4930.554
        2952.016
        0.8409286
        NA

        2
        Bayesian Linear Regression (full) 4796.795
        2888.051
        0.8429861
        1857.318
```

- Bayesian model slightly outperformed the frequentist model in both RMSE and MAE
- R² values were nearly identical, indicating similar explanatory power
- WAIC available only for Bayesian model, which aids in model comparison and validation
- Bayesian model provides uncertainty quantification and more interpretable posterior estimates

Conclusion/Limitation

Key Findings

- Bayesian regression offered competitive predictive performance
- Interaction terms and nonlinear effects improved model expressiveness
- Posterior distributions allow uncertainty visualization and deeper interpretation

Limitations

- Small dataset size (n = 1338) may limit generalizability
- The model assumes Gaussian residuals (could be improved with more flexible likelihoods)
- Regional effects are modest. more hierarchical structure (e.g., for smoker subgroups) could be explored

Thank you