Life Expectancy Trends (2000-2015)

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Introduction

Life expectancy says a lot about how people live and the conditions they face around the world. In this project, we wanted to look at how life expectancy differs across continents and how it changes over time. We started by checking whether continents already had different average life expectancies in the year 2000. That way we could get a baseline snapshot of global inequality. Then, we tested whether those differences changed between 2000 and 2015 to see if countries have been getting closer together or if the gap has stayed the same.

The main goal is to understand whether the differences in life expectancy reflect ongoing global inequality or improvements that are happening unevenly across regions.

The data come from Kaggle's Life Expectancy 2000–2015 dataset (https://www.kaggle.com/datasets/vrec99/life-expectancy-2000-2015), which combines information from the World Health Organization, World Bank, and the United Nations. It includes 119 countries across 15 years, with variables like GDP per capita, CO emissions, health expenditure, and internet access.

```
data = read.csv("Life_Expectancy.csv")
```

Section 1 – Comparing Continents in 2000

We wanted to start by establishing a baseline for global inequality in life expectancy. To see whether people in some continents were living longer than others at the start of the 21st century.

Our hypotheses were:

H_0 : The distributions of life expectancy are the same across all continents.

H_a : At least one continent differs.

Checking The Assumptions

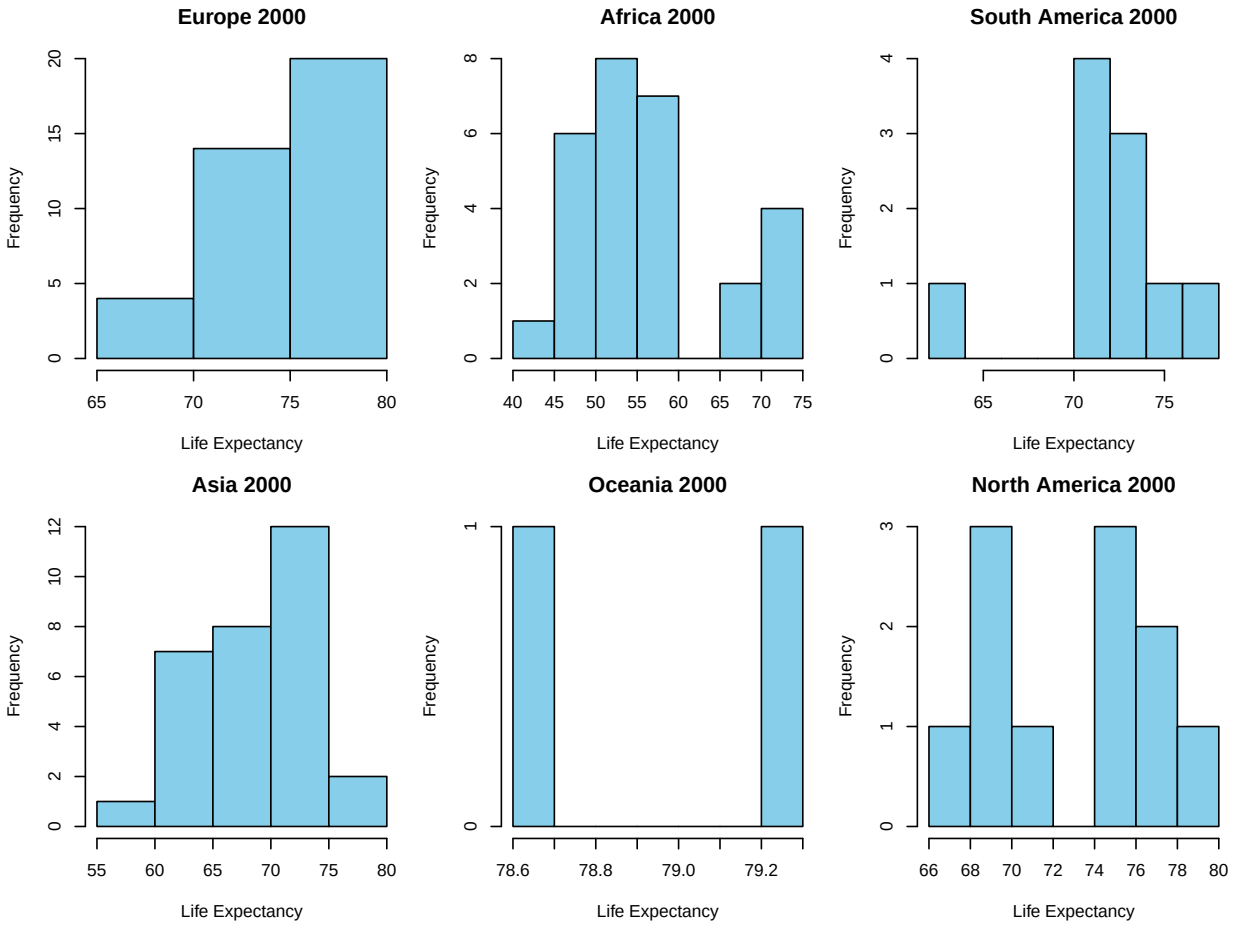
We planned to test this using a one-way ANOVA, so we first checked whether the assumptions of normality and equal variances were met.

1. Normality Normality is important because ANOVA assumes that residuals within each group are normally distributed.

H_0 : The life expectancy values within each continent are normally distributed.

H_a : The life expectancy values within at least one continent deviate from normality.

For normality, we visually inspected histograms of life expectancy for each continent.



Visual inspection of the histograms suggested that the distributions were varied, with some having approximately bell shaped curves, some with unique distributions, and some skewed. To confirm normality statistically, we used a Monte Carlo Anderson–Darling test.

This test measures how far the observed data deviates from what would be expected under a normal distribution with the same mean and standard deviation. Comparing our observed statistic to this simulated one let us estimate the p-value and decide whether the normality assumption held.

```
set.seed(123123)
nmc = 10000
n = length(x)
mc_ad = c()

# observed statistic
x_sorted = sort(x)
F_emp = (1:n) / (n+1)
F_null = pnorm(x_sorted, mean(x_sorted), sd(x_sorted))
AD_obs = sum(((abs(F_emp - F_null))^2) / (F_emp * (1 - F_emp)))

# simulated normality
for(k in 1:nmc){
  smc = sort(rnorm(n, 0, 1))
  F_emp_mc = (1:n)/(n+1)
```

```
  F_null_mc = pnorm(smc, 0, 1)
  mc_ad = c(mc_ad, sum((F_emp_mc - F_null_mc)^2 / (F_emp_mc * (1 - F_emp_mc))))
  }

alpha = 0.10
ad_crit = quantile(mc_ad, 1 - alpha)
emp_pval = mean(mc_ad >= AD_obs)
```

```
## Anderson-Darling Critical Value: 2
```

```
## Empirical P-Value: 0
```

The Anderson–Darling test gave an empirical p-value of 0.0004, which is below the alpha level of 0.10. This means we reject the null hypothesis of normality. So, the life expectancy data for 2000 aren't normally distributed. This makes sense because some continents have much higher averages while others are lower, so the data are naturally skewed instead of bell-shaped. Before deciding how to move forward, we also wanted to check whether the variability between groups was similar, because large differences in spread can also affect ANOVA results.

2. Testing Equal Variances Equal variances (homoscedasticity) matter because ANOVA assumes that all groups have about the same level of variability. If one continent's life expectancy values are way more spread out than another's, the results can be misleading.

H_0 : The variances of life expectancy among continents are equal.

H_a : At least one group's variance differs.

We used the Bartlett statistic, which tests whether the variances of life expectancy across groups (j) are equal. It compares each group's sample variance (s_j^2) to the pooled variance (s_p^2) that would be expected if all groups had the same variability. The Bartlett statistic (B_{stat}) is computed as:

$$Bstat = \frac{v * ln(s_p^2) - (\sum_{j=1}^{g} v_j * ln(s_j^2))}{1 + \frac{1}{3(g-1)} * [(\sum_{j=1}^{g} \frac{1}{v_j}) - \frac{1}{v}]}$$

First, we split the dataset by continent so that we could calculate each group's mean, variance, and sample size:

```
xs = split(x, data_2000$Continent)
xbarj = sapply(xs, mean)
s2j = sapply(xs, var)
nj= sapply (xs, length)
```

Each continent's variance (s_j^2) represents how spread out its life expectancy values are. Then we calculated each group's degrees of freedom ($v_j = n_j - 1$) and counted the number of groups (g):

```
vj= nj-1
g= length(unique(data_2000$Continent))
```

Next, we computed the pooled variance, which combines the group variances into a single weighted value based on their degrees of freedom:

$$s_p^2 = \frac{\sum_{j=1}^{g} v_j s_j^2}{\sum_{j=1}^{g} v_j}$$

```r
sp2 = sum(vj * s2j)/ sum(vj)
```

After defining the components for each continent (sample variance s_j^2, degrees of freedom v_j, and the number of groups g), we computed the Bartlett statistic:

```r
bastat = ((sum(vj) * log(sp2)) - sum(vj * log(s2j)))/
  (1+ 1/(3*(g-1))* (sum(1/vj)- 1/sum(vj)))

pval = pchisq(bastat, g-1, lower.tail= F)
```

```
## Bartlett's Test Statistic: 26.5106
```

```
## Bartlett's Test P-Value: 7.102463e-05
```

The Bartlett's test returned a test statistic of 26.51 and a p-value of 0.0001, which is below the alpha level of 0.10. This means we reject the null hypothesis and conclude that the variances of life expectancy are not equal across continents. So, the spread of life expectancy values differs depending on the region.

Welch's One-Factor ANOVA

Because Bartlett's test indicated that the variances across continents were not equal, we used Welch's ANOVA, which adjusts for unequal variances and sample sizes. This version of ANOVA is more robust when the homogeneity of variance assumption is violated.

$H_0 : \mu_{\text{Africa}} = \mu_{\text{Asia}} = \mu_{\text{Europe}} = \mu_{\text{North America}} = \mu_{\text{South America}} = \mu_{\text{Oceania}}$
$H_a :$ At least one mean differs.

Welch's F statistic is calculated as:

$$F^* = \frac{\sum_{j=1}^{g} w_j(\bar{X}_j - \bar{X}_w)^2/(g-1)}{1 + \frac{2(g-2)}{g^2-1}\sum_{j=1}^{g}\frac{(1-w_j/\sum_{k=1}^{g} w_k)^2}{n_j-1}}$$

where $w_j = \frac{n_j}{s_j^2}$ are the weights for each group.

```r
nj = sapply(xs, length)
s2j = sapply(xs, var)
wj = nj/s2j
xbarbar_h = sum(wj*xbarj)/sum(wj)
g = length(unique(data_2000$Continent))
n = length(x)

ssm_h = sum(wj*(xbarj-xbarbar_h)^2)
msm_h = ssm_h/g
v_h = ((sum(nj/s2j))^2) / (sum((nj^2) / (s2j^2 * (nj - 1))))

Fstat_h = msm_h/(1+2 * (g-2)/v_h)
p = pf(Fstat_h, g-1, v_h, lower.tail=F)
```

```
## F Statistic: 11.8083
```

```
## P-Value: 0.06788656
```

At an alpha level of 0.10, the p-value (0.0679) is slightly above the cutoff. Therefore, we fail to reject the null hypothesis, meaning that when adjusting for unequal variances, there is no statistically significant difference in mean life expectancy across continents at the 10% level.

However, since the data were not normally distributed (as shown by the Anderson–Darling test), we could not fully rely on the results of Welch's ANOVA.

Kruskal–Wallis Test

To confirm whether the previous conclusion holds, we used the Kruskal–Wallis test, a non-parametric alternative that compares the median ranks instead of the means.

The hypotheses are:

H_0 : The distributions of life expectancy are the same across all continents.

H_a : At least one continent differs.

We used the Kruskal–Wallis statistic, which tests whether the distributions of life expectancy across groups (j) are the same. It ranks all observations together, then compares the average rank within each group ($\bar{R}_j$) to the overall mean rank ($\bar{R}$). If the group ranks differ a lot, it suggests that at least one continent's distribution is different. The Kruskal–Wallis statistic (H) is computed as:

$$H = \frac{12}{N(N+1)} \sum_{j=1}^{g} n_j (\bar{R}_j - \bar{R})^2$$

```
R_all = rank(unlist(xs))
Rj = split(R_all, rep(names(xs), times = sapply(xs, length)))
nj = sapply(Rj, length)
N = sum(nj)
g = length(Rj)
Rbar_j = sapply(Rj, mean)
Rbar = (N + 1) / 2

H_stat = (12 / (N * (N + 1))) * sum(nj * (Rbar_j - Rbar)^2)
pval_kw = pchisq(H_stat, g - 1, lower.tail = FALSE)
```

```
## Kruskal-Wallis H Statistic: 65.0293
```

```
## P-Value: 1.105162e-12
```

The Kruskal–Wallis test returned an H statistic of 65.03 with a p-value of 1.10×10^{-12}, which is below the alpha level of 0.10. This means we reject the null hypothesis and conclude that life expectancy distributions differ significantly across continents in the year 2000.

Therefore, there was clear inequality in life expectancy at the start of the 21st century, some regions were already living much longer on average than others. This result confirms that the gap in global health outcomes was large even before major developments of the following decades.

Section 2 – Comparing Continents from 2000-2015

After finding that life expectancy differed across continents in 2000, we wanted to see whether those differences changed over time. Did the gap between regions decrease or have some continents continued to fall behind? To figure that out, we looked at how the average life expectancy changed from 2000 to 2015.

Our hypotheses were:

H_0 : $\mu_{2000} = \mu_{2001} = \mu_{2002} = \cdots = \mu_{2015}$
H_a : At least one mean differs.

Checking The Assumptions

We planned to test this using a repeated-measures ANOVA, so we first checked whether the assumptions of normality, sphericity, and independence were met.

1. Normality Normality is important because repeated-measures ANOVA assumes that the residuals (or differences between time points) are roughly normally distributed.

H_0 : The life expectancy values across years are normally distributed. H_a : The life expectancy values deviate from normalit

To test this, we used the Kolmogorov–Smirnov test, which compares the sample's cumulative distribution to a normal distribution with the same mean and standard deviation.

The KS statistic (D) is computed as:

$$D = \max \left| F_{\text{emp}}(x) - F_{\text{null}}(x) \right|$$

In R, it was calculated as:

```
x = data$Life.Expectancy
x_sorted = sort(x)
set.seed(123123)
nmc = 10000
n = length(x_sorted)

# observed statistic
F_emp = (1:n) / (n+1)
F_null = pnorm(x_sorted, mean(x_sorted), sd(x_sorted))
KS_obs = max(abs(F_emp - F_null))

# simulated normality
KS_mc = c()
for(k in 1:nmc){
  smc = sort(rnorm(n, 0, 1))
  F_emp_mc = (1:n) / (n+1)
  F_null_mc = pnorm(smc, 0, 1)
  KS_mc = c(KS_mc, max(abs(F_emp_mc - F_null_mc)))
  }

alpha = 0.10
KS_crit = quantile(KS_mc, 1 - alpha)
emp_pval = mean(KS_mc >= KS_obs)
```

```
## Kolmogorov-Smirnov Critical Value: 0.02790051
```

```
## Empirical P-Value: 0
```

The Kolmogorov–Smirnov test gave a critical value of 0.0279 and an empirical p-value of 0, which is below the alpha level of 0.10. This means we reject the null hypothesis of normality. So, the life expectancy values across years aren't normally distributed. Before deciding how to move forward, we also wanted to check the assumption of sphericity, which deals with the relationships between repeated measurements over time.

2. Sphericity Sphericity is the repeated-measures version of equal variances. It assumes that the variances of the differences between every pair of years are roughly equal.

H_0 : The variances of the differences between all pairs of years are equal. H_a : At least one pair of years differs in variance c

We computed Mauchly's test to evaluate the sphericity assumption. This test measures whether the covariance matrix of repeated measures is close to spherical.

The Mauchly statistic (W) is calculated as:

$$W = \frac{|\Sigma|}{\left(\frac{\text{tr}(\Sigma)}{k}\right)^k}$$

where $|\Sigma|$ is the determinant of the covariance matrix and $\text{tr}(\Sigma)$ is its trace.

The test statistic (M_{stat}) is then computed as:

$$M_{\text{stat}} = -(n-1)\ln(W)$$

```
k = ncol(x)
n = nrow(x)
c = cov(x)
tr = sum(diag(c))
det = det(c)

W = det / ((tr / k)^k)
Mstat = -(n-1) * log(W)
df = (k*(k-1)/2)
Mcrit = qchisq(1-0.10, df)
Mpval = pchisq(Mstat, df,lower.tail = F)
```

```
## Mauchly's Test Statistic: 2119.985
```

```
## Mauchly's Test P-Value: 0
```

The Mauchly's test of sphericity returned a test statistic of **2119.99** and a p-value of **0**, which is below the alpha level of 0.10. This means we reject the null hypothesis of sphericity. So, the variances of the differences between years are not equal, meaning that the correlations between time points vary.

Non-Spherical Repeated-Measures ANOVA

Since Mauchly's test showed that the data violated sphericity, we used the Greenhouse–Geisser correction to adjust the repeated-measures ANOVA. This correction adjusts the degrees of freedom to make the test more accurate when the relationships between time points aren't perfectly equal.

$H_0 : \mu_{2000} = \mu_{2001} = \mu_{2002} = \cdots = \mu_{2015}$
H_a : At least one mean differs.

The corrected F statistic is calculated as:

$$F = \frac{MS_{\text{Year}}}{MS_{\text{Error(Year)}}}$$

but both degrees of freedom are multiplied by the Greenhouse–Geisser epsilon (ε_{GG}):

$$df_1^* = \varepsilon_{GG}(k-1), \quad df_2^* = \varepsilon_{GG}(k-1)(n-1)$$

```
xbarj = colMeans(x)
xbari = rowMeans(x)
xbarbar = mean(x)
s2all = var(x)

n = nrow(x)
g = ncol(x)
Y = x - rowMeans(x)
c = cov(Y)

SSM = n*sum((xbarj - xbarbar)^2)
E = x - xbari - matrix(xbarj, n, g, byrow=T) + xbarbar
SSE = sum(E^2)
Fstat = (SSM/(g-1))/(SSE/((n-1)*(g-1)))

# Greenhouse-Geisser Correction
eps_GG = ((sum(diag(c)))^2) / ((g - 1) * sum(c^2))
df1_GG = eps_GG * (g - 1)
df2_GG = eps_GG * (g - 1) * (n - 1)

p_GG = pf(Fstat, df1_GG, df2_GG, lower.tail = FALSE)
```

```
cat("F Statistic:", Fstat, "\n")
```

```
## F Statistic: 22.95869
```

```
cat("P-Value:", p_GG, "\n")
```

```
## P-Value: 0.004653024
```

After applying the correction, the results showed a significant main effect of year, $p = 0.0047$. This means we reject the null hypothesis and conclude that mean life expectancy changed significantly between 2000 and 2015.

Bootstrap Confidence Interval

Since the Kolmogorov–Smirnov test showed that the data were not normally distributed, we can't fully rely on the repeated-measures ANOVA results. So, we used a bootstrap confidence interval to check whether mean life expectancy changed between 2000 and 2015.

By resampling the data 10,000 times and recalculating the mean difference each time, the bootstrap method builds an empirical distribution of possible mean changes. This lets us estimate a confidence interval without assuming that the data are normal.

```
set.seed(123123)
data_2000 = subset(data, Year == 2000)$Life.Expectancy
data_2015 = subset(data, Year == 2015)$Life.Expectancy
obs_diff = mean(data_2015) - mean(data_2000)

nboot = 10000
boot_diffs = c()
for (i in 1:nboot) {
  s1 = sample(data_2000, replace = TRUE)
  s2 = sample(data_2015, replace = TRUE)
  boot_diffs[i] = mean(s2) - mean(s1)
}

alpha = 0.10
ci_lower = quantile(boot_diffs, alpha / 2)
ci_upper = quantile(boot_diffs, 1 - alpha / 2)
```

```
cat("Bootstrap CI:", ci_lower, "to", ci_upper, "\n")
```

```
## Bootstrap CI: 3.157008 to 6.605049
```

The 90% bootstrap confidence interval ranged from 3.16 to 6.61 years. Since the interval does not include zero, we reject the null hypothesis and conclude that life expectancy changed significantly across this period. This supports the results from the Greenhouse–Geisser–corrected ANOVA, showing that global life expectancy changed over time and that this change was statistically meaningful.

Section 3 – Life Expectancy and CO2 Emissions

bootstrap regression and add in a graph