# Selection Intensity is not linear

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I want to demonstrate that selection intensity does not follow a linear pattern. While increasing selection intensity is beneficial up to a certain point, beyond a specific threshold, the returns diminish. This is specially important in the context of response to selection and the breeder's equation to measure genetic gain as the breeder's equation is proportional to selection intensity.

$$R = \frac{ir\sigma_A}{L}$$

Where R is the response to selection, i is the selection intensity,  $\sigma_A$  is the additive genetic variance and r is the square root of the heritability, also known as accuracy. L is an optional parameter that relates genetic gain to time in terms of the generation interval.

#### What is selection intensity?.

Selection intensity is a measure of how strongly selection pressures act on a population. It quantifies the extent to which certain individuals, are selected as parents for the next generation.

The selection intensity is given by the expression:

$$i = \frac{\phi\left(\Phi^{-1}\left(1 - \frac{z}{100}\right)\right)}{\frac{z}{100}}$$

where i is the selection intensity,  $\phi()$  is the probability density function of the normal distribution,  $\Phi^{-1}()$  is the quantile function of the normal distribution, and z is the percent of selected individuals.

We can write the expression above in R as follows

```
intensity <- function (z) {
  numerator <- dnorm(qnorm(1-z/100))
  return(numerator/(z/100))
}</pre>
```

Using the function above we can compute the selection intensity for 0.0001% to 95% by 0.01 % increments of the population rounded to two decimal places.

```
# Create a vector of percentages from 0.001% to 95%
percentages <- seq(0.001, 95, by = 0.1)

# Apply the function to calculate selection intensity for each percentage
selection_intensity_values <- sapply(percentages, intensity)

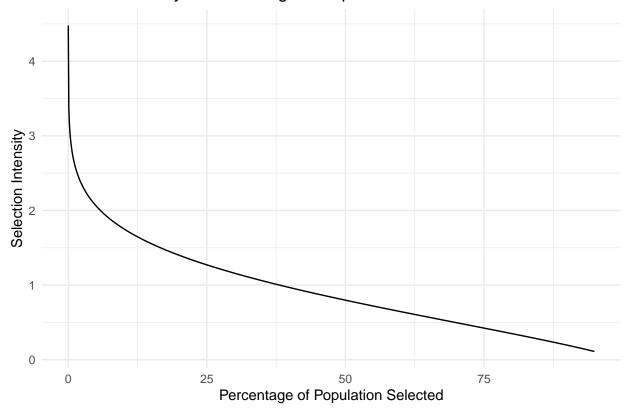
# Create a dataframe
selection_df <- data.frame(Percentage = percentages, Intensity = selection_intensity_values)</pre>
```

The code above creates a dataframe with two columns: Percentage of the population selection and its corresponding Intensity. This is advantageous because quantitative genetics books report this numbers but often the percentage of the population you wish to select does not correspond to the tabulated values. This function allows you to compute any intensity value for any

### Visualization

How does the relationship between percent of the population selected and the intensity of look like?

### Selection Intensity vs Percentage of Population Selected



We can see that the relationship is not linear. To illustrate this further let's zoom in into selection percentages between 10 and 0.001.

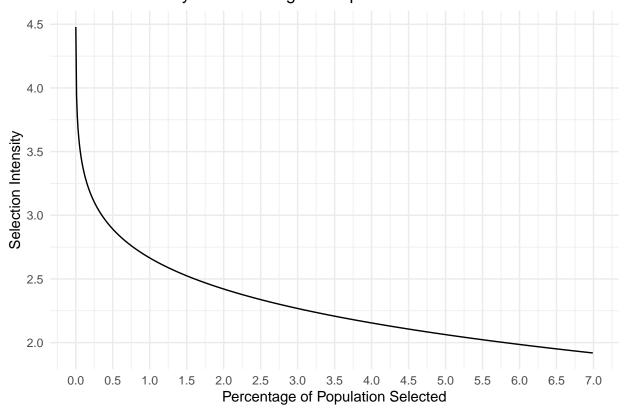
```
# Create a vector of new percentages from 0.001% to 10%
new_percentages <- seq(0.001, 7, by = 0.01)

# Apply the function to calculate selection intensity for each percentage
selection_intensity_values_new <- sapply(new_percentages, intensity)</pre>
```

```
# Create a dataframe
selection_df_new <- data.frame(Percentage = new_percentages, Intensity = selection_intensity_values_new)</pre>
```

Let's vizualise this

## Selection Intensity vs Percentage of Population Selected



Note in the plot above for example that selection intensity jumps from 3.5 to 4.5 with a very small increment of the proportion of individuals selected.

I hope this helps highlight that high selection intensities can drive genetic gain up to a certain point, but if pushed to high, the returns diminish.

### References

Professor Endelman Selection Theory 812 Lectures