

# Machine learning for regression problems

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### Introducing the dataset

#### **DNA** methylation and age in European bats



- Wild Bechstein's bats (Myotis bechsteinii)
- N = 62
- seven CpG sites (<u>here</u>)
- % methylation
- age: [0-14] years





Source: <a href="https://en.wikipedia.org/wiki/Bechstein%27s\_bat">https://en.wikipedia.org/wiki/Bechstein%27s\_bat</a>

#### **DNA** methylation and age in European bats



Received: 26 February 2018

Revised: 21 April 2018

Accepted: 2 May 2018

DOI: 10.1111/1755-0998.12925

#### RESOURCE ARTICLE



Application of a novel molecular method to age free-living wild Bechstein's bats

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### DNA methylation and age in European bats



		Age	CpG 1	CpG 2	CpG 3	CpG 4	CpG GRIA2	CpG GRIA2	
Sample	Age	category	TET2	TET2	TET2	TET2	1	2	ASPA 1
BabyBechs_SHW	0	Age 0-3	29	21	26	31	2	2	61
Dd_Juv_Hamgree									
n	0	Age 0-3	30	21	24	32	1	2	59
A2402	1	Age 0-3	44	38	51	53	1	5	48
A2414-2014	1	Age 0-3	48	36	50	46	1	2	53

#### Regression problems



**Demonstration 2.1** 

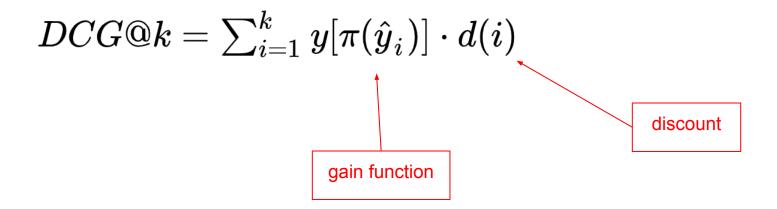
 $\rightarrow$  linear\_regression.Rmd

## Normalized discounted cumulative gain (NDCG)



NDCG is a **ranking metric** developed in information theory which has been applied to evaluation of genomic selection models

NDCG evaluates the **top** (e.g. 20%) **individuals in the ranking**, which are supposed to be the most relevant when comparing models



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$$DCG@k = \sum_{i=1}^{k} y[\pi(\hat{y}_i)] \cdot d(i)$$

The higher the DCG, the better

However, DCG is difficult to interpret (unbounded)

NDCG

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$$NDCG(y,\hat{y}) = rac{\sum_{i=1}^k \left(y[\pi(\hat{y})]_i \cdot d(i)
ight)}{\sum_{i=1}^k \left(y[\pi(y)]_i \cdot d(i)
ight)}$$

NDCG values lie in [0,1]

#### Regression problems



Exercise 2.1

 $\rightarrow$  linear\_regression.Rmd