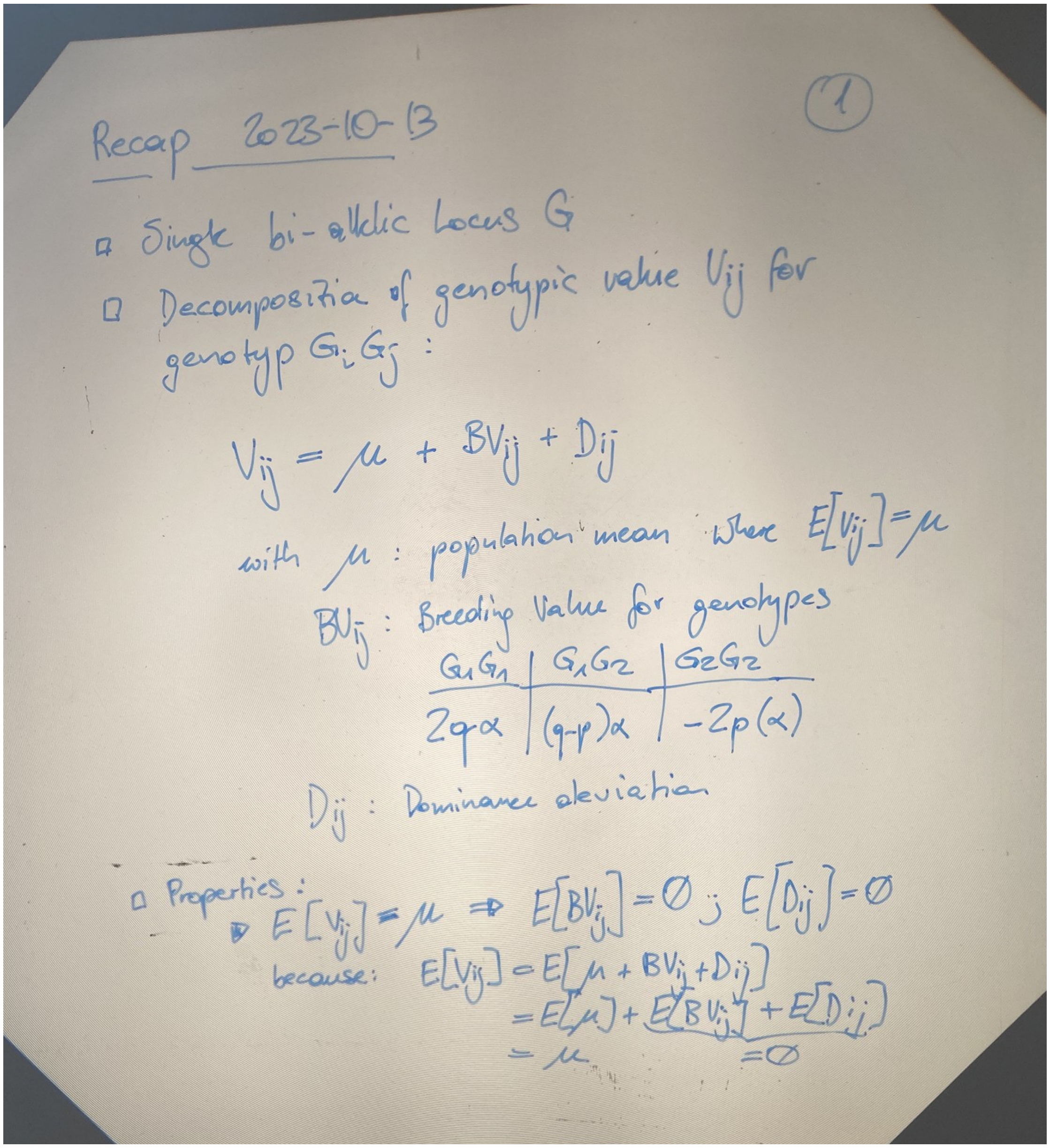
OHP Picture 1



Recap 2023-10-13 ①

- Single bi-allelic Locus G
- Decomposition of genotypic value V_{ij} for genotyp G_iG_j:

$$V_{ij} = \mu + BV_{ij} + D_{ij}$$

with μ : population mean where $E[V_{ij}] = \mu$

BV_{ij} : Breeding Value for genotypes

G_1G_1	G_1G_2	G_2G_2
$2q\alpha$	$(q-p)\alpha$	$-2p(\alpha)$

D_{ij} : Dominance deviation

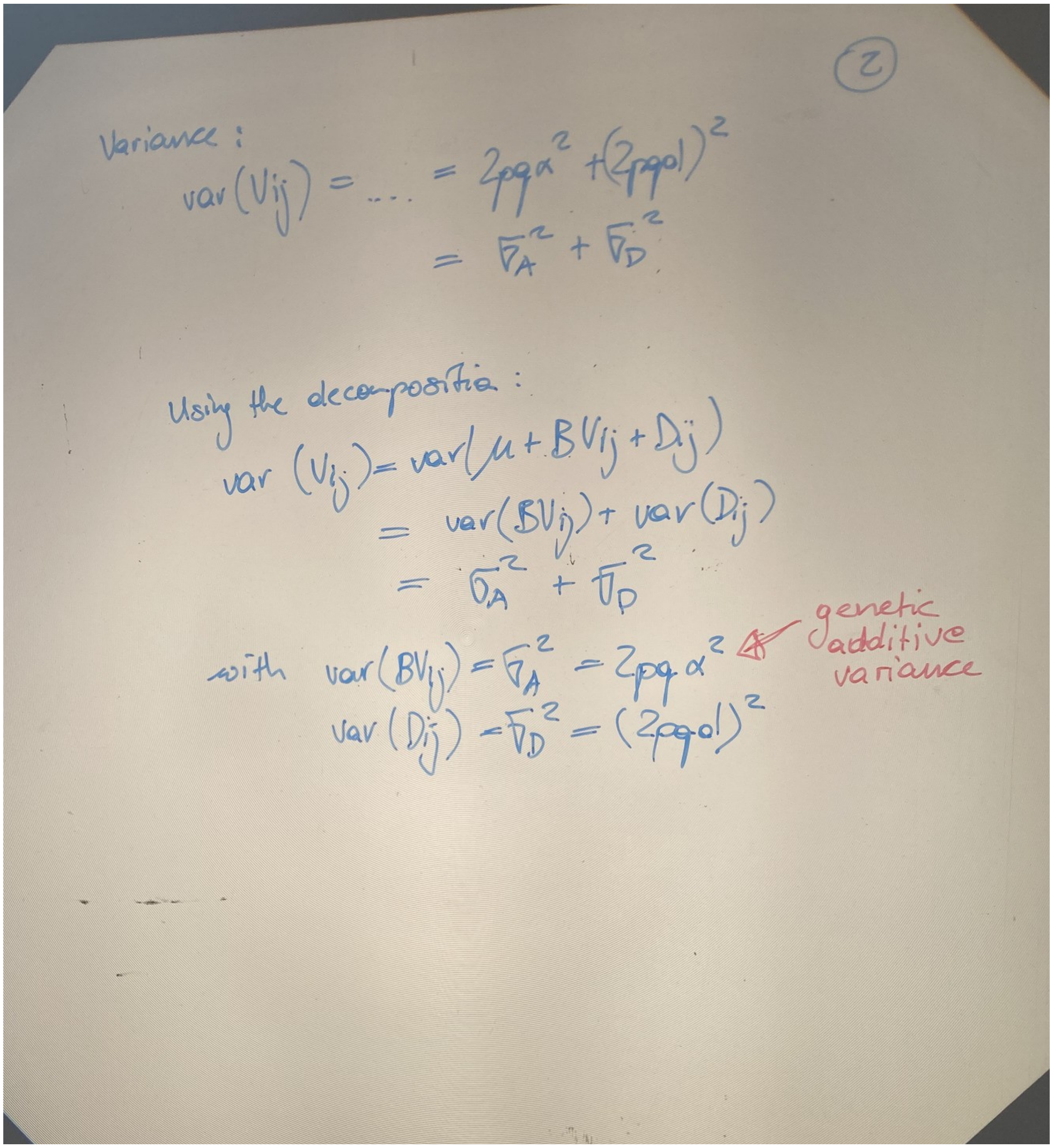
- Properties:
  - $E[V_{ij}] = \mu \Rightarrow E[BV_{ij}] = 0 \,;\, E[D_{ij}] = 0$

because: $E[V_{ij}] = E[\mu + BV_{ij} + D_{ij}]$

$$= E[\mu] + \underbrace{E[BV_{ij}] + E[D_{ij}]}_{=0}$$

$$= \mu$$

OHP Picture 2



②

Variance :

$$\mathrm{var}(V_{ij}) = \dots = 2pq\alpha^2 + (2pqd)^2$$

$$= \sigma_A^2 + \sigma_D^2$$

Using the decomposition :

$$\mathrm{var}(V_{ij}) = \mathrm{var}(\mu + BV_{ij} + D_{ij})$$

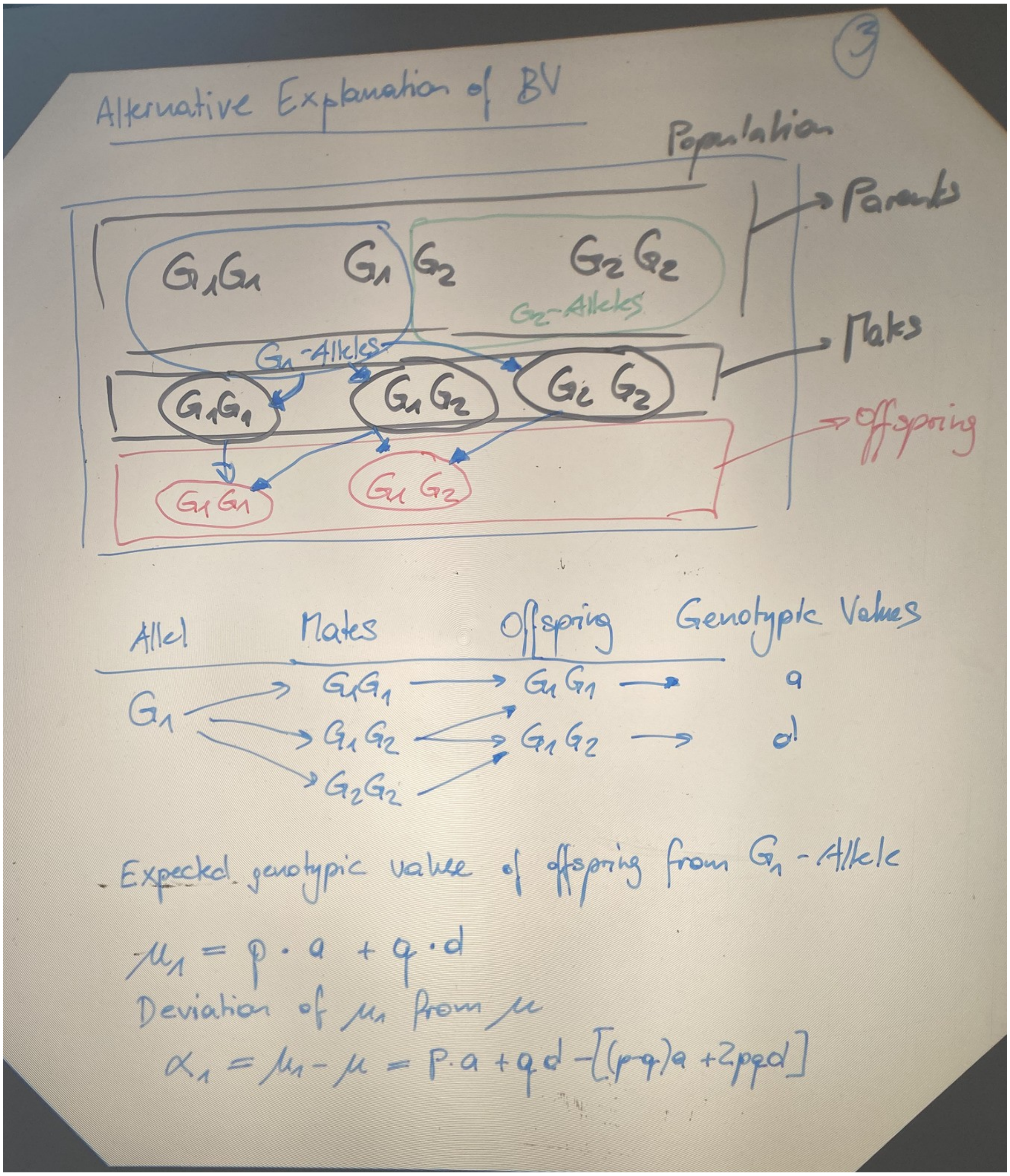
$$= \mathrm{var}(BV_{ij}) + \mathrm{var}(D_{ij})$$

$$= \sigma_A^2 + \sigma_D^2$$

with $\mathrm{var}(BV_{ij}) = \sigma_A^2 = 2pq\alpha^2 \leftarrow$ genetic additive variance

$\mathrm{var}(D_{ij}) = \sigma_D^2 = (2pqd)^2$

OHP Picture 3



Alternative Explanation of BV

Allel	Mates	Offspring	Genotypic Values
G_1	G_1G_1	G_1G_1	a
	G_1G_2	G_1G_2	d
	G_2G_2		

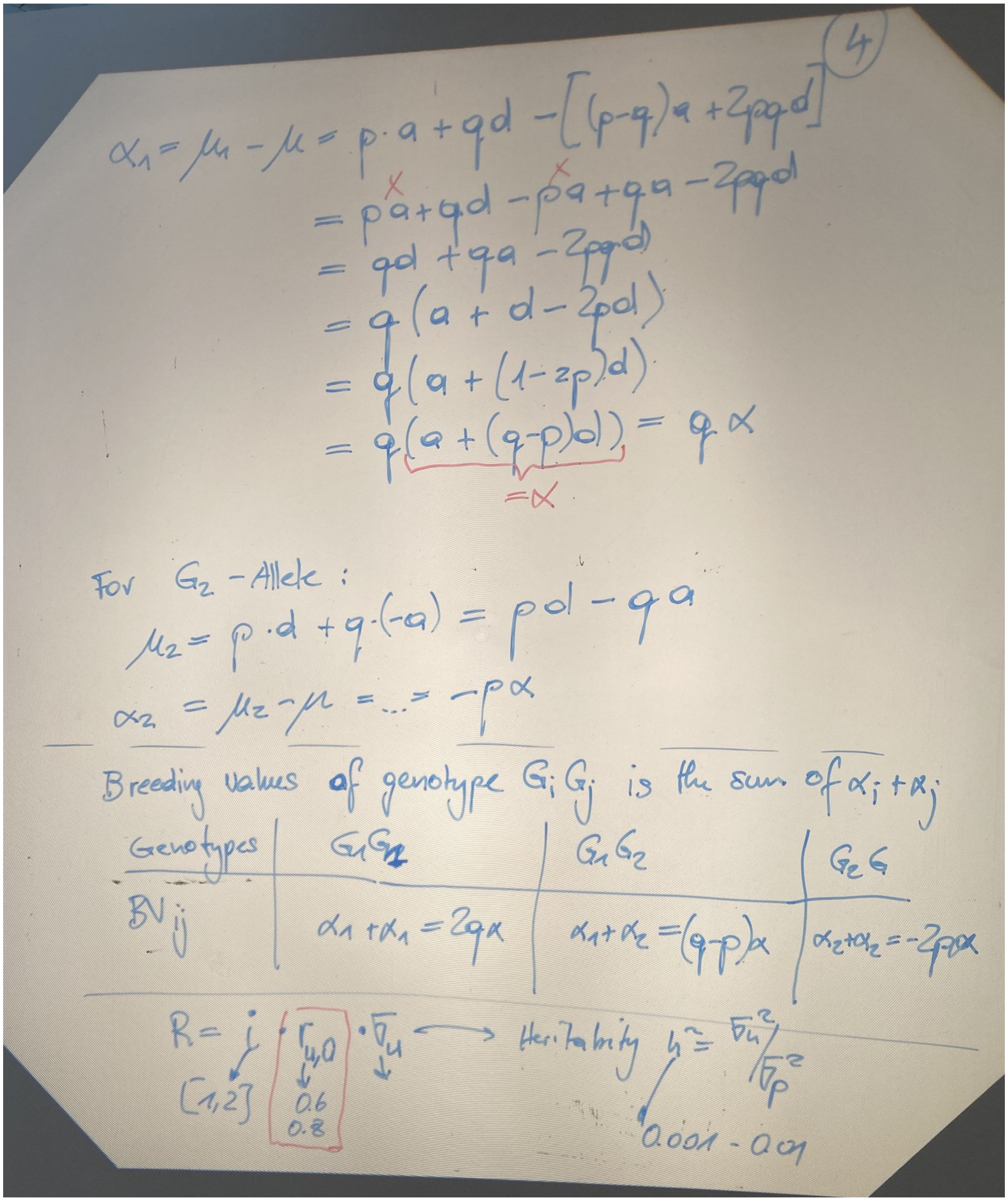
- Expected genotypic value of offspring from G_1-Allele

$$\mu_1 = p \cdot a + q \cdot d$$

Deviation of μ_1 from μ

$$\alpha_1 = \mu_1 - \mu = p \cdot a + q \cdot d - [(p-q)a + 2pqd]$$

OHP Picture 4



④

$$\alpha_1 = \mu_1 - \mu = p \cdot a + qd - \left[(p-q)a + 2pqd\right]$$
$$= \cancel{p}a + qd - \cancel{p}a + qa - 2pqd$$
$$= qd + qa - 2pqd$$
$$= q(a + d - 2pd)$$
$$= q(a + (1-2p)d)$$
$$= q\underbrace{(a + (q-p)d)}_{=\alpha} = q\alpha$$

For G_2 - Allele :

$$\mu_2 = p \cdot d + q \cdot (-a) = pd - qa$$
$$\alpha_2 = \mu_2 - \mu = \ldots = -p\alpha$$

Breeding values of genotype $G_i G_j$ is the sum of $\alpha_i + \alpha_j$

Genotypes	G_1G_1	G_1G_2	G_2G
BV_{ij}	$\alpha_1 + \alpha_1 = 2q\alpha$	$\alpha_1 + \alpha_2 = (q-p)\alpha$	$\alpha_2 + \alpha_2 = -2p\alpha$

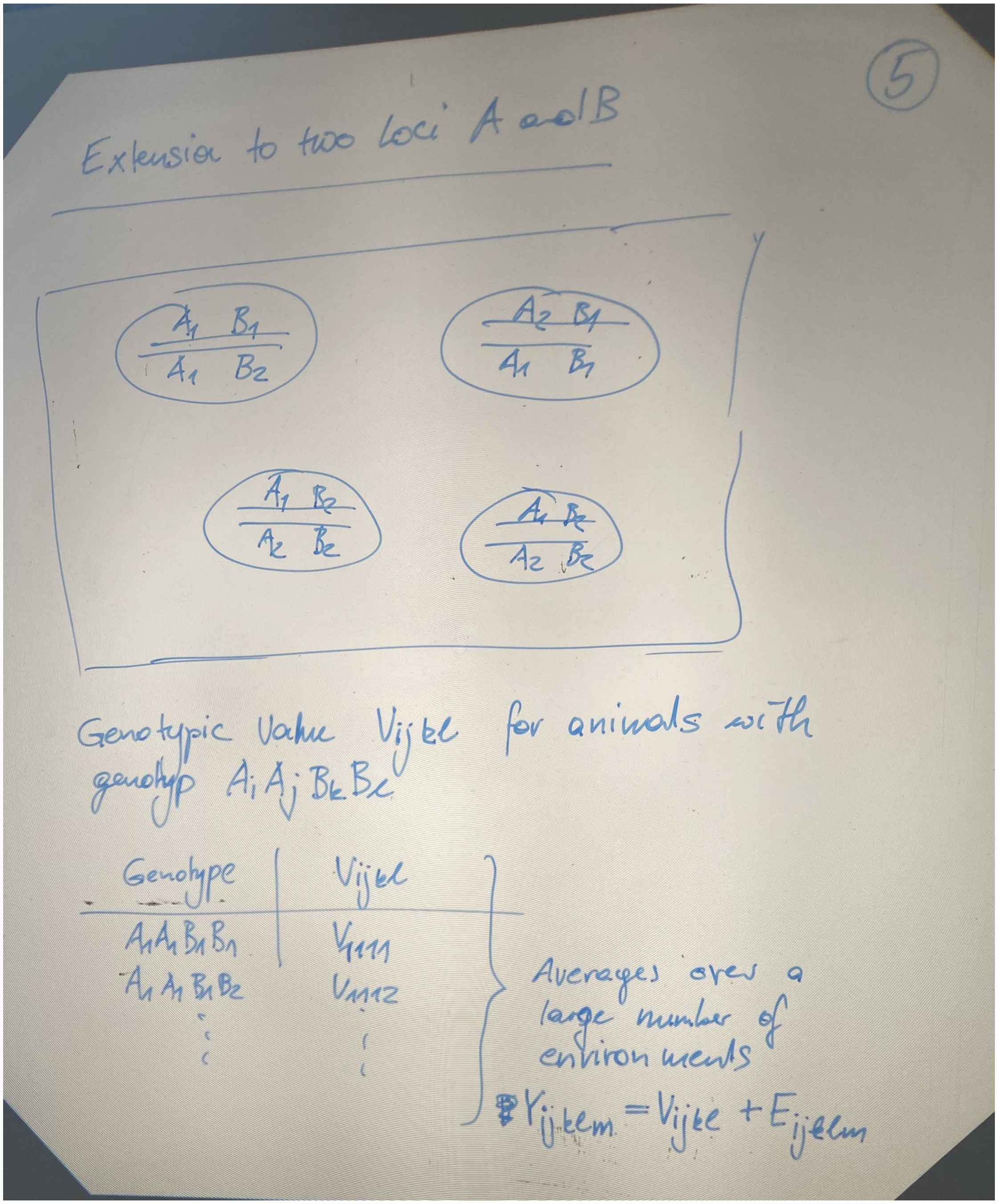
$$R = i \cdot \boxed{r_{u,a}} \cdot \sigma_u \longleftrightarrow \text{Heritability } h^2 = \sigma_u^2 / \sigma_p^2$$

i: [1,2]

$r_{u,a}$: 0.6 0.8

h^2: 0.001 - 0.01

OHP Picture 5



⑤

Extension to two loci A and B

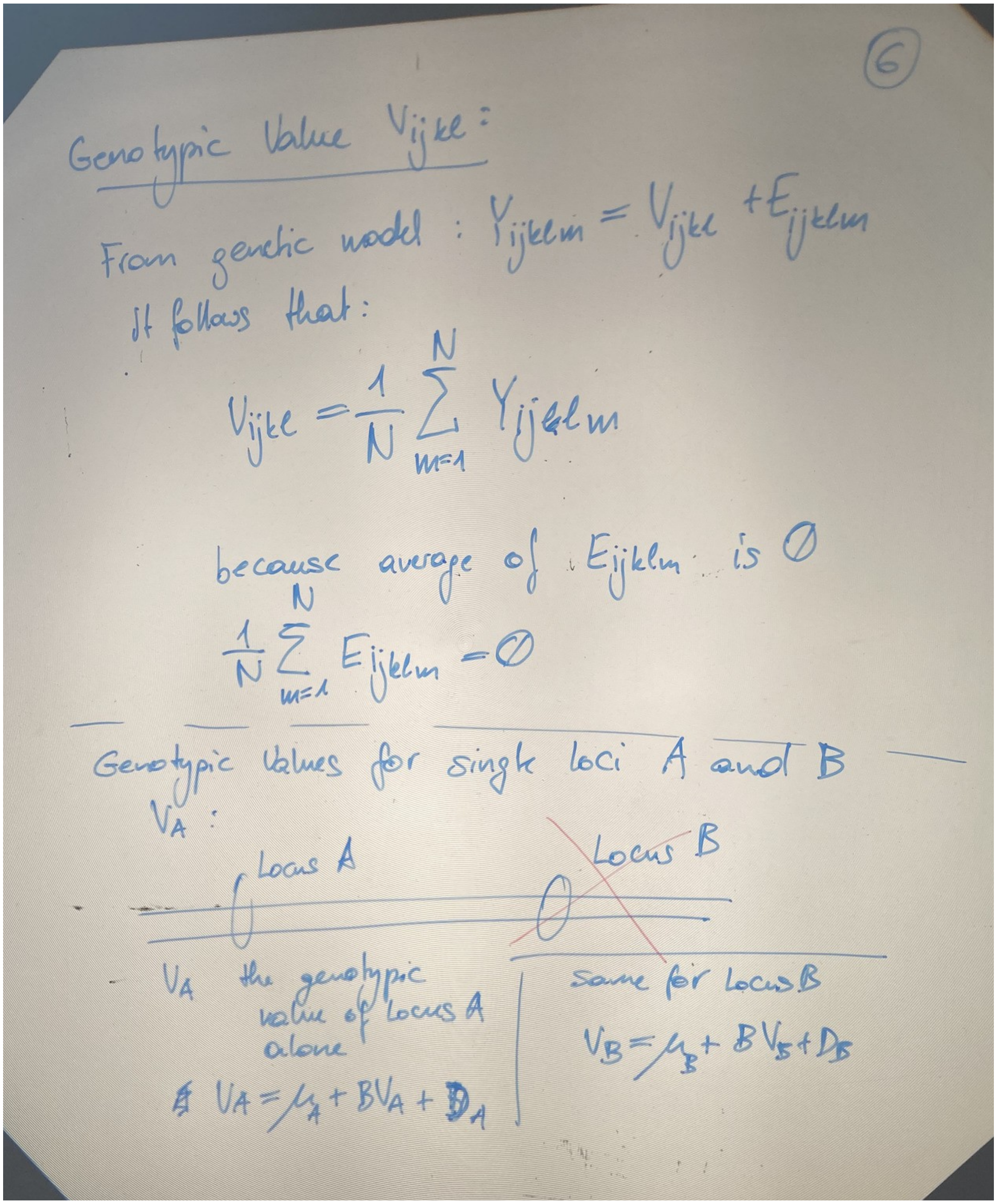
Genotypic Value V_{ijkl} for animals with genotyp $A_iA_jB_kB_l$

Genotype	V_{ijkl}
$A_1A_1B_1B_1$	V_{1111}
$A_1A_1B_1B_2$	V_{1112}
$\vdots$	$\vdots$

Averages over a large number of environments

$Y_{ijklm} = V_{ijkl} + E_{ijklm}$

OHP Picture 6



⑥

Genotypic Value V_{ijkl}:

From genetic model: $Y_{ijklm} = V_{ijkl} + E_{ijklm}$

It follows that:

$$V_{ijkl} = \frac{1}{N}\sum_{m=1}^{N} Y_{ijklm}$$

because average of E_{ijklm} is 0

$$\frac{1}{N}\sum_{m=1}^{N} E_{ijklm} = 0$$

Genotypic Values for single loci A and B

V_A:

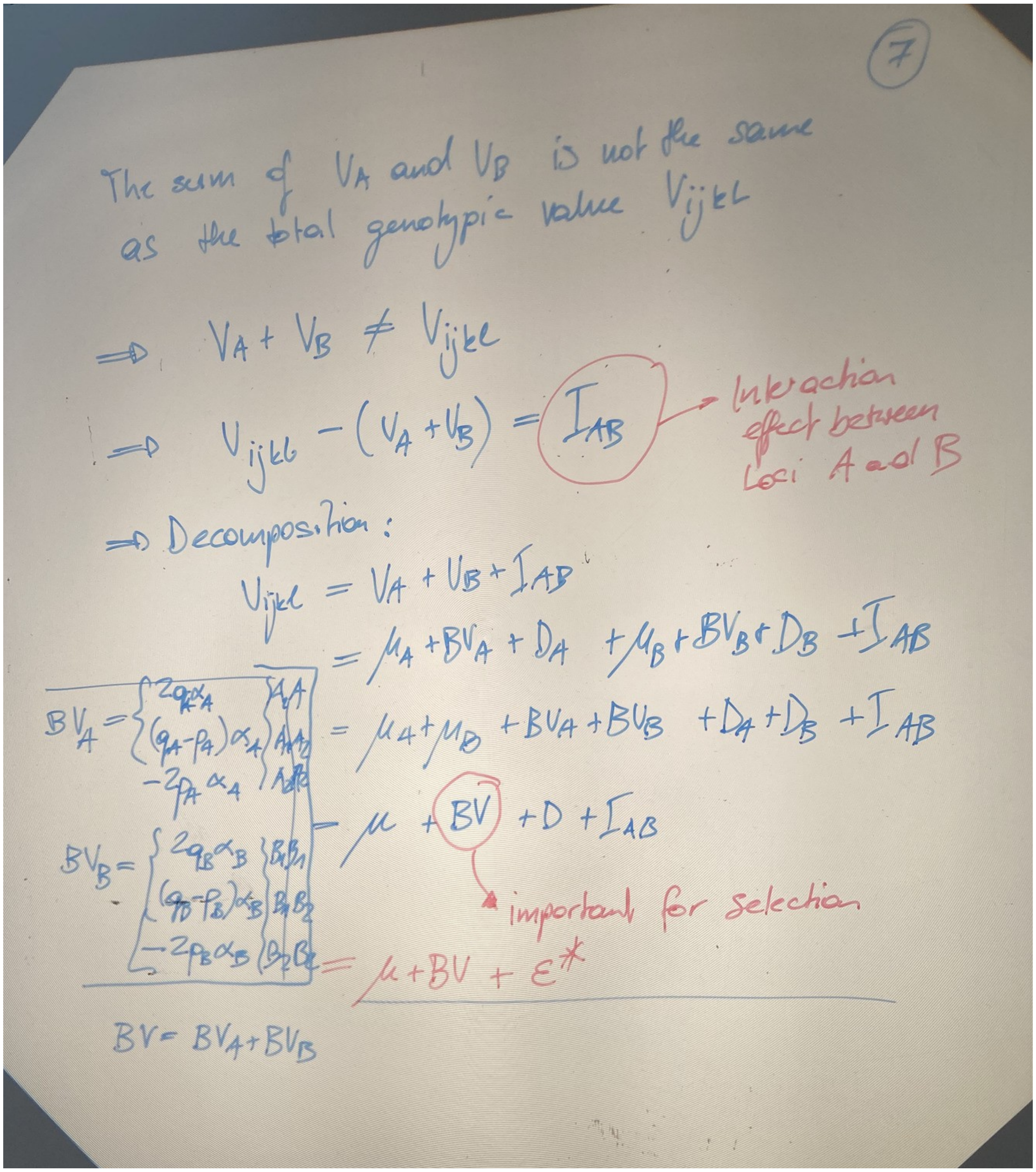
V_A the genotypic value of Locus A alone

$V_A = \mu_A + BV_A + D_A$

Same for Locus B

$V_B = \mu_B + BV_B + D_B$

OHP Picture 7



⑦

The sum of V_A and V_B is not the same as the total genotypic value V_{ijkl}

$$\Rightarrow \quad V_A + V_B \neq V_{ijkl}$$

$$\Rightarrow \quad V_{ijkl} - (V_A + V_B) = \boxed{I_{AB}}$$

Interaction effect between Loci A and B

⇒ Decomposition:

$$V_{ijkl} = V_A + V_B + I_{AB}$$

$$= \mu_A + BV_A + D_A + \mu_B + BV_B + D_B + I_{AB}$$

$$= \mu_A + \mu_B + BV_A + BV_B + D_A + D_B + I_{AB}$$

$$= \mu + \boxed{BV} + D + I_{AB}$$

important for selection

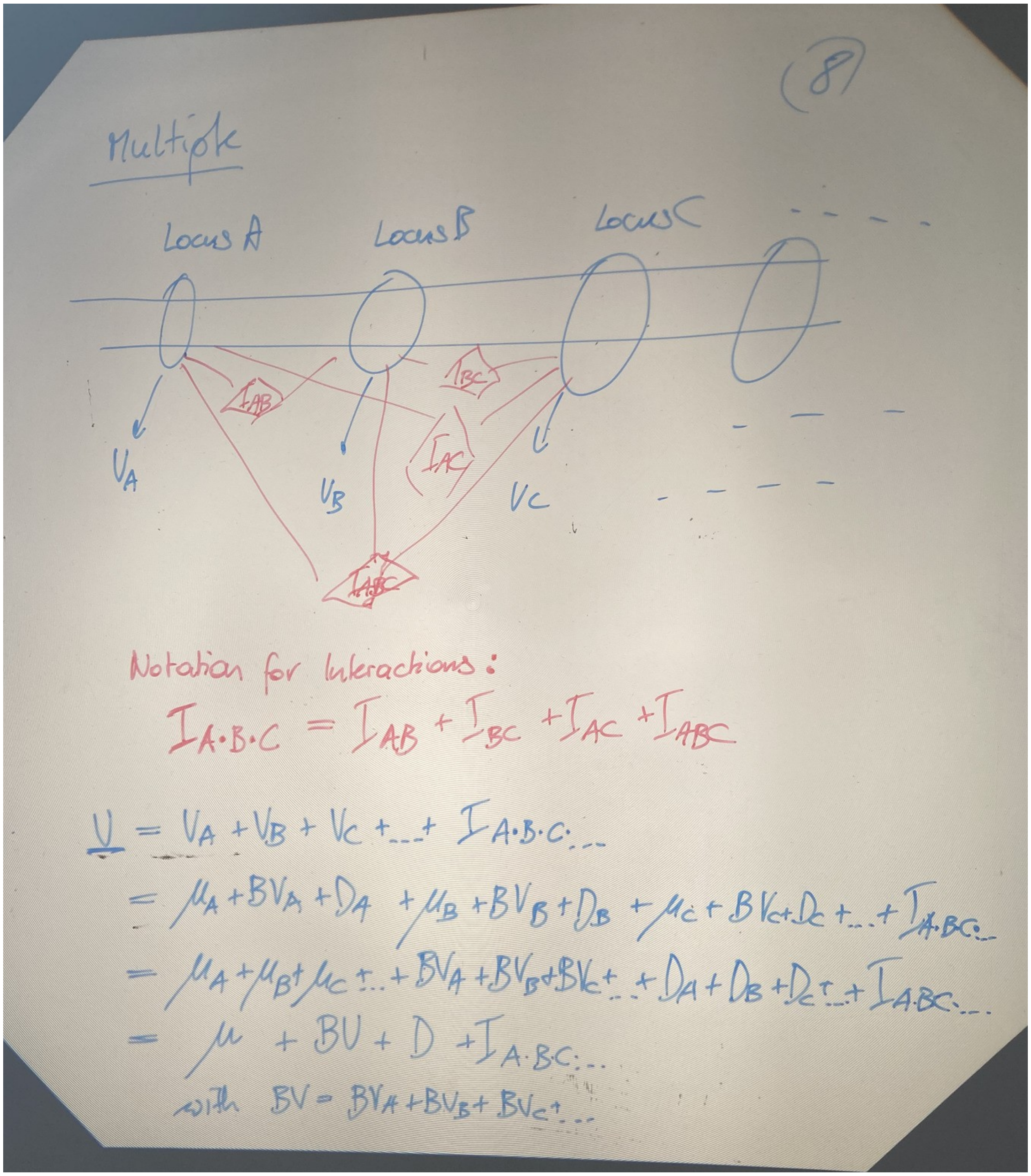
$$= \mu + BV + \varepsilon^*$$

$$BV_A = \begin{cases} 2q_A\alpha_A & A_1A_1 \\ (q_A - p_A)\alpha_A & A_1A_2 \\ -2p_A\alpha_A & A_2A_2 \end{cases}$$

$$BV_B = \begin{cases} 2q_B\alpha_B & B_1B_1 \\ (q_B - p_B)\alpha_B & B_1B_2 \\ -2p_B\alpha_B & B_2B_2 \end{cases}$$

$$BV = BV_A + BV_B$$

OHP Picture 8



⑧

Multiple

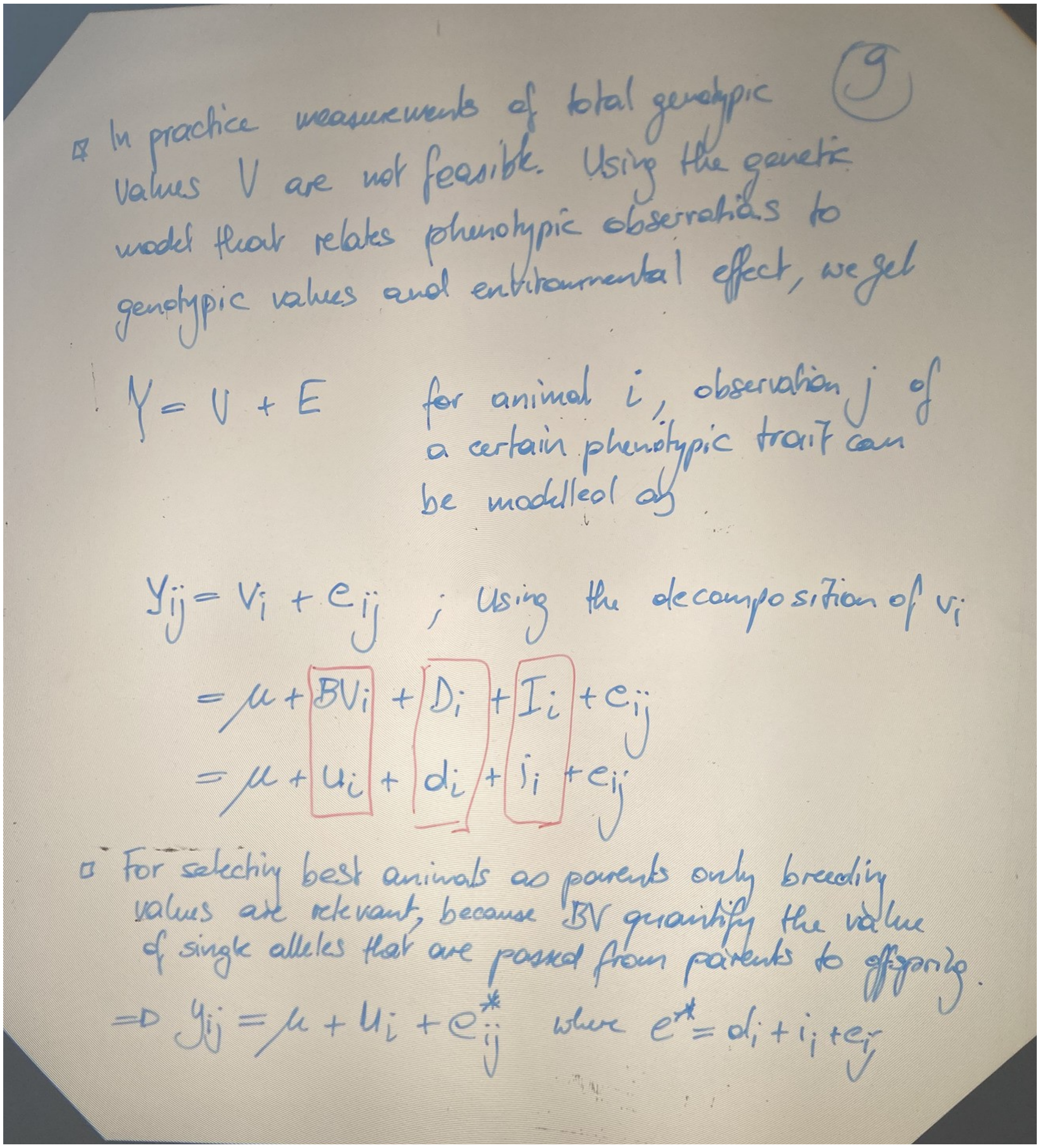
Notation for Interactions:

$$I_{A\cdot B\cdot C} = I_{AB} + I_{BC} + I_{AC} + I_{ABC}$$

$$\begin{aligned}\underline{V} &= V_A + V_B + V_C + \ldots + I_{A\cdot B\cdot C\cdot\ldots} \\ &= \mu_A + BV_A + D_A + \mu_B + BV_B + D_B + \mu_C + BV_C + D_C + \ldots + I_{A\cdot B\cdot C\cdot\ldots} \\ &= \mu_A + \mu_B + \mu_C + \ldots + BV_A + BV_B + BV_C + \ldots + D_A + D_B + D_C + \ldots + I_{A\cdot B\cdot C\cdot\ldots} \\ &= \mu + BV + D + I_{A\cdot B\cdot C\cdot\ldots}\end{aligned}$$

with $BV = BV_A + BV_B + BV_C + \ldots$

OHP Picture 9



(9)

☒ In practice measurements of total genotypic values V are not feasible. Using the genetic model that relates phenotypic observations to genotypic values and environmental effect, we get

$Y = V + E$ for animal i, observation j of a certain phenotypic trait can be modelled as

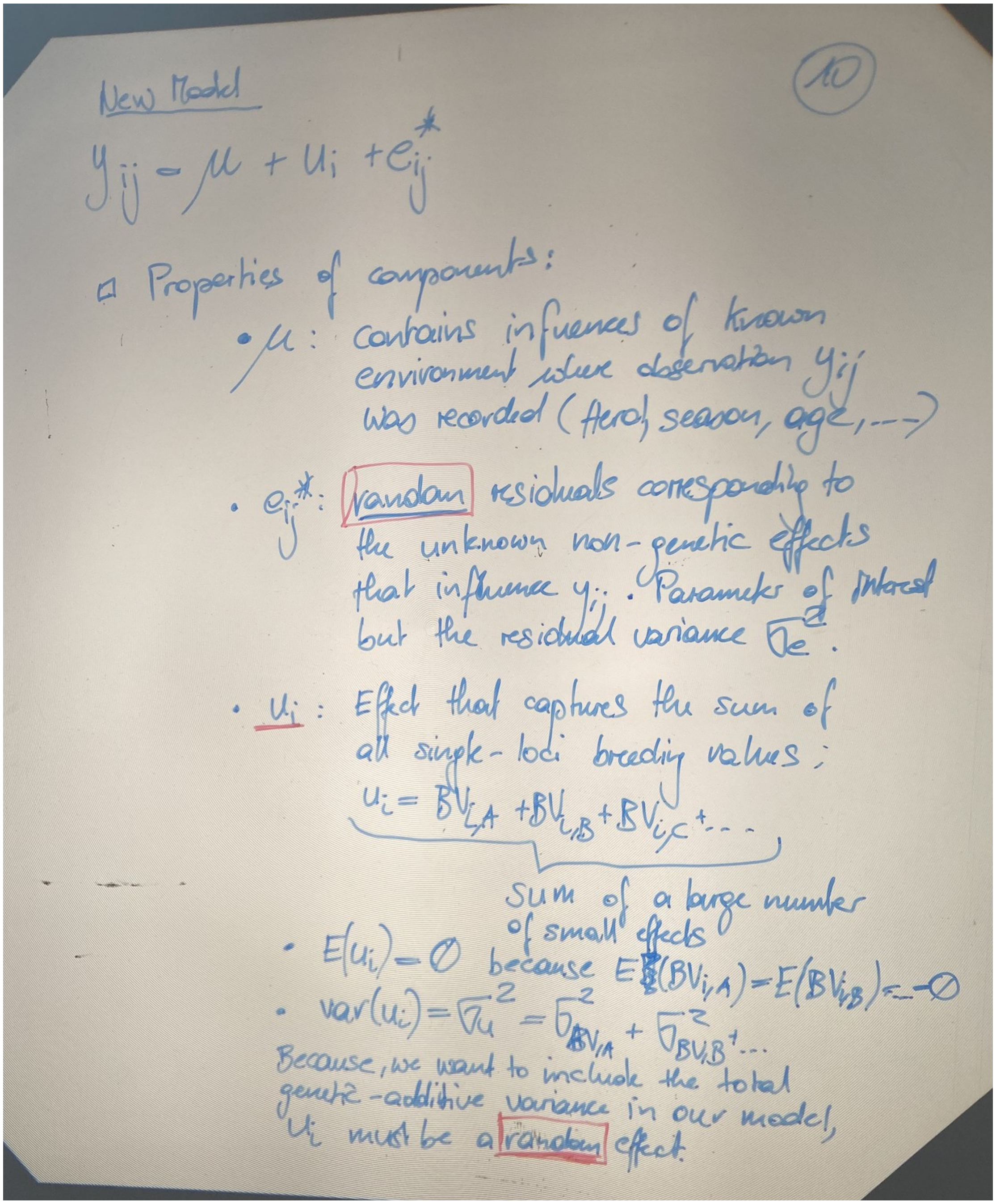
$$y_{ij} = v_i + e_{ij}$$; Using the decomposition of v_i

$$= \mu + \boxed{BV_i} + \boxed{D_i} + \boxed{I_i} + e_{ij}$$
$$= \mu + \boxed{u_i} + \boxed{d_i} + \boxed{i_i} + e_{ij}$$

☐ For selecting best animals as parents only breeding values are relevant, because BV quantify the value of single alleles that are passed from parents to offspring.

$\Rightarrow y_{ij} = \mu + u_i + e^*_{ij}$ where $e^* = d_i + i_i + e_{ij}$

OHP Picture 10



⑩

New Model

$$y_{ij} = \mu + u_i + e_{ij}^*$$

☐ Properties of components:

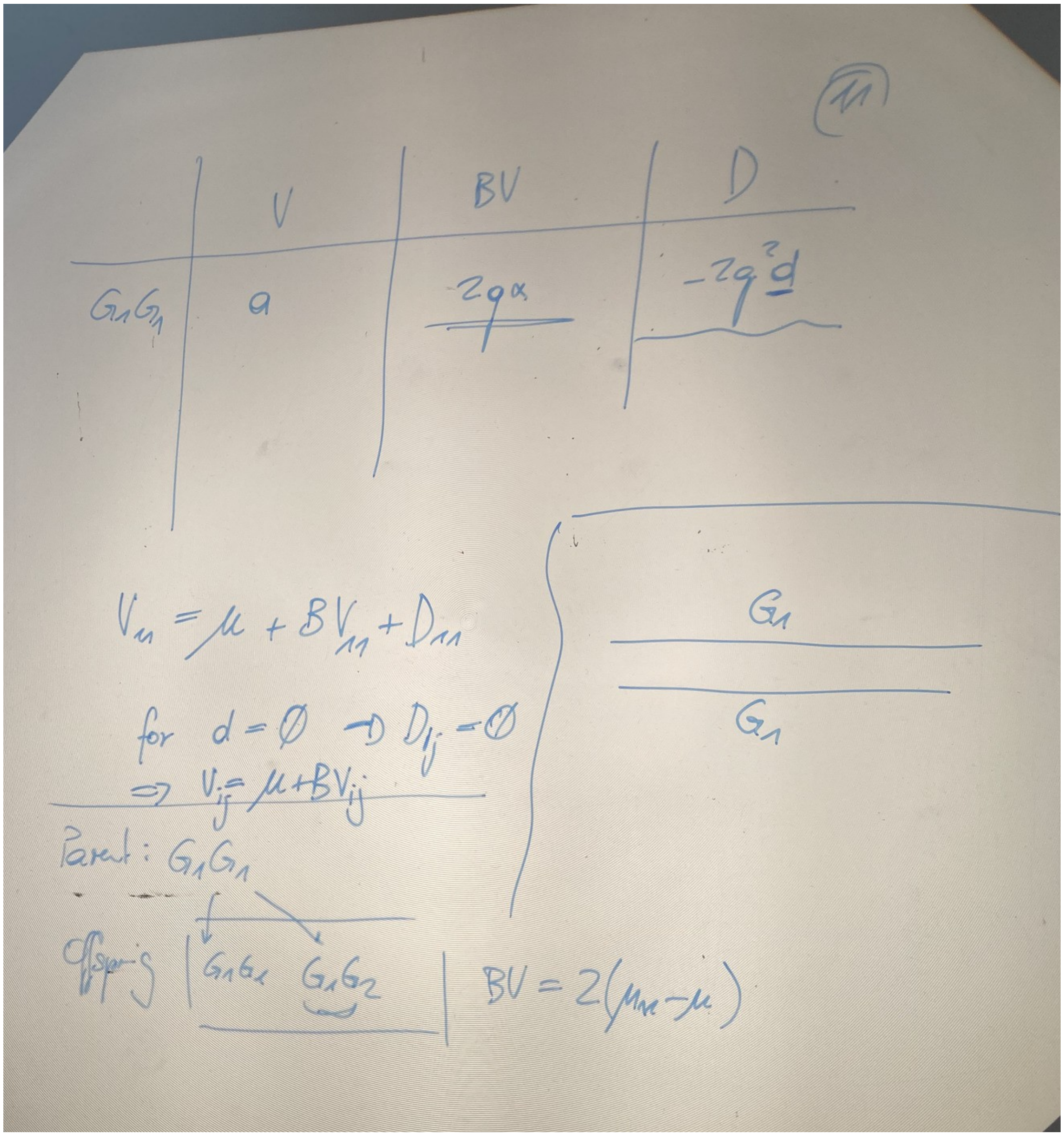
- μ: contains influences of known environment where observation y_{ij} was recorded (herd, season, age, ...)
- e_{ij}^*: random residuals corresponding to the unknown non-genetic effects that influence y_{ij}. Parameters of interest but the residual variance σ_e^2.
- u_i: Effect that captures the sum of all single-loci breeding values:

$$\underbrace{u_i = BV_{i,A} + BV_{i,B} + BV_{i,C} + \ldots}_{\text{sum of a large number of small effects}}$$

- $E(u_i) = 0$ because $E(BV_{i,A}) = E(BV_{i,B}) = \ldots = 0$
- $var(u_i) = \sigma_u^2 = \sigma^2_{BV_{i,A}} + \sigma^2_{BV_{i,B}} + \ldots$

Because, we want to include the total genetic-additive variance in our model, u_i must be a random effect.

OHP Picture 11



⑪

	V	BV	D
G_1G_1	a	$2q\alpha$	$-2q^2d$

$$V_{11} = \mu + BV_{11} + D_{11}$$

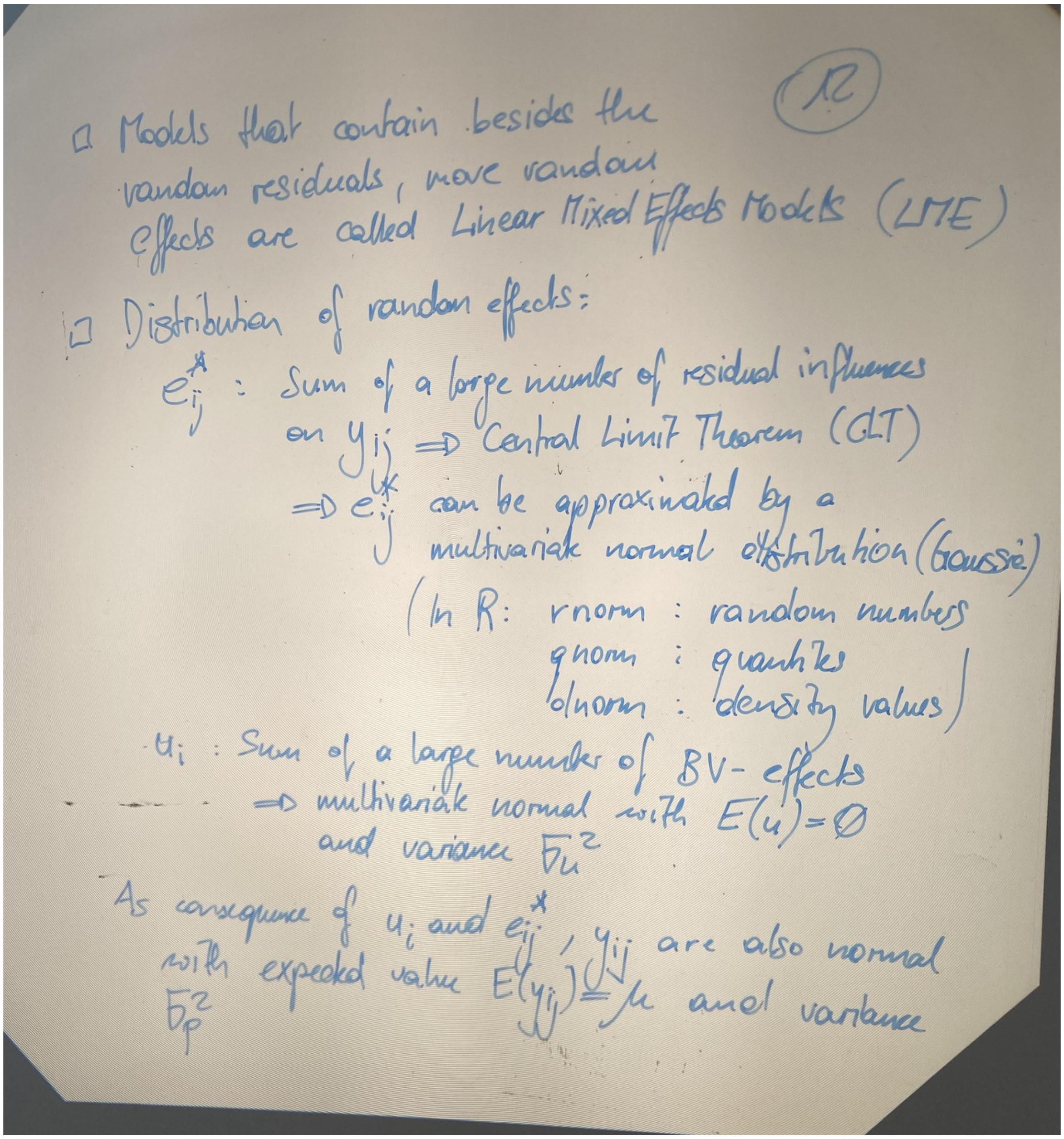
for $d = 0 \rightarrow D_{ij} = 0$

$\Rightarrow V_{ij} = \mu + BV_{ij}$

Parent: G_1G_1

Offspring | G_1G_1 $\underbrace{G_1G_2}$ | $BV = 2(\mu_{11} - \mu)$

OHP Picture 12



⑫

☐ Models that contain besides the random residuals, more random effects are called Linear Mixed Effects Models (LME)

☐ Distribution of random effects:

e^*_{ij} : Sum of a large number of residual influences on y_{ij} ⇒ Central Limit Theorem (CLT)

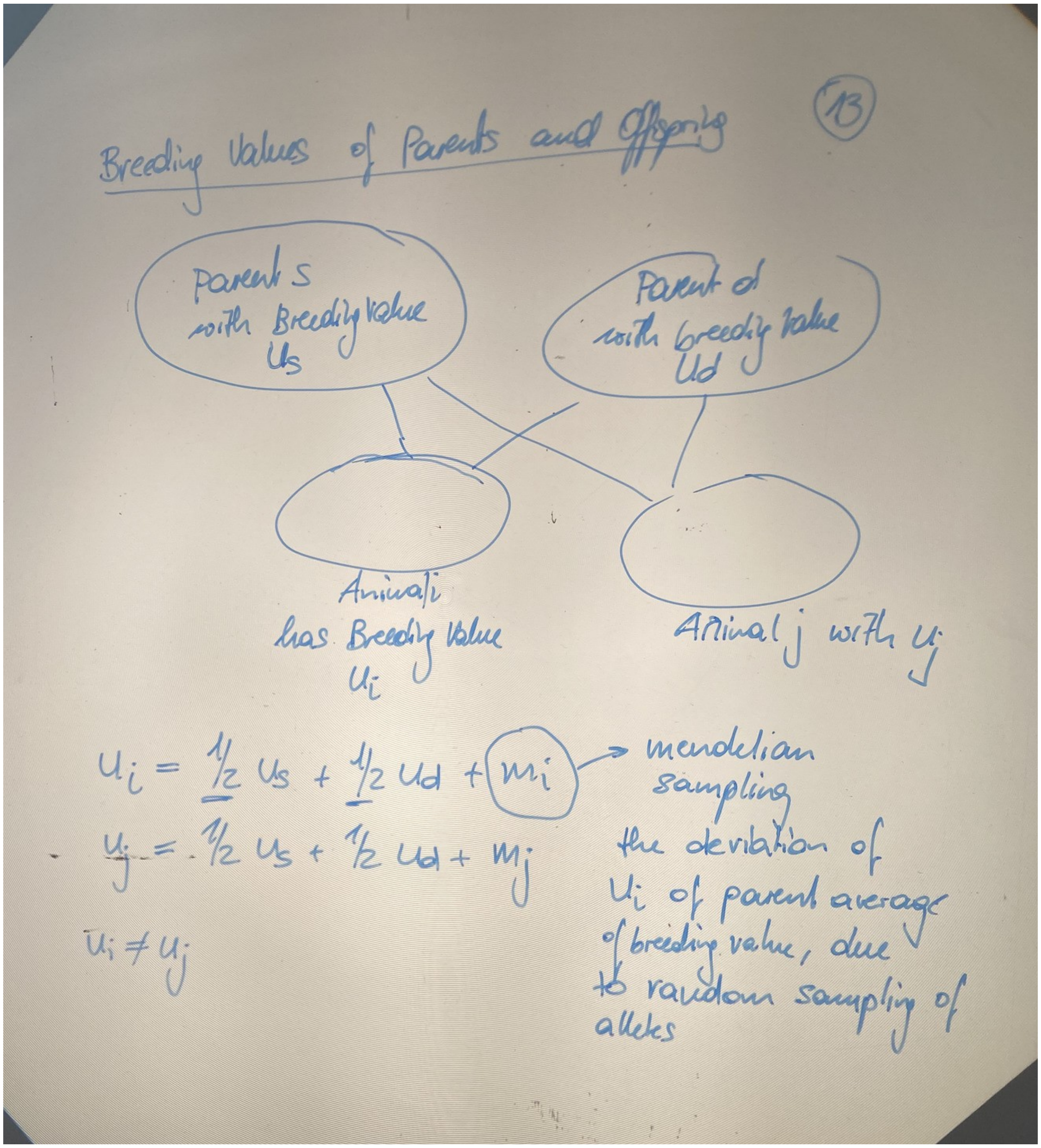
⇒ e^*_{ij} can be approximated by a multivariate normal distribution (Gaussé)

(In R: rnorm : random numbers
qnorm : quantiles
dnorm : density values)

u_i : Sum of a large number of BV-effects
⇒ multivariate normal with $E(u) = 0$ and variance σ_u^2

As consequence of u_i and e^*_{ij}, y_{ij} are also normal with expected value $E(y_{ij}) = \mu$ and variance σ_p^2

OHP Picture 13



Breeding Values of Parents and Offspring

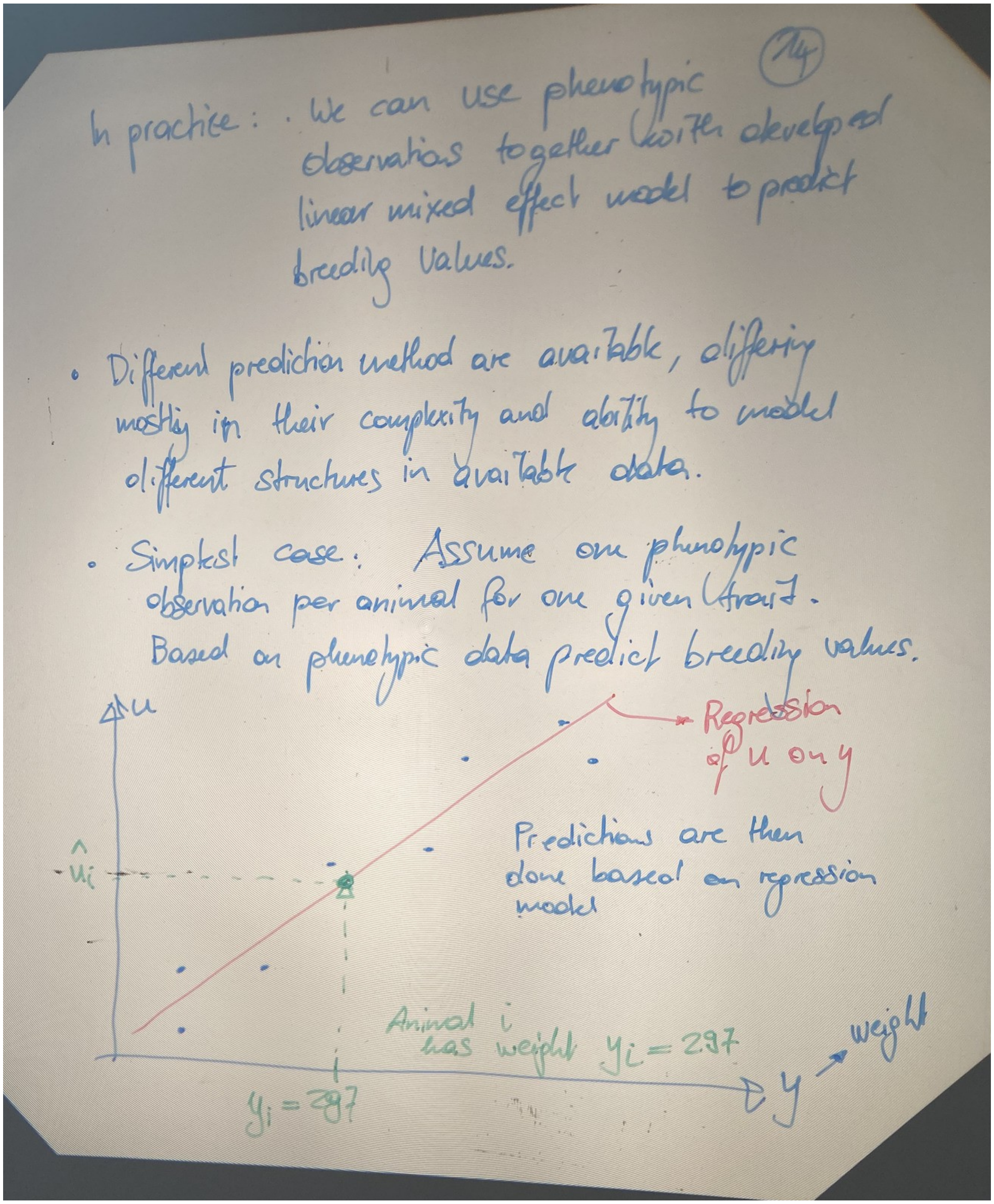
$$u_i = \underline{1/2}\, u_s + \underline{1/2}\, u_d + \boxed{m_i} \rightarrow \text{mendelian sampling}$$

$$u_j = 1/2\, u_s + 1/2\, u_d + m_j$$

$$u_i \neq u_j$$

the deviation of u_i of parent average of breeding value, due to random sampling of alleles

OHP Picture 14



⑭

In practice: . We can use phenotypic observations together (with developed linear mixed effect model to predict breeding values.

- Different prediction method are available, differing mostly in their complexity and ability to model different structures in available data.
- Simplest case: Assume one phenotypic observation per animal for one given (trait. Based on phenotypic data predict breeding values.

Predictions are then done based on regression model