

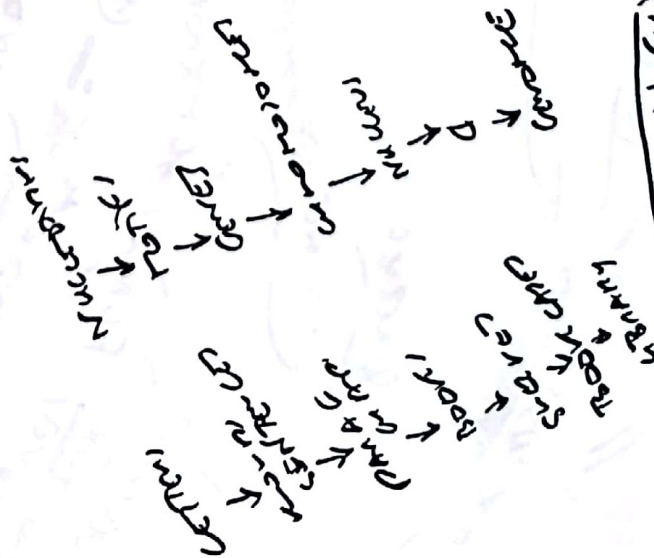
OVERVIEW

DATA

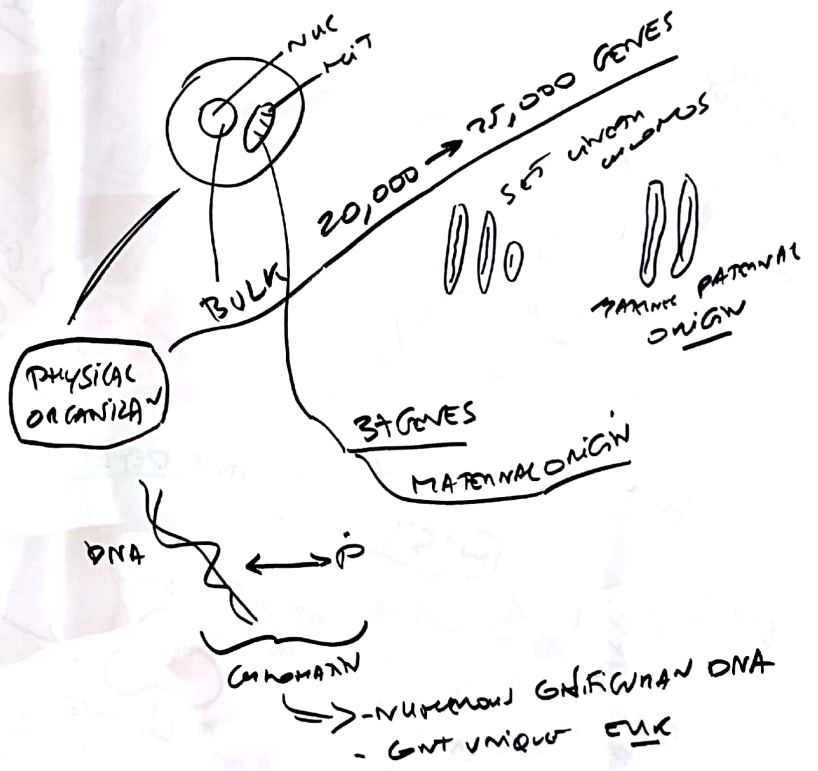
SPACE
PRINT

NEVER USED
DATA

INITIAL TO REMOVE IN THEIR MANNER

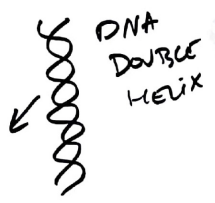


DATA STORAGE ANALOGY



NUC STR EUR DNA

H BONDS



5' END

3' END

PENTOSE

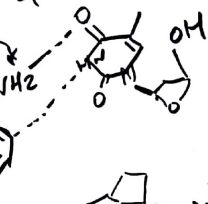
PHOSPHATE DIESTER BACKBONE

PHOSPHATE DEOXYRIBOSE

DNA BUILDING BLOCKS

ASYMMETRICALLY JOINED TO PHOSPHATE GROUPS BY PHOSPHATE DIESTER BONDS

GUANINE BINDING NUCLEOTIDE



A::T
C::G

5' END

3' END

5'

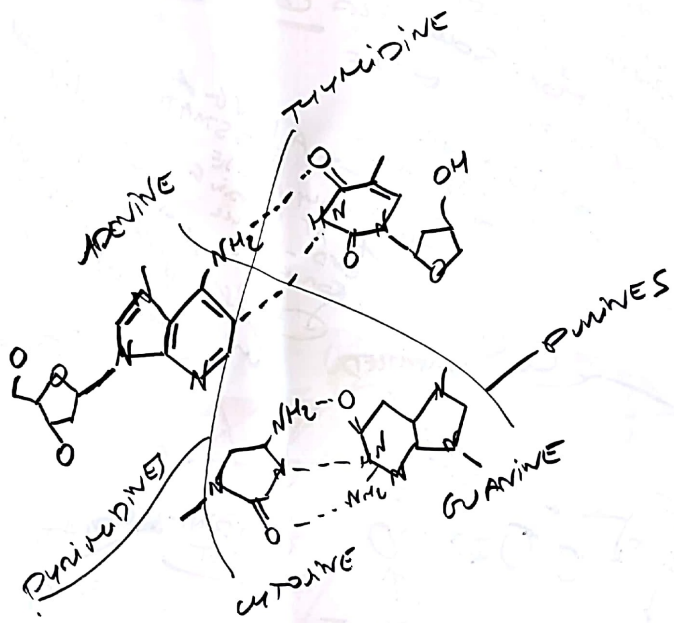
3'

3'

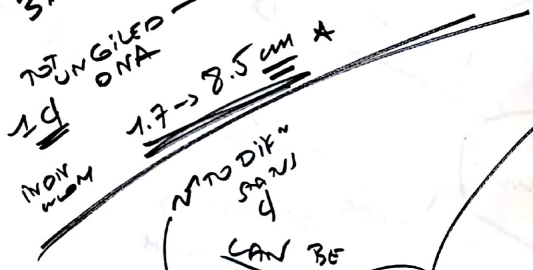
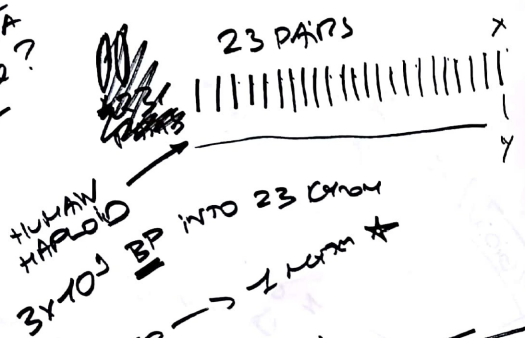
5'

NUCLEOTIDE = NUCLEOTIDE UNKIND TO A SUGAR & ONE OR MORE P

A G HETEROCYCLIC GUANINES PURINES
CYTOSINE THYMINE PYRIMIDINE C T

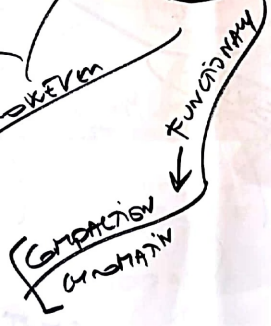
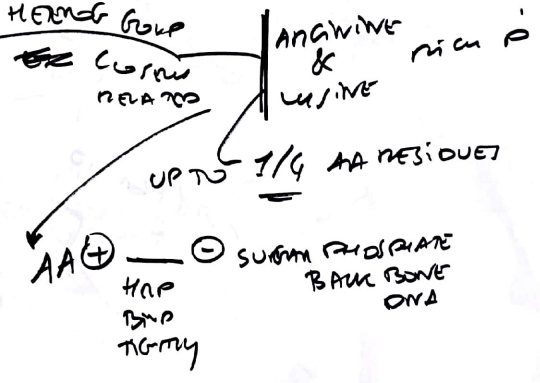
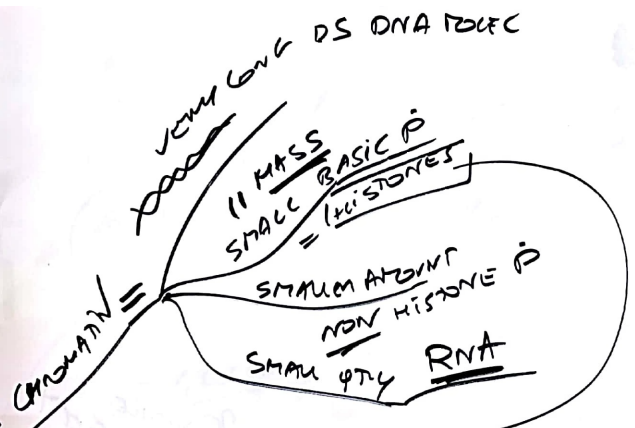


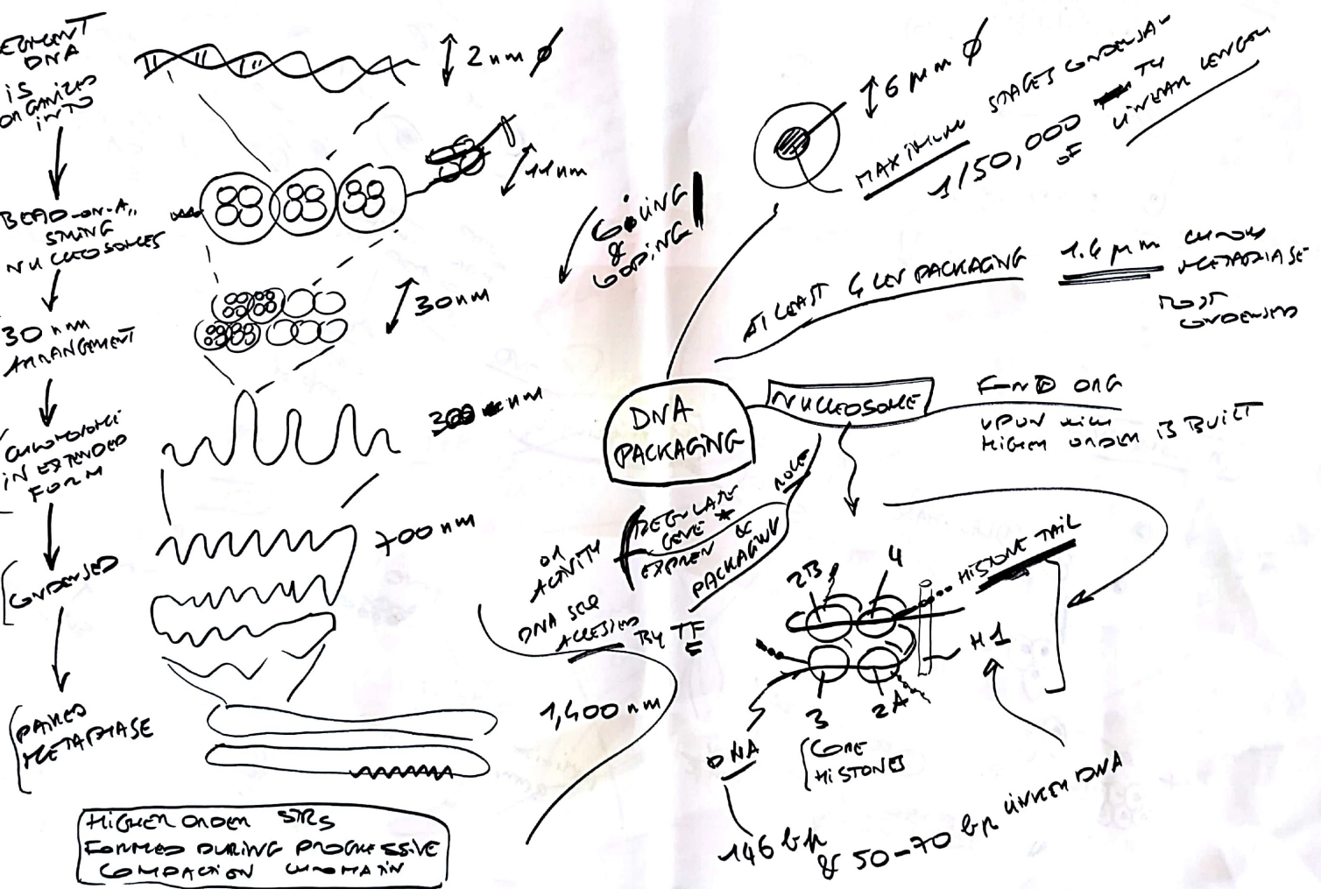
Just how much DNA is there?

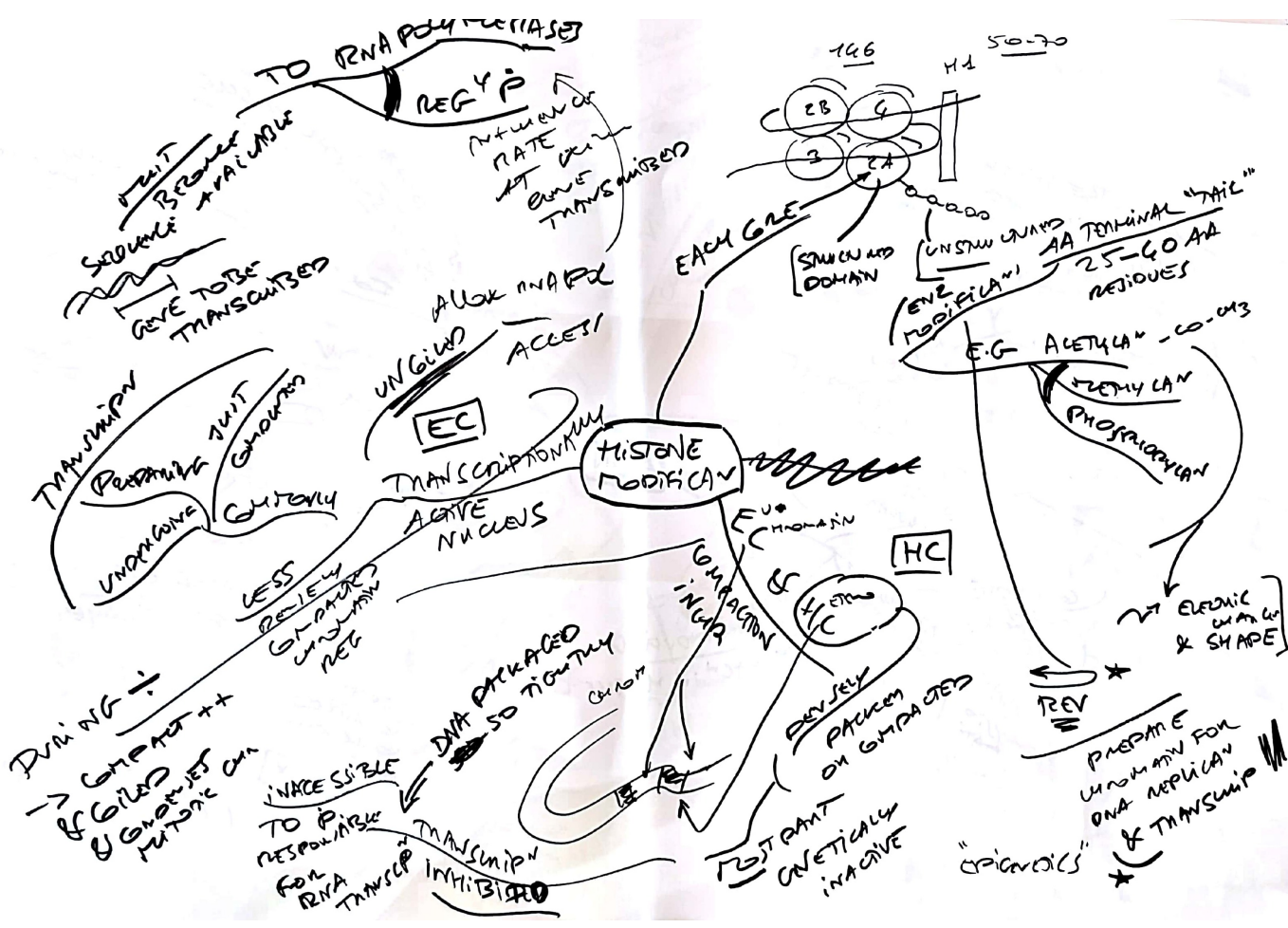


MODIFIED
 CAN BE
 + CAN BE DYNAMIC
 HOWEVER
 FROM STATIC

MISIONS







SEQUENCE AVAILABLE
 GENE TO BE TRANSCRIBED
 TO RNA POLYMERASE
 REG P
 AUX IN AND ACCESS
 RATE AT WHICH GENE TRANSCRIBED

EACH CORE
 STRUCTURE DOMAIN
 UNSTRUCTURED AA TERMINAL "TAIL"
 25-60 AA RESIDUES
 E.G. ACETYLATION - CO-CH3
 METHYLATION
 PHOSPHORYLATION
 ELECTRIC CHARGE & SHAPE

TRANSCRIPTION
 PERSISTENT WITH GROWTH
 UNORGANIC GLYCEROL
 TRANSCRIPTIONALLY ACTIVE NUCLEUS
 LESS REVIEW STAPLES AND WITH REG
 DNA PACKAGED SO TIGHTLY
 POST PART GENETICALLY INACTIVE
 INACCESSIBLE TO P RESPONSIBLE FOR RNA TRANSCRIPTION INHIBITED

HISTONE MODIFICATION
 UNGILDED
 GILDED
 E+ CHROMATIN
 H3, H4, H2B, H2A
 LINKER
 H1
 H.C.
 REVERSE PACKING OF GMPACKED
 "EPICENTERS" *
 PREPARE FOR UNIFORM DNA REPLICATION & TRANSCRIPTION

DURING
 GROWTH ++
 GILDED
 GROWTH INHIBITION

EACH 2
MULTIPLE
ORIGINS
REPLICAN
DISPENSOR

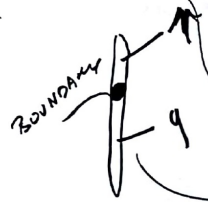
ACTS AS
DNA REPLICAN
ORIGIN

SPECIFIC
NUCLEOTIDE
SEQ

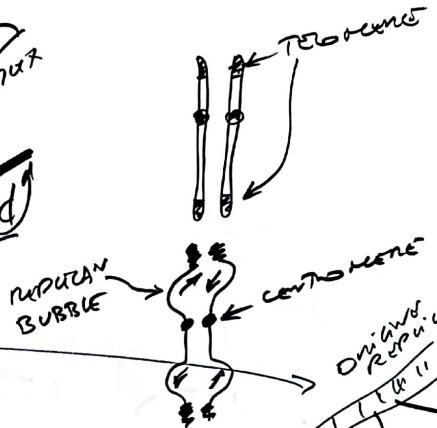
HISTONES
ONE VERY
LONG
LINKING
DUPLICATE NON GV
INDIVIDUAL
GENOME STRAT

IN ORDER
DNA TO
REPLICATE

CHROMOSOME
STRUCTURE



KINETOCORE
"HANDLES"
SPINDLE
CENTROMERE



ORIGINS
REPLICAN
SPEZ
DS DNA
BINDING PROT
+ SEVES DIRECT
REPEAT DNA SEQ

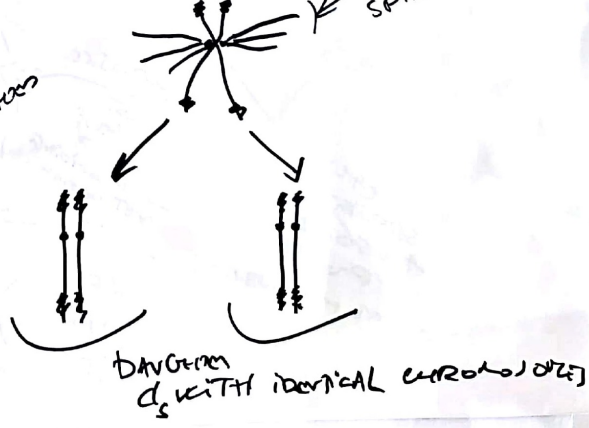
FROM
PROTEIN
HEXA NUCLE
DNA REPEATS

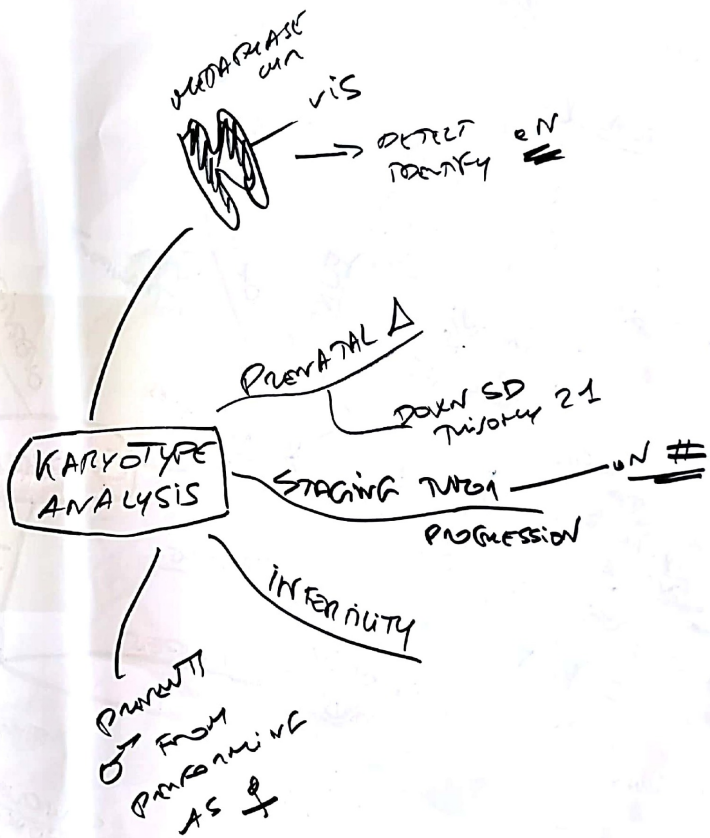
TELOMERE
NARROWER
ELEMENTS
SEQUENCE

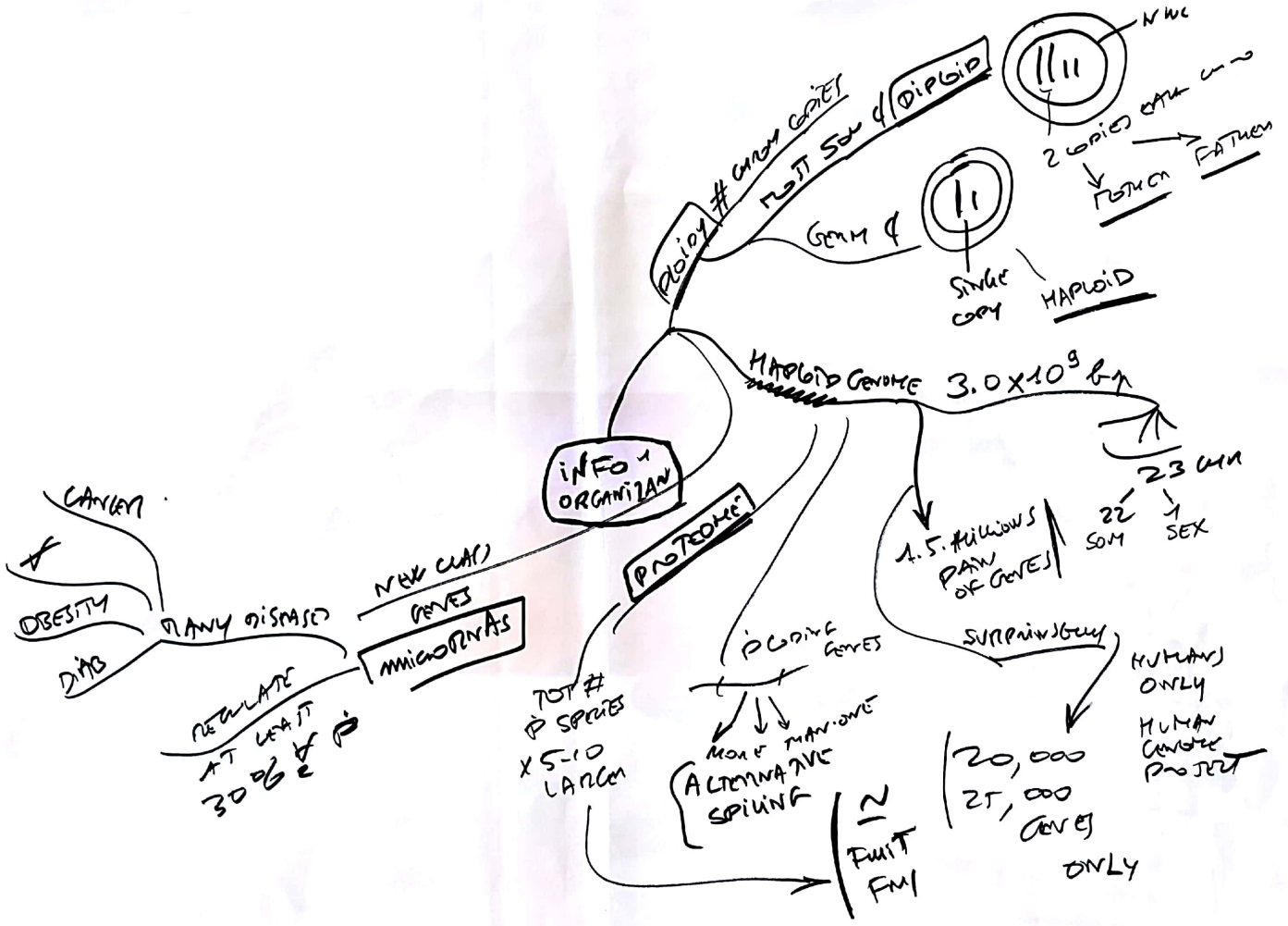
OSSE TURNS LIKE
O-1
DIGITAL CALIBRATOR
M

[TAGGGG]

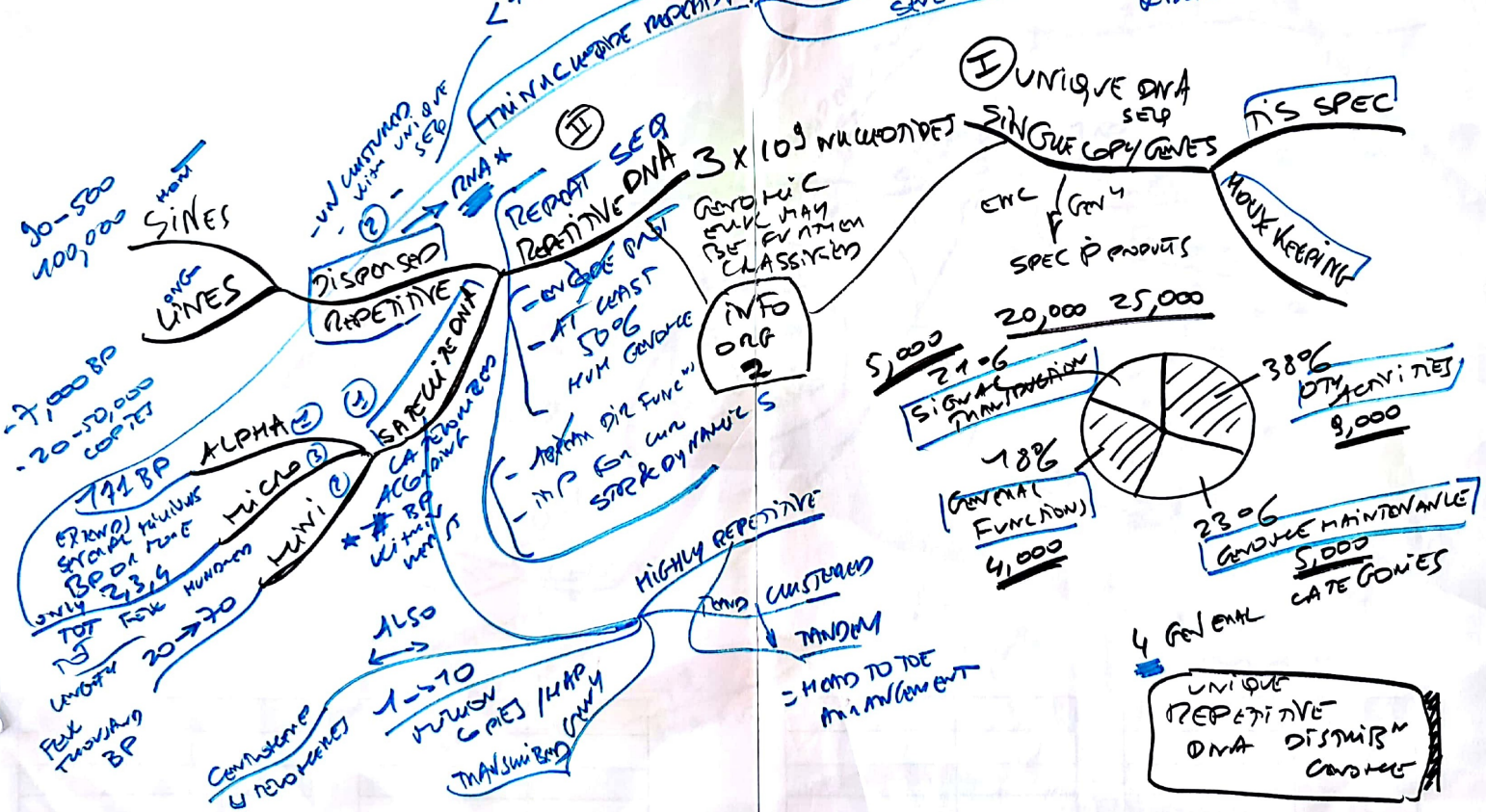
FROM
PROTEIN
MAINWAY
AS INDIV
UNITS





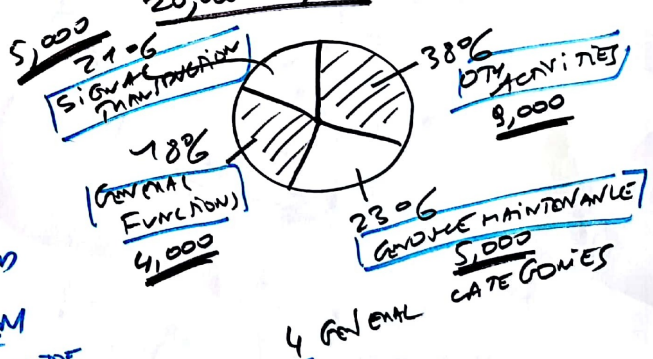


KENNEDY	CAG	11-35	→ 40-62	PCOING REGION S'UNTIMULATED REZ
HUNTINGTON	CAG	11-35	→ 42-60	
FRAGILE X	CGG	6-55	→ 270-4,000	
MYOTONIC DYSTROPHY	CTG	5-30	→ > 50	

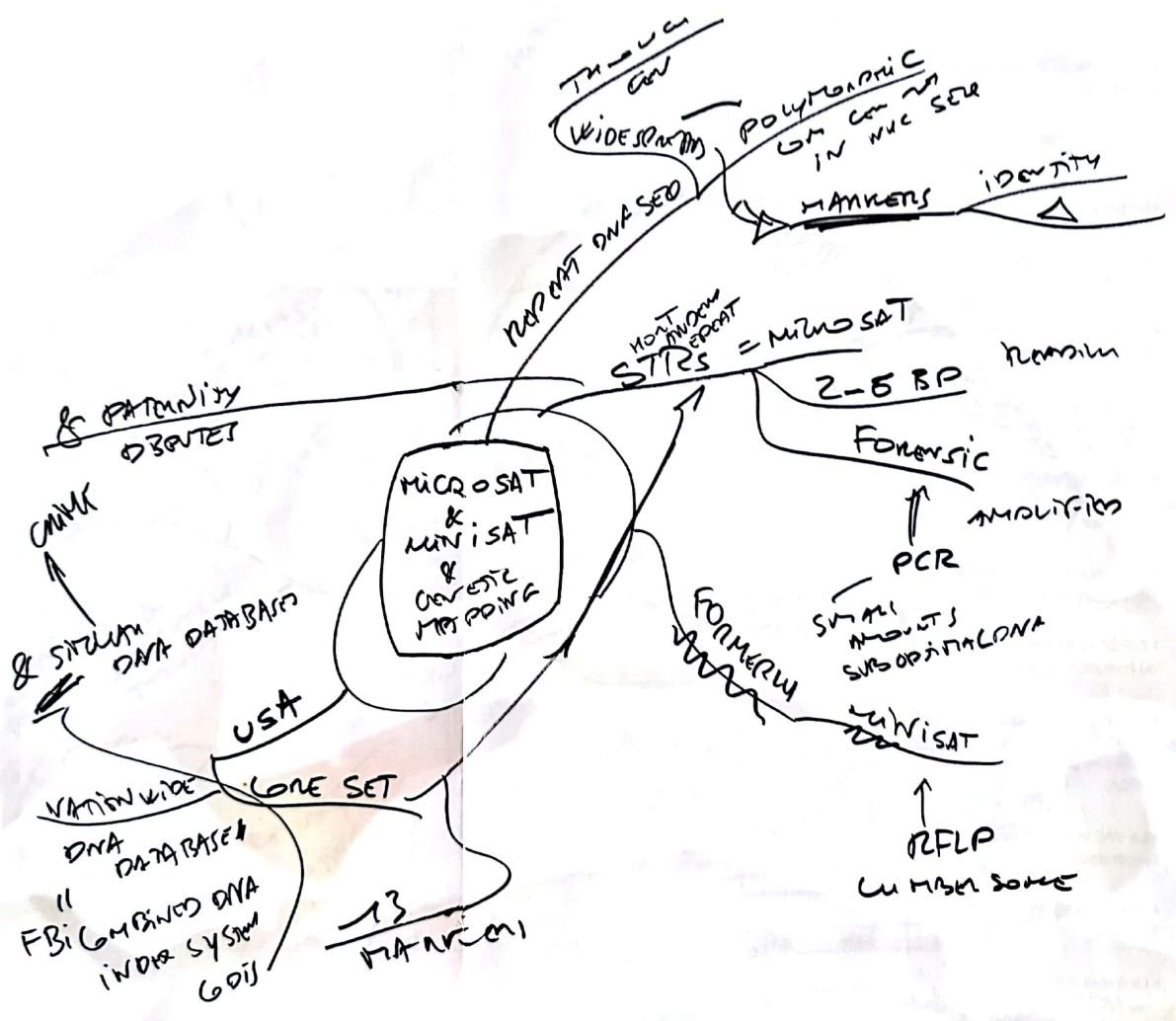


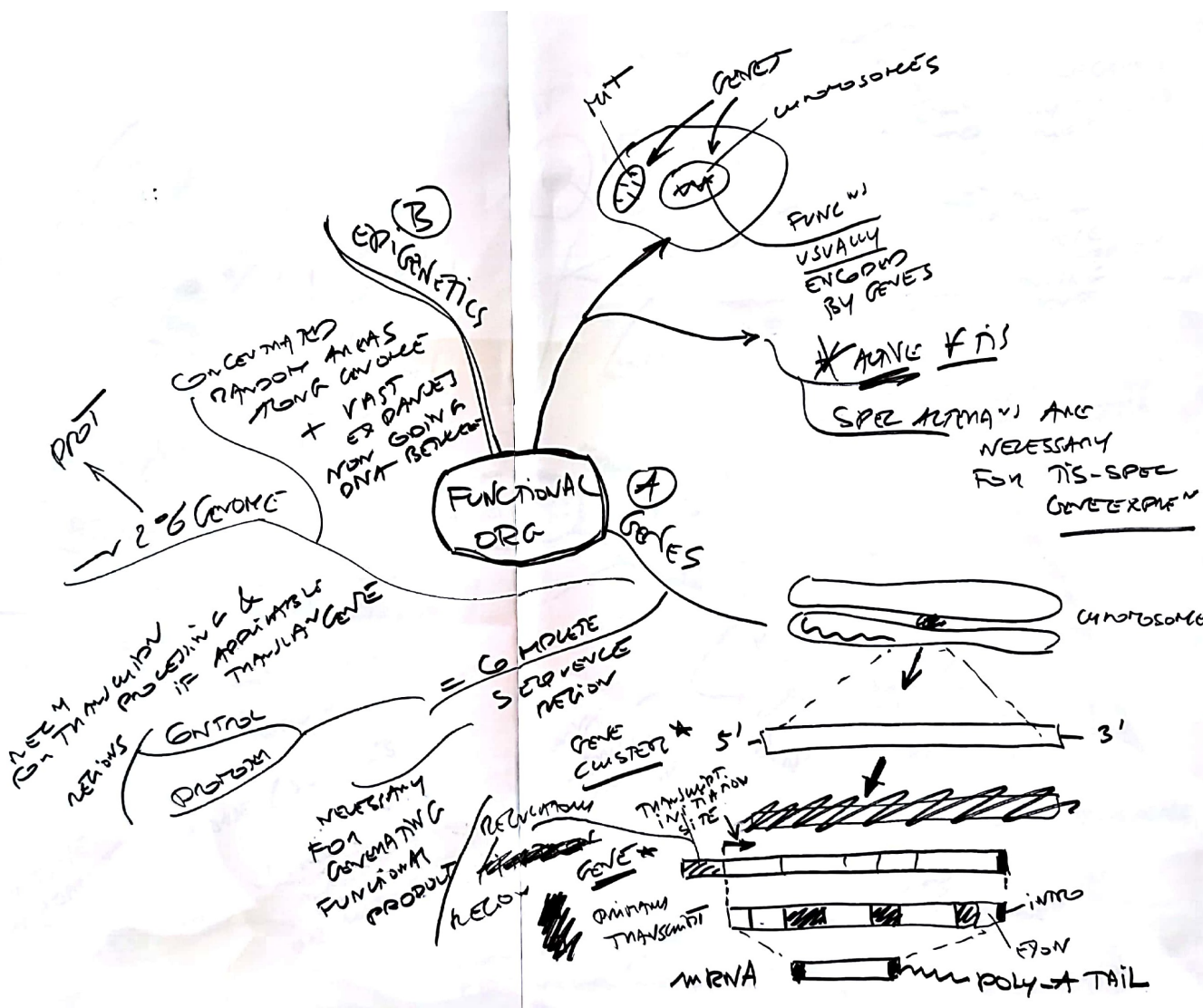
1 PRESENT
 CONTAIN GENES
 CAN EXPANSION
 SEVERAL HUNDRED TIMES
 EXPANSION N
 UNUSABLE
 DEFERIVE GENES

I UNIQUE DNA SET
 SINGULAR COPY GENES
 THIS SPEC
 MAINTENANCE



UNIQUE REPTITIVE DNA DISTRIBUTION
 GENES

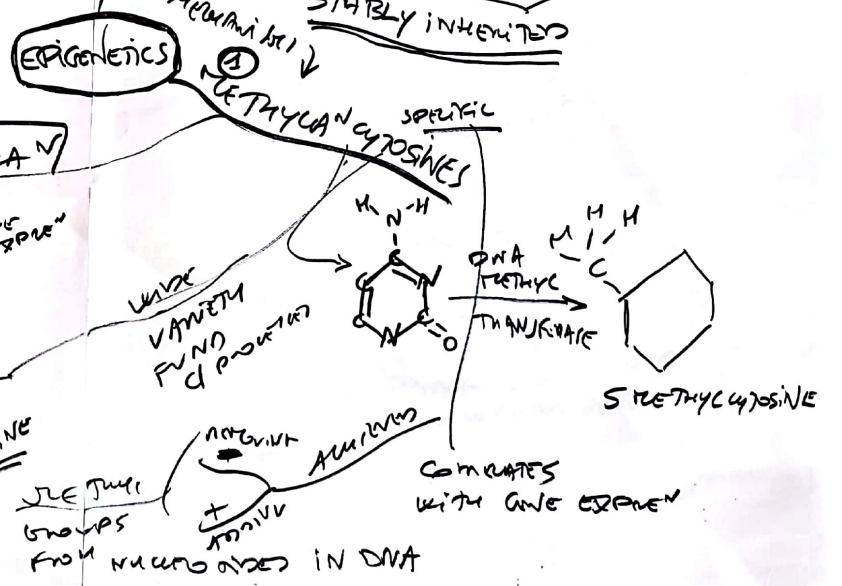




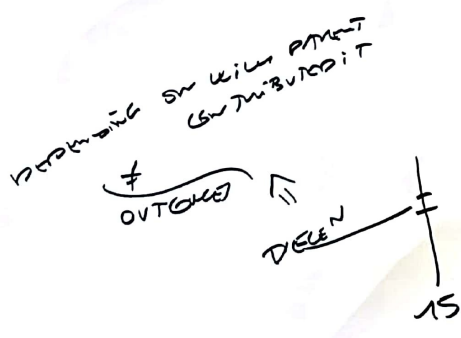
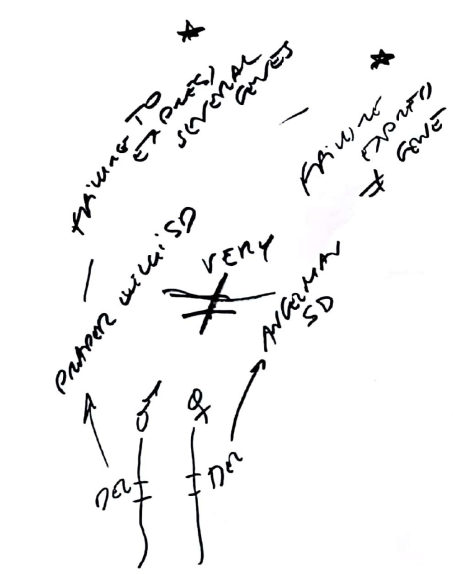
HOUSEKEEPING
 ACTIVE IN KDTM
 CONSTITUTIVE
 + HYPO METHYLATED
 SOMETIMES
 TISSUE
 + METHYLATED WHEN NOT NECESSARY
 TEND TO BE CONSTITUTIVELY EXPRESSED
 GLOBIN
 + METHYLATED & HYPO METHYLATED
 + METHYLATED & HYPO METHYLATED

TEND TO BE CONSTITUTIVELY EXPRESSED
 IN CELL STEM PROGENITORS
 5'-CG-3' RESIDUES
 GENE METHYLATION
 STERIC HINDRANCE TO P THAT INHIBITS GENE EXPRESSION
 5' CYTOSINE ADJACENT TO A GUANINE BASE (5'-CG-3')
 ESPECIALLY IN NATURAL ON CYTOSINE
 METHYL GROUPS FROM NUCLEOTIDES IN DNA

ASIDE FROM MUTN
 IDENTICAL DNA I CAN GET
 DIFFERENT SET OF GENES TO CHURN OUT THEIR FUN
 SPECIFIC TO CELL TYPE
 STABLE INHERITED
 COMMONLY OCCUR IN GENOME
 HELP EXPLAIN ALTERNATIVE GENE EXPRESSION
 = EPIGENETIC



GEN AND GENOMIC IMPRINTING



SOME APPROX TO BE EXPRESSED EXCLUSIVELY FROM ONE CONTRIBUTING FROM EITHER MOTHER OR FATHER



"IMPRINTING" = HAVE ABILITY TO TURN ON OR OFF DEPENDING ON WHICH PARENT CONTRIBUTED GENE

CANONICAL STR
IS TIS SPEC



SAME DNA
BUT
≠ CANONICAL
STR
⇒ TIS SPEC FN



TIS SPEC &
CANONICAL
ALTERATIONS

EC & HC

STABLY INHERITED CHANGE
OF SPEC

ALTERATIONS MAINTAINED WITH \div *

DEF FN

≠ CLASS OF

MAINTAINING TIS-SPEC
C STR

EX

H-MODIFYING ENZ

C REMOVING
COMPLEXES

PROPAGATION
UBIQUITIN
METHYL
PROTEIN

H PROTEIN INHERITABLE

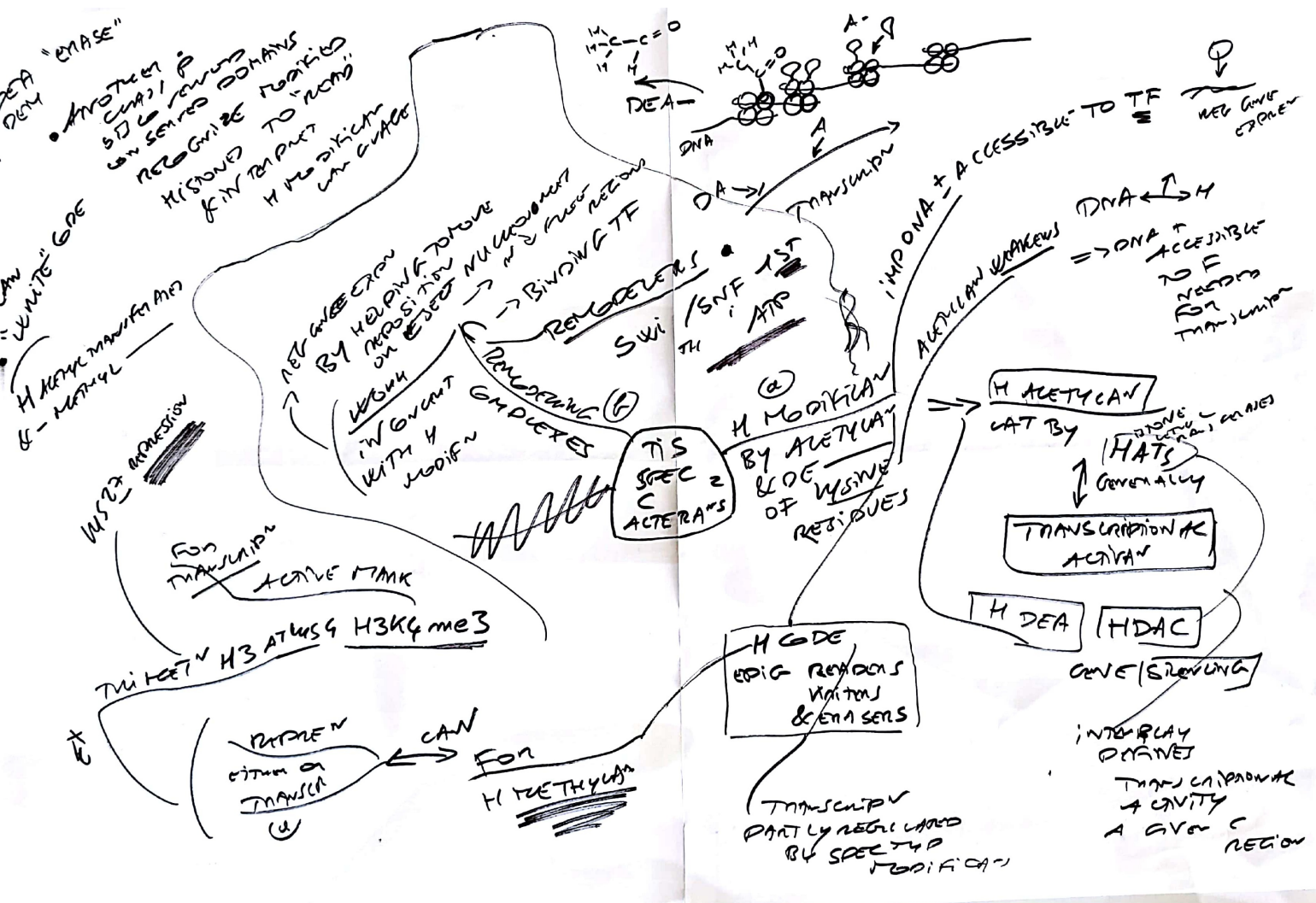
ALTHOUGH
CAN OCCUR
AT LOCAL
TRANSMISSION
EVENTS

MAINT
& PROP N
STABLE TIS STR

DEACETYLASE
REST
UNDERSTOOD

V N STRUCTURE N-TERMINAL
TAILS

PARTICULARLY
HIGHLY
MODIFIED



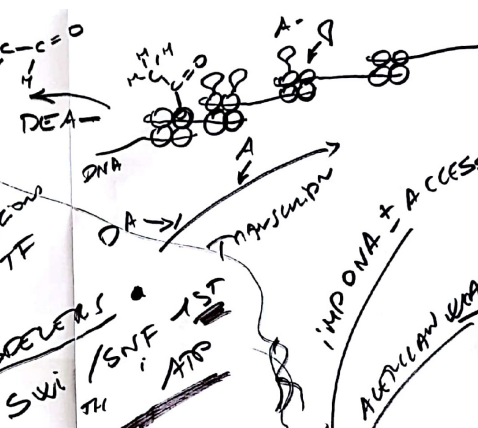
DEA
DEM
"EMASE"

STRUCTURE
BY 2 REPEATING
UNITS
RECOGNIZE DOMAINS
RESPOND TO "RNA"
FIN TEMPLAT
H MODIFICATION
CAN GATE

WST REPRESSION
FOR TRANSCRIPTION
ACTIVE MARK
H3K9me3 H3K4me3
H3K9me3 H3K4me3
PATTERN
OF TRANSCRIPTION
CAN
FOR
H3 METHYLATION

NET REJECTION
BY HELPING TO MOVE
OR POSITION
ON ESECT MULTIMOMENT
→ BINDING TF
REMOVERS
SWI
SNF
ATP
1ST

REMOVING
EMPLETES
IN GOVANT
WITH H
MODIFN



H MODIFICATION
BY ACETYLATION
& DE
OF HISTONE
RESIDUES
HAT BY
HATS
GENERALY
TRANSCRIPTIONAL
ACTIVAT
H DEA
HDAC
GIVE/SILENCING
INTERPLAY
PARTNER
TRANSCRIPTIONAL
& CAVITY
A GIVEN
REGION

HAT BY
HATS
GENERALY
TRANSCRIPTIONAL
ACTIVAT
H DEA
HDAC
GIVE/SILENCING
INTERPLAY
PARTNER
TRANSCRIPTIONAL
& CAVITY
A GIVEN
REGION

TRANSCRIPTION
IMP DNA + ACCESSIBLE TO TF
DNA ACCESSIBLE TO TF
NEED GIVE
EXPOSE

TRANSCRIPTION
PARTLY REGULATED
BY SPECIFIC
MODIFICATION