Test: DELPHi / DIY (circle one)

Universidad de La Laguna (Spain), 26 January 2022

Your initials:

- **Question 1:** Is the candidate gene a transcription factor or part of a transcription complex?

Gene	Transcription factor / part of transcription complex? (Y/N)	
HIF1A		
SMAD3		
TRAF2		
CEBPA	Y	Y

- **Question 2:** Is the candidate gene involved in an immune signalling pathway, i.e. a pathway that is immune cell-specific or a generic pathway known to operate in immune cells (e.g. the JAK-STAT, MAPK, NF-kappa B or TNF signalling pathways) ?

  You can also consider blood cell-specific pathways like leukaemias.

Gene	Annotate relevant pathways	
HIF1A		
SMAD3		
TRAF2		
CEBPA	AML	AML

- **Question 3:** Can you write down the known protein binding partners (if any) of each candidate gene ?

Gene	Annotate relevant pathways
HIF1A	
SMAD3	
TRAF2	
CEBPA	FOXO1_MOUSE KDM1A_MOUSE

CDK2
CDK4
DDT3

- **Question 4:** Can you write down the diseases each candidate gene is associated with?

Gene	Annotate relevant pathways
HIF1A	
SMAD3	
TRAF2	
CEBPA	ACUTE MYELOID LEUKEMIA

ACUTE MYELOID LEUKEMIA

- **Question 5:** For each candidate gene, can you find a genetic phenotype that produces an abnormal immune phenotype or disease?

Gene	Annotate relevant pathways
HIF1A	
SMAD3	
TRAF2	
CEBPA	ABNORMAL B CELL PROLIFERATION ABNORMAL CO-POINTET

- **Question 6:** Are any of the candidate genes expressed in a type of immune cell or in a tissue or organ where immune cells are known to reside (e.g. the bone marrow, thymus, spleen and lymph nodes) ?

Gene	Annotate relevant pathways
HIF1A	
SMAD3	
TRAF2	
CEBPA	EMBRYONIC BODY 19.0. (BONE MARROW)

BONE MARROW

- **Question 7:** Have any of the candidate genes been studied in the context of macrophages?

Gene	PMID of paper
HIF1A	
SMAD3	
TRAF2	
CEBPA	YES! 4.

YES!

System Usability Scale

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	Strongly disagree				Strongly agree	
1. I think that I would like to use this system frequently					X	4
	1	2	3	4	5	
2. I found the system unnecessarily complex	X					4
	1	2	3	4	5	
3. I thought the system was easy to use					X	4
	1	2	3	4	5	
4. I think that I would need the support of a technical person to be able to use this system	X					4
	1	2	3	4	5	
5. I found the various functions in this system were well integrated					X	4
	1	2	3	4	5	
6. I thought there was too much inconsistency in this system	X					4
	1	2	3	4	5	
7. I would imagine that most people would learn to use this system very quickly					X	4
	1	2	3	4	5	
8. I found the system very cumbersome to use	X					4
	1	2	3	4	5	
9. I felt very confident using the system					X	4
	1	2	3	4	5	
10. I needed to learn a lot of things before I could get going with this system	X					4
	1	2	3	4	5	

40 × 2.5 = 100

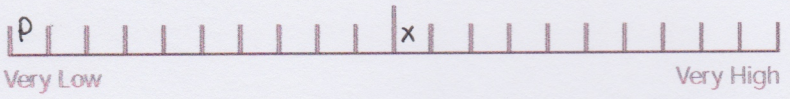
Figure 8.6

NASA Task Load Index

Hart and Staveland's NASA Task Load Index (TLX) method assesses work load on five 7-point scales. Increments of high, medium and low estimates for each point result in 21 gradations on the scales.

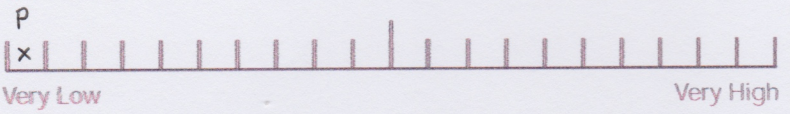
Name	Task	Date

Mental Demand — How mentally demanding was the task?



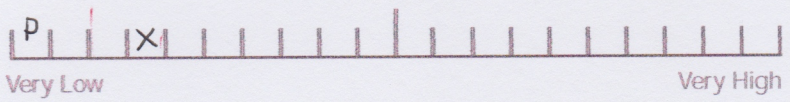
Very Low — Very High

Physical Demand — How physically demanding was the task?



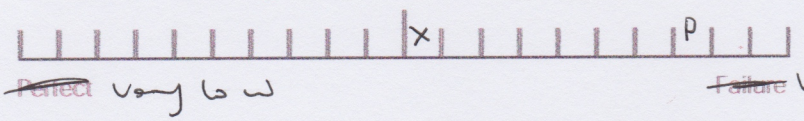
Very Low — Very High

Temporal Demand — How hurried or rushed was the pace of the task?



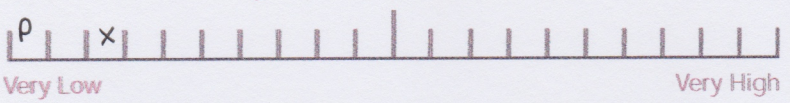
Very Low — Very High

Performance — How successful were you in accomplishing what you were asked to do?



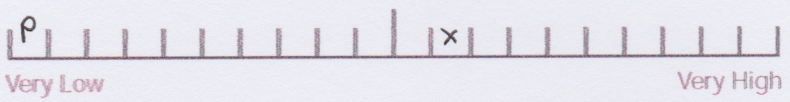
~~Perfect~~ very low — ~~Failure~~ very high

Effort — How hard did you have to work to accomplish your level of performance?



Very Low — Very High

Frustration — How insecure, discouraged, irritated, stressed, and annoyed wereyou?



Very Low — Very High

PO22

[redacted]

	P	X	Faculty Paleogenomics
Q1	11"	Google → Gene Cards	17"
Q2	35"	Google → KEGG	1'45"
Q3	19"	Google → PubMed	3'48"
Q4	29"	Google → ~~2~~	26"
Q5	16"	~~Ne~~ Google → NCBI → Google → PhreGenI database → Google → PubMed	3'30"
Q6	20"	Google → The Human Protein Atlas	26"
Q7	17"	PubMed → papers	23"

• Qué te gustó + y qué −?

⊕ Hay mucha info. estructurada de manera que no tienes que estar de un lado a otro, y que sabes que todo está estructurado

⊕ Me gustó mucho la parte de las publicaciones y a veces es complicado y pesado leer la búsqueda bibliográfica de las últimas publicaciones

• Qué cambiarías?

⊖ Sería posible poner los datos más relevantes para mí?

Es decir → variantes genéticas de cada gen y un link a una BD donde se encuentre las frecuencias alélicas en poblaciones.

• Algo más?

— Qué se pueden analizar listas.