P016

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 KMMIA.

C/EBP RB1
β-PPAR
HDAC1

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

Gene	Annotate relevant pathways
HIF1A	
SMAD3	
TRAF2	
CEBPA	AML

AML

- **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	Anormal B cell prolyferat is

- **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	Bone marrow

Bone
White cell

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

Gene	PMID of paper
HIF1A	
SMAD3	
TRAF2	
CEBPA	Y ly

System Usability Scale

© Digital Equipment Corporation, 1986.

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

36x

2.5 = 90

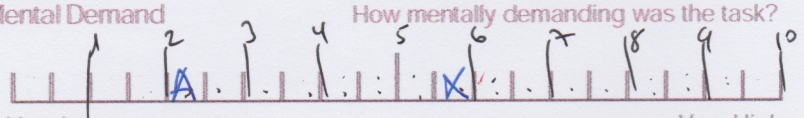
Figure 8.6

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.

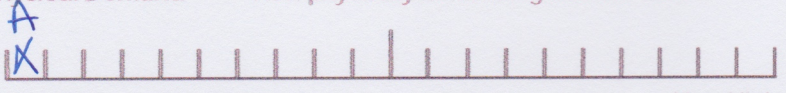
Name	Task	Date

Mental Demand — How mentally demanding was the task?



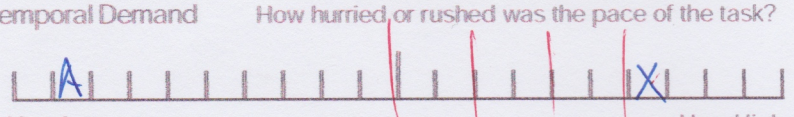
Very Low — Very High

Physical Demand — How physically demanding was the task?



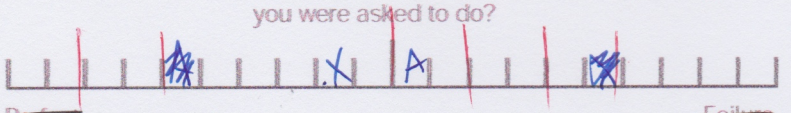
Very Low — Very High

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



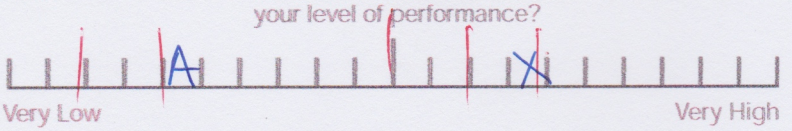
Very Low — Very High

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



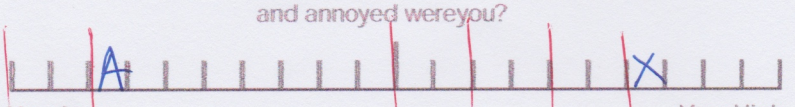
~~Perfect~~ very low — ~~Failure~~ very high

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 were you?



Very Low — Very High

1 [redacted]

Q1

Q2

1h duró

PTA – debriefing

1 How useful do you think the interface is?

Sí y he sorprendido porque la información que de esta que uno siempre está buscando. Lo quisiera mucho que tuviera links para profundizar más.

2 What would you like to add / improve?

– ponerlo en humano

– el tamaño de la letra, era demasiado pequeño, las ventanas en vez de ponerlas en mosaico ponerlas en vertical, scroll es más fácil

3 What thinks did you not like?

4 Otro comentario?

– Lo usaría con frecuencia si estuviera disponible.

– ~~cuesta~~ customizar ings. para su campo, centrarlo únicamente en la bioquímica

		Errors	que no es la fuente primaria.	Error
Q1	11.28 - 30	0	NCBI Gene 51"	
Q2	30:32	0	NCBI gene	1 no hay encuentro en NCBI,
Q3	32:33	0	NCBI gene	
Q4	1 min		Fue a la web de enfermedades del NCBI	1 no encontró nada 2 fue a NCBI/protein 3 se metió en CEBIA humano a ver si salía algo.
Q5	1 min			
Q6	1 min			
Q7			1 se metió en NCBI/Gene se metió en ~~Genetards~~ Genetards humano	
Total	6'		Fue al PubMed directamente	
			Total 18'	

→ Estaba más familiarizado con la interfaz del NCBI que con la ~~de~~ del prototypo y eso jugó a mi contra.

→ Fue difícil controlar lo que estaban haciendo porque saltaban de un sitio a otro. Por eso les pedí el trouble ahead.

→ Julio está principalmente familiarizado con el sitio de NCBI y e intenta explotarlo para todo lo que puede sin darse cuenta de que hay otros sitios más óptimos.

"Este tipo de información no se busca a diario y por eso una herramienta donde está todo protocolizado ayudaría mucho"

↓

cuando el re-visita las páginas de costumbre (herecards, etc) se da cuenta de que han cambiado el formato o

learnability

han incluido más información.

(cada vez más carga cognitiva)

tiende a la complicación y no a la sencillez.

↓

es la filosofía contraria a lo que yo está planteando.

• Hacerlo en humanos.

• Le gustaría una herramienta que reduzca la learnability.

• importante que se da acceso a la fuente primaria.

Uniprot etc