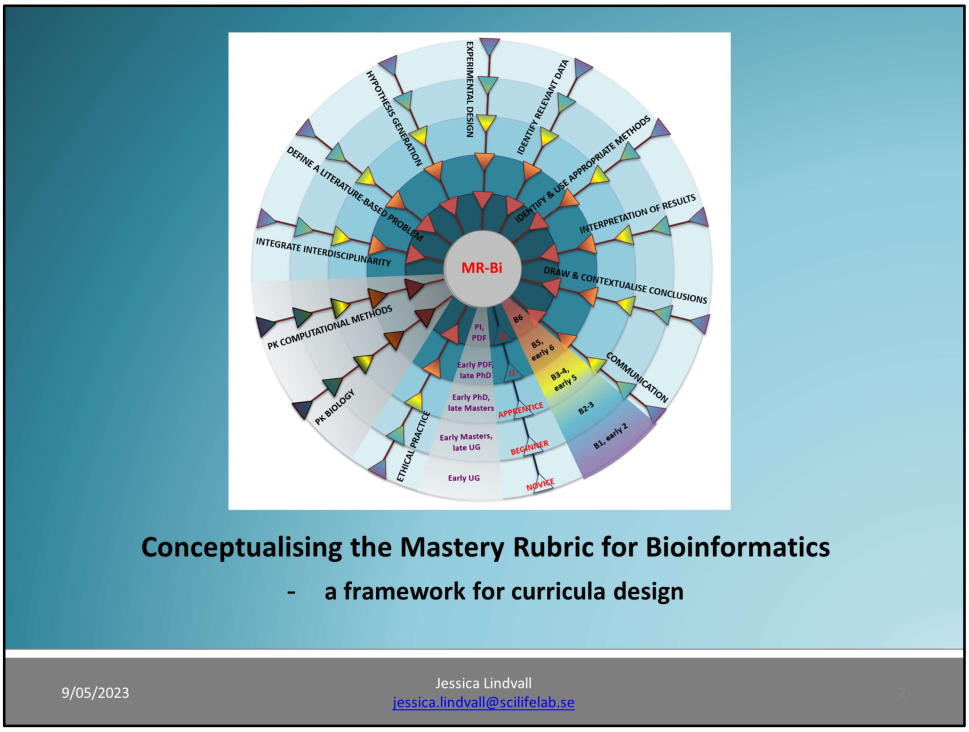
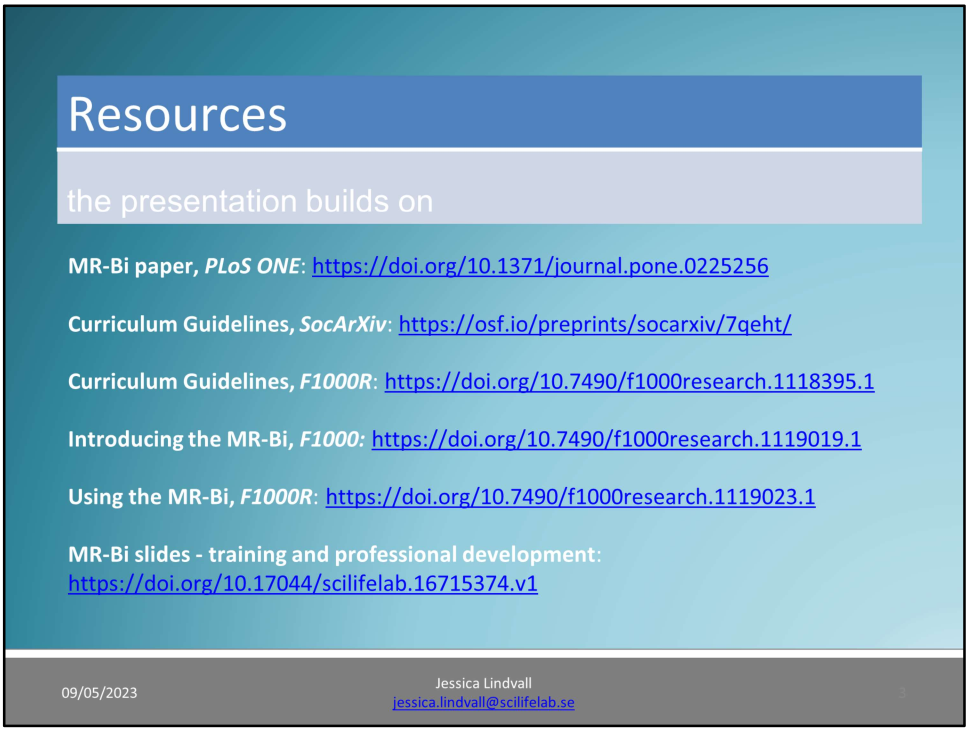
Presentation from the plenary session at the conference BioSB, which is the 9th edition of the Dutch Bioinformatics & Systems Biology conference held on 9 and 10 May 2023.

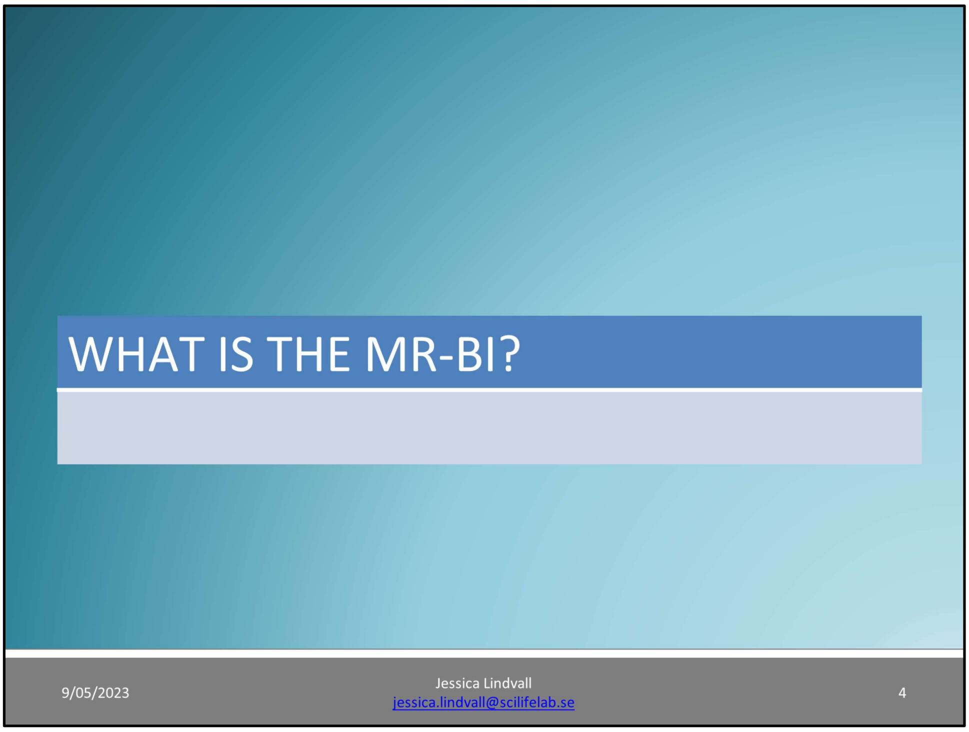
I was invited to give the plenary session on the 9th of May and to take part in the discussions around a national, Dutch, educational framework for Bioinformatics and Systems Biology (primarily aimed at MSc students/programmes). This framework is in tandem with a European framework for Bioinformatics that has been independently formulated from the ISCB (see here).



The presentation bears the title of “Conceptualising the Mastery Rubric for Bioinformatics - a framework for curricula design” and is a collaborative work spanning many years and different work.



The presentation are built from the resources listed on the slide. The slide will appear again in the end of the presentation.



I will first take you to a tour across the framework itself, what is the Mastery Rubric for Bioinformatics?


RESEARCH ARTICLE

The Mastery Rubric for Bioinformatics: A tool to support design and evaluation of career-spanning education and training

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Abstract

As the life sciences have become more data intensive, the pressure to incorporate the requisite training into life-science education and training programs has increased. To facilitate curriculum development, various sets of (bio)informatics competencies have been articulated; however, these have proved difficult to implement in practice. Addressing this issue, we have created a curriculum-design and -evaluation tool to support the development of specific Knowledge, Skills and Abilities (KSAs) that reflect the scientific method and promote both bioinformatics practice and the achievement of competencies. Twelve KSAs were extracted via formal analysis, and stages along a developmental trajectory, from uninitiated student to independent practitioner, were identified. Demonstration of each KSA by a performer at each stage was initially described (Performance Level Descriptors, PLDs), evaluated, and revised at an international workshop. This work was subsequently extended and further refined to yield the Mastery Rubric for Bioinformatics (MR-Bi). The MR-Bi was validated by demonstrating alignment between the KSAs and competencies, and its consistency with principles of adult learning. The MR-Bi tool provides a formal framework to support curriculum building, training, and self-directed learning. It prioritizes the development of independence and scientific reasoning, and is structured to allow individuals (regardless of career stage, disciplinary background, or skill level) to locate themselves within the framework. The KSAs and their PLDs promote scientific problem formulation and problem solving, lending the MR-Bi durability and flexibility. With its explicit developmental trajectory, the tool can be used by developing or practicing scientists to direct their (and their team's) acquisition of new, or to deepen existing, bioinformatics KSAs. The MR-Bi is a tool that can contribute to the cultivation of a next generation of bioinformaticians who are able to design reproducible and rigorous research, and to critically analyze results from their own, and others', work.

OPEN ACCESS

Citation: Tractenberg RE, Lindvall JM, Attwood TK, Via A (2019) The Mastery Rubric for Bioinformatics: A tool to support design and evaluation of career-spanning education and training. PLoS ONE 14(11): e0225256. https://doi.org/10.1371/journal.pone.0225256

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Data Availability Statement: All of the data are included in this manuscript; the data are qualitative and are included in the tables.

You can find out all the details of the tool in the paper we published at the end of 2019 in ***PLoS One***: *The Mastery Rubric for Bioinformatics: a tool to support design & evaluation of career-spanning education & training.*

The DOI is at the bottom, here - for anyone who's interested, this URL appears again in the final slide, as do all other URLs mentioned in later slides – so you don't need to write them down now.

A descriptive '3D' table
KSAs, Stages, PLDs

Performance Level:	Novice	Beginner	Apprentice	J1 Journeyman	J2 Journeyman
General description of bioinformatics practitioner	Reads, generally understands, but does not question, life science research (results). Beginning to recognise that 'facts' are actually just the best-currently-supported theory. Limited engagement with uncertainty associated with 'facts'; developing understanding of experimental design paradigms in biology, & own specific area of study.	Consolidates reading & understanding, beginning to learn how to analyze given biology problems (with software). Growing recognition that 'facts' are typically the best-currently-supported theory. Engaging consistently with uncertainty associated with 'facts'; deepening understanding of experimental design paradigms in biology, & own specific area of study.	Reads & understands; reliably identifies methods (software & programming) for given problems. Chooses & executes correct analysis, not necessarily able to identify several methods that could be equally viable, depending on given research objectives. Qualified as a fluent, but not as an independent, scientist who uses bioinformatics as a tool, but does not yet synthesise techonolgy with biology to generate new research problems.	Qualified as an independent scientist who uses bioinformatics methodologies as part of routine practice. Poses novel scientific questions, & identifies data & technology to align appropriate statistical/ analytical methods to desired scientific objectives. Experienced reviewer of relevant technical features of available bioinformatics methods. Newly-independent expert in integrating bioinformatics technology/ techniques into novel research problems in their area of expertise.	Independent scientist who expertly integrates bioinformatics & more traditional methodologies, as needed, to achieve desired objectives & contribute to the body of knowledge. Expert reviewer of relevant technical features of available bioinformatics options.
Considerations for evidence of performance at this level	Bloom's 1, early 2: remember, understand. Problems the Novice can engage with are well-defined, with solutions already known. Work does not generally reflect self-assessment.	Bloom's 2-3: understand & apply, but only what they are told to apply. Problems the Beginner can engage with are well-defined. Work reflects some self-assessment, when directed to do so.	Bloom's 3-4, early 5: *choose* & apply techniques to problems that have been defined (either jointly or by others). Can analyze & interpret appropriate data, identify basic limitations & conceptualise a need for next steps/contextualization of results with extant literature. Seeks guidance to improve self-assessment of own work.	Bloom's 5, early 6: evaluate (review) & synthesise novel life-science knowledge while developing abilities to integrate bioinformatics into research practice. Shows independent expertise in a specific life-science area, & confidently integrates current bioinformatics technology into that area. Beginning to critically evaluate experimental paradigms & their results, without knowing/ requiring that there be 'one right answer'. Consistently self-assesses own work.	Bloom's 6: prepared for independent scientific work. Expert in design & critical evaluation of experimental paradigms & their results. Self-assesses in own work, & encourages others to develop this skill.
Ethical practice	Exhibits respect for community standards/rules for public behavior & personal interaction. Learning how to recognise, & manifest respect for, intellectual property, professional accountability, & scientific contributions.	Learning to recognise 'misconduct' in the scientific sense. Learning to avoid, & respond to, misconduct; & the importance of neither condoning nor promoting it.	Learning the principles of ethical professional & scientific conduct. Seeks guidance to strengthen applications of these principles in own practice. Learning how to respond to unethical practice.	Practices bioinformatics in an ethical way, & does not promote or tolerate any type of professional or scientific misconduct. Seeks guidance in how/when to take appropriate action when aware of unethical practices by others.	Practices, & encourages all others to practice, bioinformatics in an ethical way. Does not promote or tolerate any type of professional or scientific misconduct. Takes appropriate action when aware of unethical practices by others.
Prerequisite knowledge – biology (includes statistical inference & experimental design considerations)	Basic knowledge of biology; little-to-no awareness of the uncertainty inherent in experimental designs common in the life sciences. Thinking about the life sciences is based on uncritical acceptance of information as 'factual' or 'true'.	Advanced knowledge of biology, & basic knowledge of key bioinformatics methods. Very simple statistics/programs are run to answer pre-defined scientific questions. Learning to understand the uncertainty inherent in the scientific method, questions assumptions in the data & their relevance for given	Thinking about life sciences integrates both experimental & bioinformatics/technological sources for data & knowledge. Understands the uncertainty inherent in the scientific method, questions assumptions in the data & their relevance for given scientific problems (which typically arise from others, or with others). Experimental design & statistical	Recognises the importance of, & is able to critically evaluate, the relevant literature, & understands historical background of the relevant biological system(s). Sufficient knowledge of a biological system(s) to be able to draw functional conclusions from analytical results. Collaborates with experts to inform the next stages in the experimental design process (validating	Makes predictions to inform next stages of experimental design process. Evaluates relevant experimental methods that can be applied in any problem. Can generalise to other biological systems; independently solves biological problems that are innovative & move the field forward.

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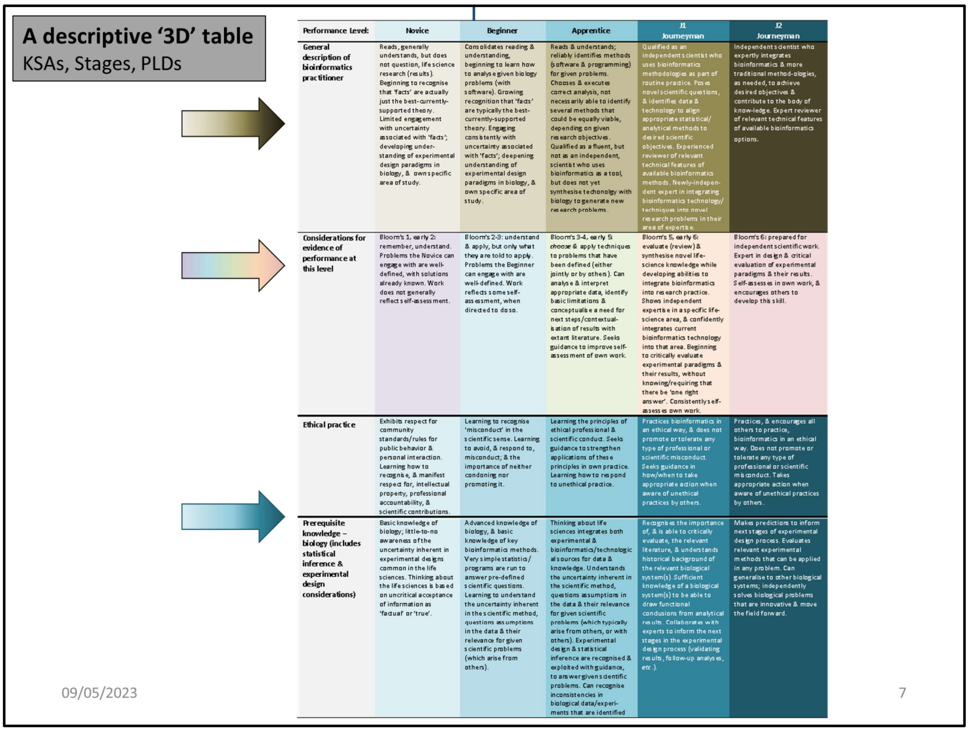
For those who've read the paper, you'll already have discovered Table 1. Table 1 ***is*** the MR-Bi, essentially a descriptive table with 3 'dimensions':

* the **y-axis** lists the **Knowledge Skills & Abilities** (the **KSAs**) that are intended to be delivered by a course or programme;

* the **x-axis** outlines a **developmental trajectory** from less to more expert – i.e., from **novice** to (independent) **journeyman**;

* & the individual **cells** (like the one shown) describe in detail how a learner might be expected to perform, & thence to change over time, when progressing along that trajectory (these are the so-called Performance Level Descriptors, or **PLDs**). As you can see, at first glance, there's quite a lot to take in…



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General description of bioinformatics practitioner	Reads, generally understands, but does not question, life science research (results). Beginning to recognise that 'facts' are actually just the best-currently-supported theory. Limited engagement with uncertainty associated with 'facts'; developing under-standing of experimental design paradigms in biology, & own specific area of study.	Consolidates reading & understanding, beginning to learn how to analyse given biology problems (with software). Growing recognition that 'facts' are typically the best-currently-supported theory. Engaging consistently with uncertainty associated with 'facts'; deepening understanding of experimental design paradigms in biology, & own specific area of study.	Reads & understands; reliably identifies methods (software & programming) for given problems. Chooses & executes correct analysis, not necessarily able to identify several methods that could be equally viable, depending on given research objectives. Qualified as a fluent, but not as an independent, scientist who uses bioinformatics as a tool, but does not yet synthesise techonolgy with biology to generate new research problems.	Qualified as an independent scientist who uses bioinformatics methodologies as part of routine practice. Poses novel scientific questions, & identifies data & technology to align appropriate statistical/ analytical methods to desired scientific objectives. Experienced reviewer of relevant technical features of available bioinformatics methods. Newly-indepen-dent expert in integrating bioinformatics technology/ techniques into novel research problems in their area of expertise.	Independent scientist who expertly integrates bioinformatics & more traditional method-ologies, as needed, to achieve desired objectives & contribute to the body of know-ledge. Expert reviewer of relevant technical features of available bioinformatics options.
Considerations for evidence of performance at this level	Bloom's 1, early 2: remember, understand. Problems the Novice can engage with are well-defined, with solutions already known. Work does not generally reflect self-assessment.	Bloom's 2-3: understand & apply, but only what they are told to apply. Problems the Beginner can engage with are well-defined. Work reflects some self-assessment, when directed to do so.	Bloom's 3-4, early 5: *choose* & apply techniques to problems that have been defined (either jointly or by others). Can analyse & interpret appropriate data, identify basic limitations & conceptualise a need for next steps/contextual-isation of results with extant literature. Seeks guidance to improve self-assessment of own work.	Bloom's 5, early 6: evaluate (review) & synthesise novel life-science knowledge while developing abilities to integrate bioinformatics into research practice. Shows independent expertise in a specific life-science area, & confidently integrates current bioinformatics technology into that area. Beginning to critically evaluate experimental paradigms & their results, without knowing/requiring that there be 'one right answer'. Consistently self-assesses own work.	Bloom's 6: prepared for independent scientific work. Expert in design & critical evaluation of experimental paradigms & their results. Self-assesses in own work, & encourages others to develop this skill.
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Prerequisite knowledge – biology (includes statistical inference & experimental design considerations)	Basic knowledge of biology; little-to-no awareness of the uncertainty inherent in experimental designs common in the life sciences. Thinking about the life sciences is based on uncritical acceptance of information as 'factual' or 'true'.	Advanced knowledge of biology, & basic knowledge of key bioinformatics methods. Very simple statistics/ programs are run to answer pre-defined scientific questions. Learning to understand the uncertainty inherent in the scientific method, questions assumptions in the data & their relevance for given scientific problems (which arise from others).	Thinking about life sciences integrates both experimental & bioinformatics/technologic al sources for data & knowledge. Understands the uncertainty inherent in the scientific method, questions assumptions in the data & their relevance for given scientific problems (which typically arise from others, or with others). Experimental design & statistical inference are recognised & exploited with guidance, to answer given scientific problems. Can recognise inconsistencies in biological data/experi-ments that are identified	Recognises the importance of, & is able to critically evaluate, the relevant literature, & understands historical background of the relevant biological system(s). Sufficient knowledge of a biological system(s) to be able to draw functional conclusions from analytical results. Collaborates with experts to inform the next stages in the experimental design process (validating results, follow-up analyses, *etc*.).	Makes predictions to inform next stages of experimental design process. Evaluates relevant experimental methods that can be applied in any problem. Can generalise to other biological systems; independently solves biological problems that are innovative & move the field forward.

So, to help navigate through the table, or to better orientate ourselves, we can highlight its main features (this is exactly the same thing, but just coloured in).

* At the top, there's a **general description** of an individual at a given stage (I should say that you're not meant to be able to read this – this is just for you to note that there ***is*** a progression as an individual advances from novice to journeyman).

* Alongside this are the requisite stages of **Bloom's hierarchy of cognitive complexity** as it builds from lower- to higher-order **'critical' thinking skills** (Blooms **level 1** to Blooms **level 6**).

* Then, beneath these are the **12 KSAs &** the **corresponding PLDs** for **each stage**. But this is just the first page of the table…
* As you can see, it's actually massive…

A descriptive '3D' table
KSAs, Stages, PLDs

	not even contextualise conclusions with the protocol that was followed. Not aware of the difference between conclusions about the null hypothesis & those about the research hypothesis. Conclusions may over- or under-state results & be driven by *p*-values or other superficial cues. Does not recognise the importance of identifying & acknowledging methodological limitations, or their implications, for conclusions. Does not or cannot apply rules of logic to scientific arguments, & commits logical fallacies when drawing conclusions.	not be able to draw those conclusions from given results themselves. Learning to differentiate between conclusions about the null hypothesis & those about the research hypothesis. Learning why *p*-value-driven conclusions, & the lack of FDR controls, are not conducive to reproducible work. Conclusions are generally aligned with given results, but when multiple methods are used, does not recognise the dependencies among methods that appear to reinforce, but actually replicate, results. Conclusions are neither fully contextualised with the rest of a document (write-up, paper, *etc.*) or study/ experiments/ paradigm (contextualisation for *coherence*), nor with the literature (*critical contextualisation*).	hypothesis/hypotheses & across the entire manuscript/writeup (as appropriate). Learning to critically contextualise results; is able to draw the most obvious conclusions, but struggles to see patterns, or draw more subtle conclusions. Learning that 'full' contextualisation of conclusions requires consideration of limitations deriving from methods & their applications, & their effects on results & conclusions. Learning to recognise how independence of multiple methods applied to similar data/problems supports reproducible conclusions.	statistical & biological significance. In their own & others' work, seeks competing, plausible alternative conclusions. Can judge the scientific importance of their results, & draws conclusions accordingly. Can draw conclusions & contextualise results with respect to an entire manuscript/writeup in a given project or study, or with literature (as appropriate). Can detect when conclusions are not aligned with other aspects of the work (*e.g.*, introduction/ background, methods &/or results, or other experiments in the project). Gives careful consideration to limitations deriving from the method & its application in a specific study. Sees patterns, & perceives more subtle conclusions than earlier-stage scientists, & collaborates to fully articulate & motivate them. Writes the Discussion & Conclusions sections, including limitations, of own articles, with collaboration.	within any given document (*e.g.*, manuscript, writeup, *etc.*). Strives to fully contextualise conclusions in own work, & also requires this in others' work. Draws & contextualises more subtle conclusions than at earlier stages. Can conceptualise new experiments based on the lack of robust &/or defensible conclusions in others' work. Carefully considers consistency of conclusions with the other parts of own or others' work.
Communication	Does not communicate scientific information clearly or consistently; is unaware of community standards for scientific communication. Generally relies on lay summaries to support own communication; does not recognise that using original literature strengthens scientific communication. Does not differentiate appropriate & inappropriate scientific communication, nor understand the ethical implications of each.	Learning both to recognise the value of clear communication, & about the role of communication in sharing & publishing research, data, code, data management, tools & resources. Developing an awareness of community standards for scientific communication, & that these include documenting code, annotating data, & adding appropriate metadata. Does not adapt communication to fit the receiver. Learning to differentiate appropriate & inappropriate scientific communication, but does not yet understand that transparency in all communication represents ethical practice, *even when* the desired results have not been achieved.	Understands the roles of sharing & publishing research, data, code, data management, tools & resources in scientific communication. Seeks guidance so that own communication is coherent, accurate & consistent with community standards (*e.g.*, following FAIR‡ principles; ensuring socially responsible science). Learning to document code, annotate data, & add appropriate metadata – & the importance of these (as appropriate given their research/ context) for sharing & integration. Learning the importance of adapting communication to fit the receiver, seeking opportunities to practice this. Learning that transparency in all communication represents ethical practice, even when the desired results have not been achieved.	Consistently & proficiently uses technical language to correctly describe what was done, why, & how. Sufficient consideration given to limitations, with explicit contextualisation of results consistently included in the communication of results & their interpretation. Can adapt communication to fit the receiver; recognises that sometimes communication must be consistent with community standards beyond their own discipline. Appropriately documents/annotates all data, code, tools, & resources for sharing, integration, & re-use. Understands that transparency in all communication represents ethical practice.	Is an expert communicator & reviewer of scientific communication; adheres to & promotes disciplinary standards for communication. Communicates in a manner that is consistent with standards across communities beyond their own discipline, as appropriate. Ensures communication is appropriate for a target audience, expertly adapting to fit the receiver(s). Communication is transparent, & appropriate to support reproducibility – & thereby, ethical practice - in every context.

*Framework of the workflow supports decisions; workflow is not necessarily linear and can be multidirectional and iterative; any point can be re-iterated, or new starts from within the workflow can be made. A pipeline is unidirectional, not iterative within its structure (it is ballistic: once initiated, it runs), and has no decision points. Pipelines can exist within workflows, but workflows do not exist in pipelines.
‡ FAIR: Findable, Accessible, Interoperable, Reusable.

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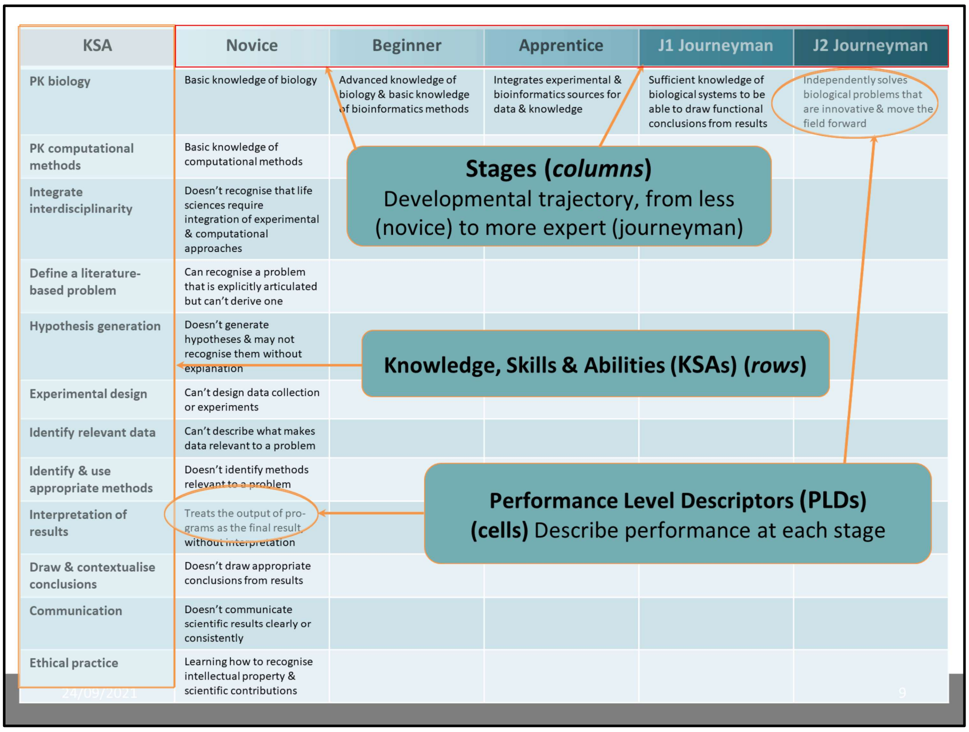
…covering a total of 6 pages!

* Clearly, this isn't the easiest thing to digest! But we can summarise the whole thing in a much simpler table…



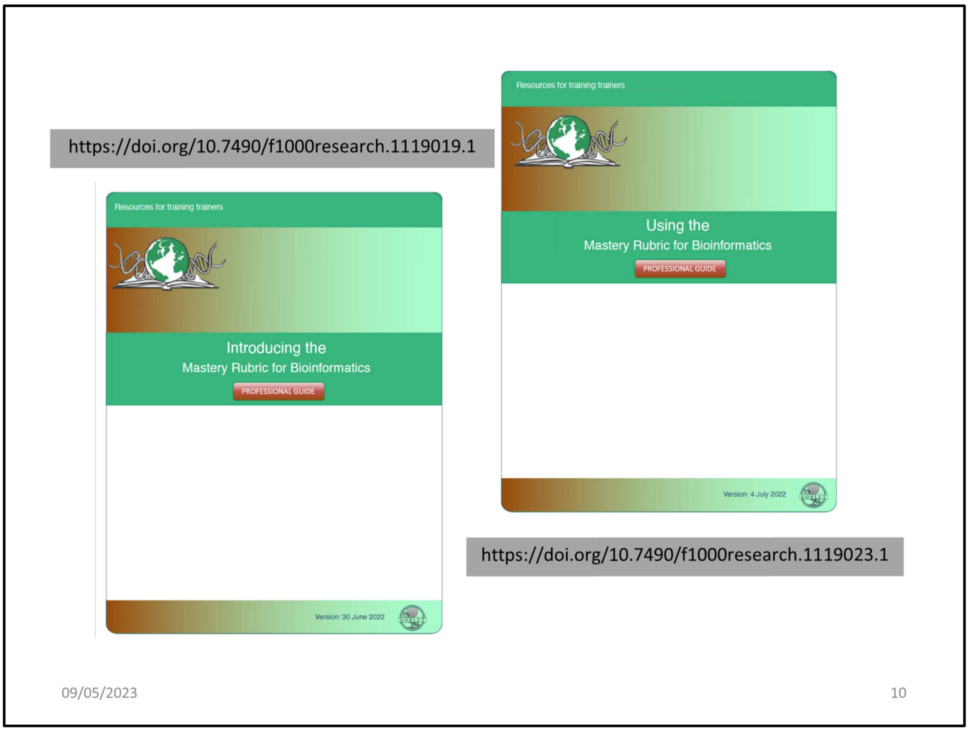
…which looks like this

* Again, note the **12 KSAs** on the y-axis, one on each row. I should point out that these are *not to be confused* with the KSAs encapsulated in various competency frameworks – the KSAs referred to here are much broader or higher-level concepts.

* As before, the **stages** are along the x-axis, denoting in each column a particular point in the developmental trajectory, from less to more expert.

* & the **descriptions** of learner performance (the PLDs) at those levels are given in each cell.

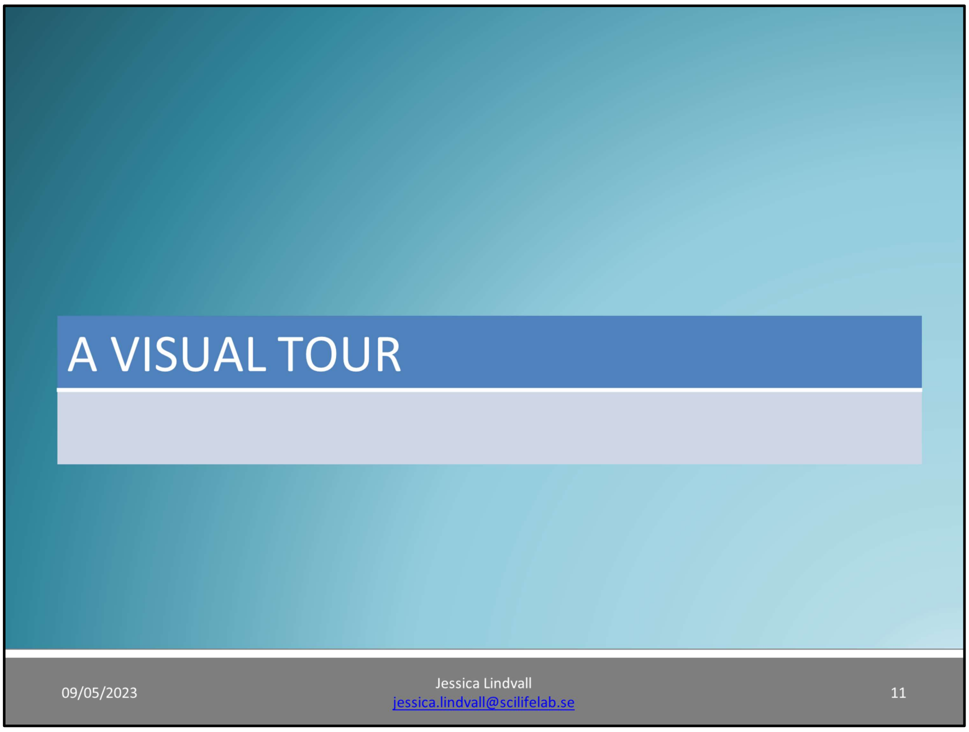
* So the key take-homes here are the **KSAs**, the **stages** & the **PLDs**.



In addition to the original paper in PLoS One we have written 2 papers for the ELIXIR-GOBLET Professional Guidelines collection (the *F1000R Bioinformatics Education & Training Collection)* outlining the usage of the framework in a more "hands-on" and practical manner

1) introduces the Master Rubric for Bioinformatics as a framework, and the
2) show you "how to use" the Mastery Rubric for Bioinformatics framework

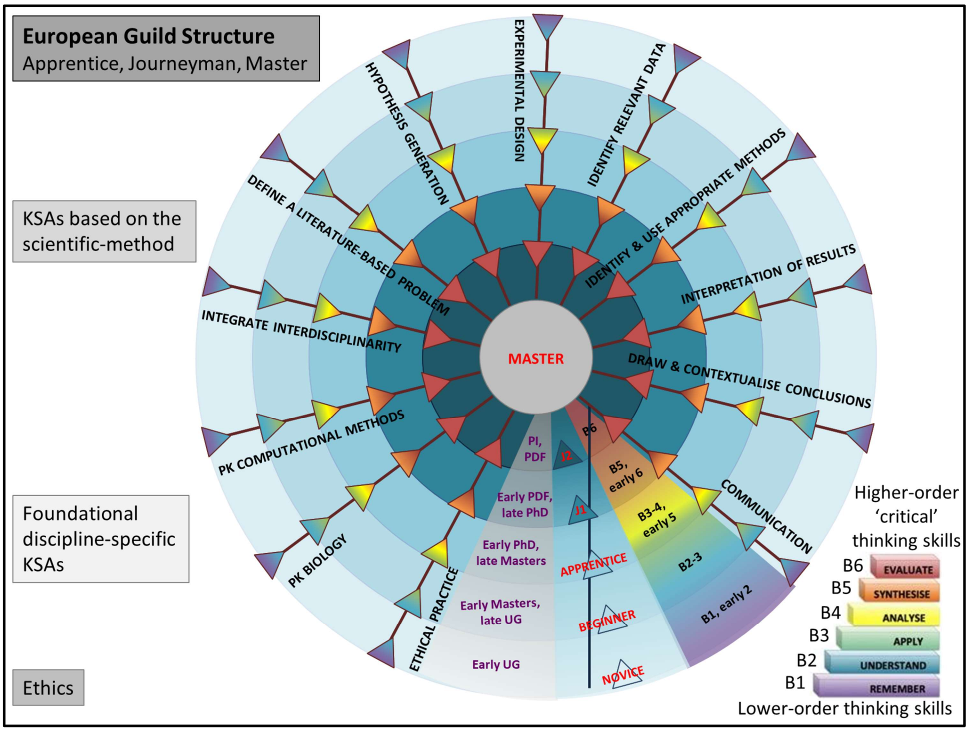
This presentation outlines these two guides.



It's a big ask to expect anyone to take all of this in in one go, so we're now going to look at the MR-Bi from a slightly different perspective – hopefully, this will help you to mentally unpack its components, & better show how they work together…

It's important to stress at this point that the key thing here is the **concepts**, ***not* the nitty-gritty detail**…

But again, please shout if anything's unclear



The first thing to note is that the Mastery Rubric builds on the (ancient) **European Guild Structure**, which outlines a trajectory from **Apprentice** through **Journeyman** to what was originally **Master Craftsman** or Tradesman.

* But the MR adds two further stages – **Novice**, **Beginner**.

* It also differentiates the **Journeyman stage into early & late (J1 & J2) stages**, recognising that the Journeyman period is generally the *longest* phase of 'training'– there are hence ***observable differences*** between a newly qualified individual (**a new PhD**) & one with, say, 10 or more years of experience (say **an independent research fellow or PI**)...who has *arguably* achieved **mastery** of his/her subject.

* Each of these **stages** can be mapped to the relevant **Bloom's level** – from remember/understand (**B1,B2**) through apply/analyse (**B3,B4**) to synthesise & evaluate (**B5 & B6**).

* Similarly, each stage can be mapped to stages in a **traditional academic trajectory**, from UG through Masters, to PhD & PDF, & ultimately independent PI.

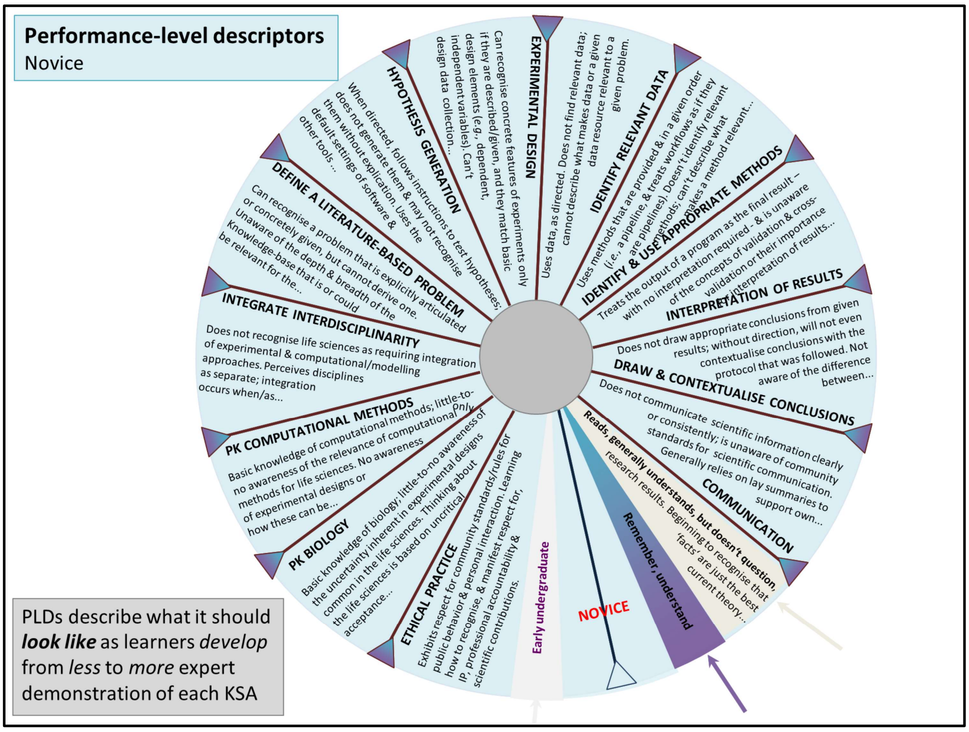
* As shown earlier, the MR lists the **KSAs** a programme is intended to deliver: for bioinformatics, these are based on **foundational, discipline-specific KSAs – PK**

Biology & **PK Computational Methods**

***** Then 9 further KSAs based on the **scientific method**;

***** & last, but not least, **ethical practice**.

Hopefully, this is beginning to give you a feel for how each of the stages **builds,** layer upon layer, onto the next in terms of **cognitive complexity** (advancing Blooms) as an individual progresses from **less** to **more** expert, from **Novice** (outside layer) to **Independent scientist** (inside layer). We can now take a closer look at this, layer by layer.

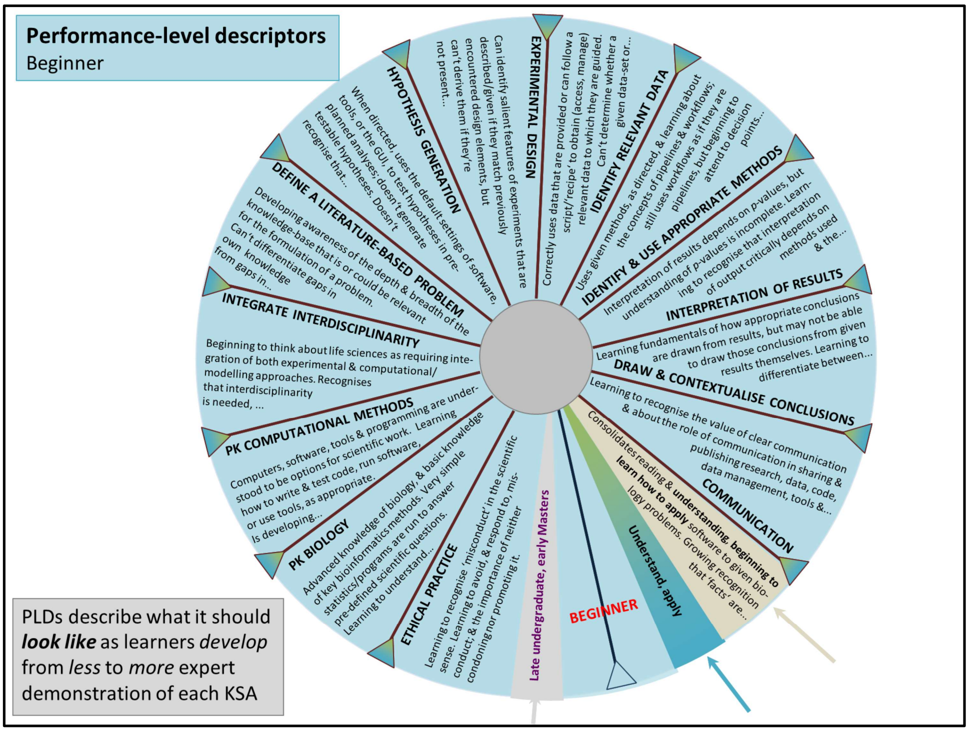


Hidden within each of the layers, at each level, are the **Performance Level Descriptors** (the **PLDs**) that describe what it should look like as learners develop from less to more expert *demonstration* of each KSA… (again, you're not meant to read this!)

* As we saw before, alongside the PLDs are a **General description** of an individual at this stage,

* the requisite **Bloom's level…** & **stage of academic training**.

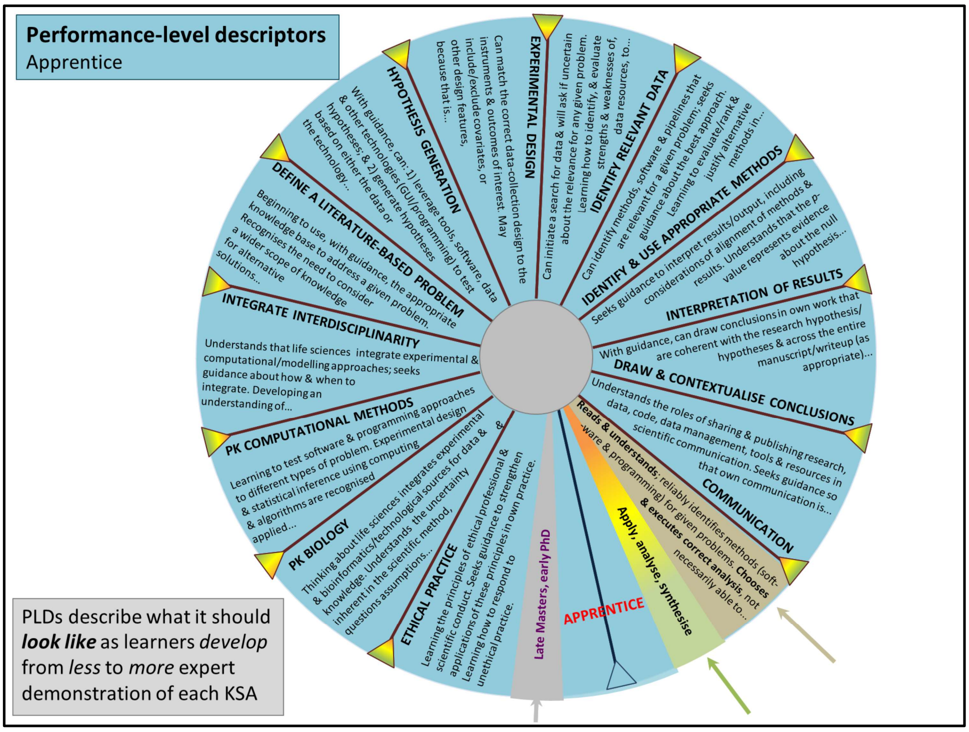
Here, for example, the **Novice** is somebody who "*Reads & **generally understands**, but **doesn't question** research results…etc.*" & the Blooms levels (**remember, understand - 1,2**) reflect this; & this would be a typical description of **early undergraduate** thinking.



And so on at each stage.

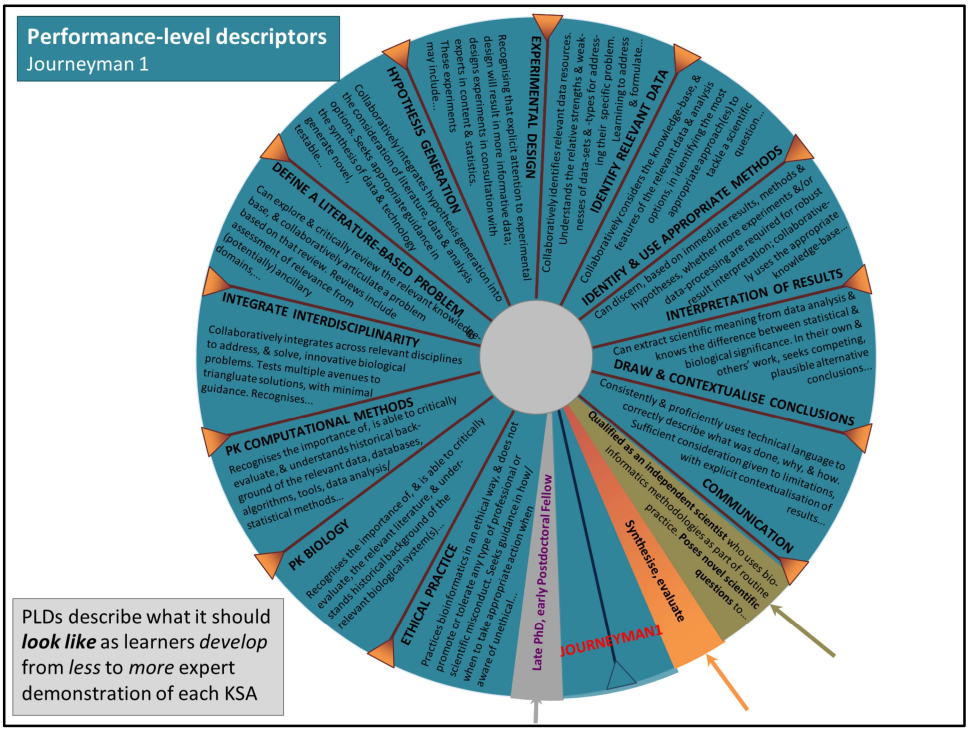
Moving to the next level ‘up’, the **Beginner** is “***beginning to learn** how to **apply** software to given biological problems…etc.*”,

the Bloom’s levels have changed accordingly (**understand, *apply* - B2-B3**), & this might be a typical description of an **early Masters** student.



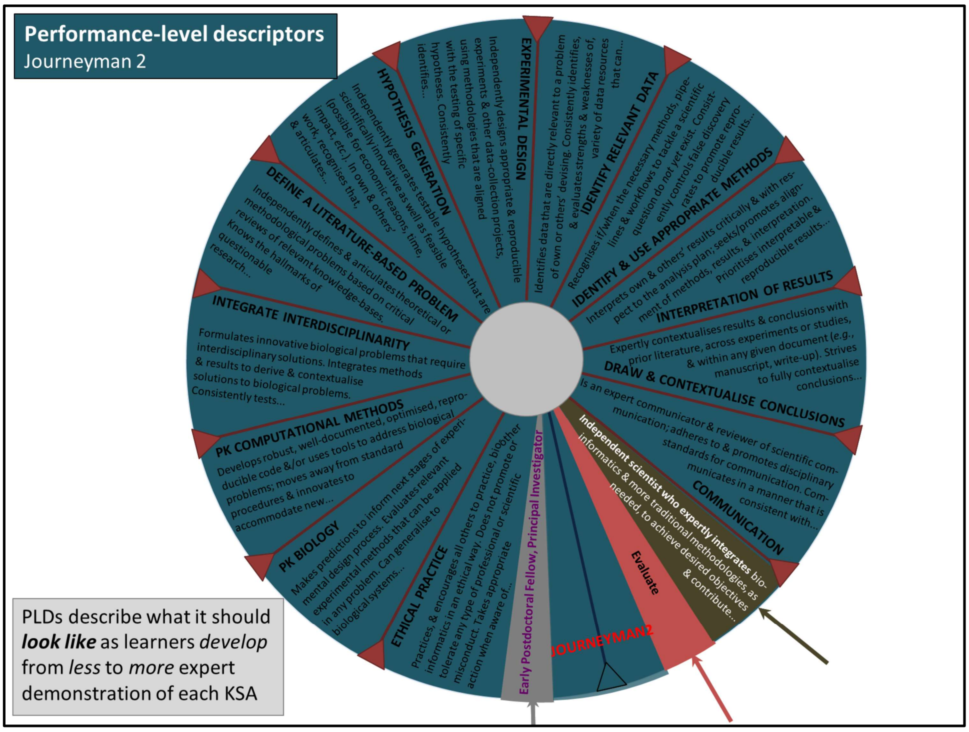
At the next level, the **Apprentice** is becoming more expert at **analyses**, but may not be aware of other equally viable approaches… & will need **guidance**.

The **Blooms** levels have progressed from **applying, analysing** & **beginning to synthesise** (**B3** to **early B5**), which might be a typical description of **late Masters/early PhD students**.



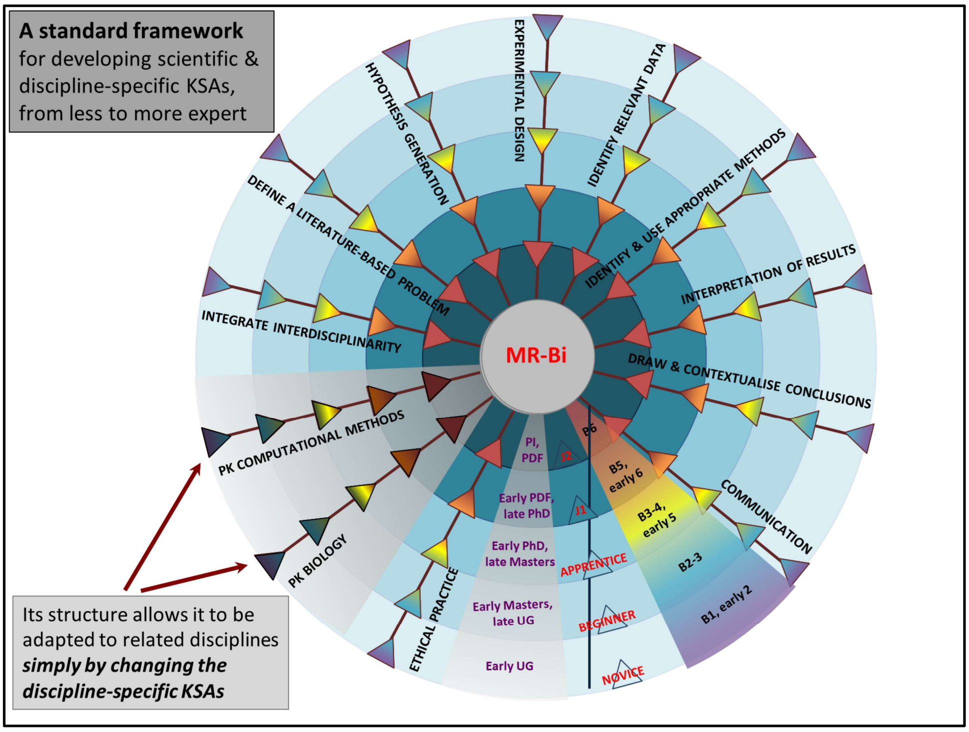
At the first Journeyman level, **J1** is newly qualified as an '**independent**' scientist, but in fact **generally still requires some supervision**, as is typical of early **PDFs**.

The **Blooms** level has moved on to include the ability of such individuals to **evaluate**, but with guidance.



And at the second Journeyman level, **J2** is the **confident expert** in his or her field, most likely a **PI** with an independent research group…

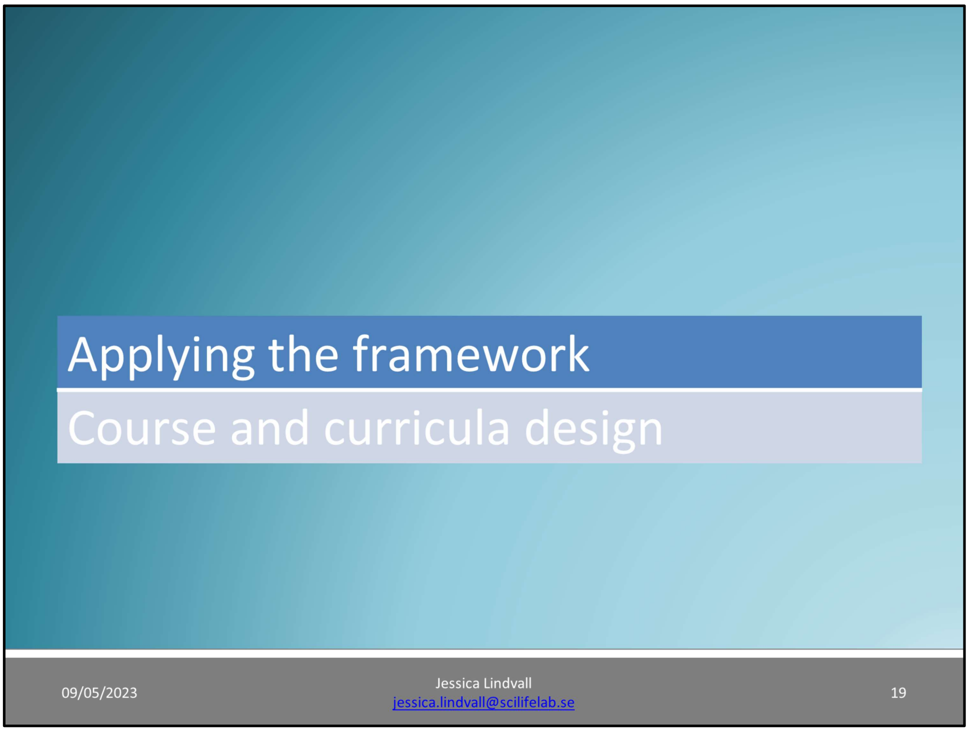
…whose cognitive abilities are at the highest **Blooms** level (evaluate – B6).



Bringing all of these components together - these cognitive layers - this *is* the Mastery Rubric for Bioinformatics (MR-Bi), a standard framework for developing **scientific & discipline-specific KSAs**, from **less** to **more expert**…

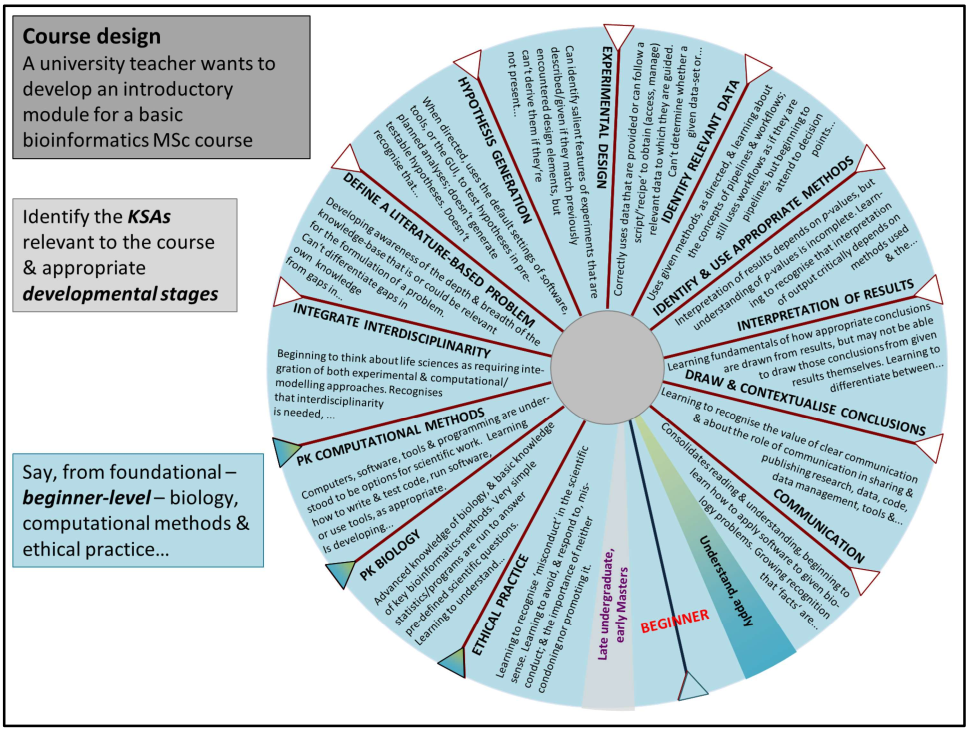
* And one of the really useful things about it is that its structure readily allows it to be adapted to related disciplines, ***simply by changing the discipline-specific KSAs***, while the scientific-method-related KSAs remain essentially the same – a plug-&-play tool, if you like, for related scientific disciplines.

So how can we use it?



For this last part. Let’s see how we can apply the MR-Bi framework to **course and curricula design**

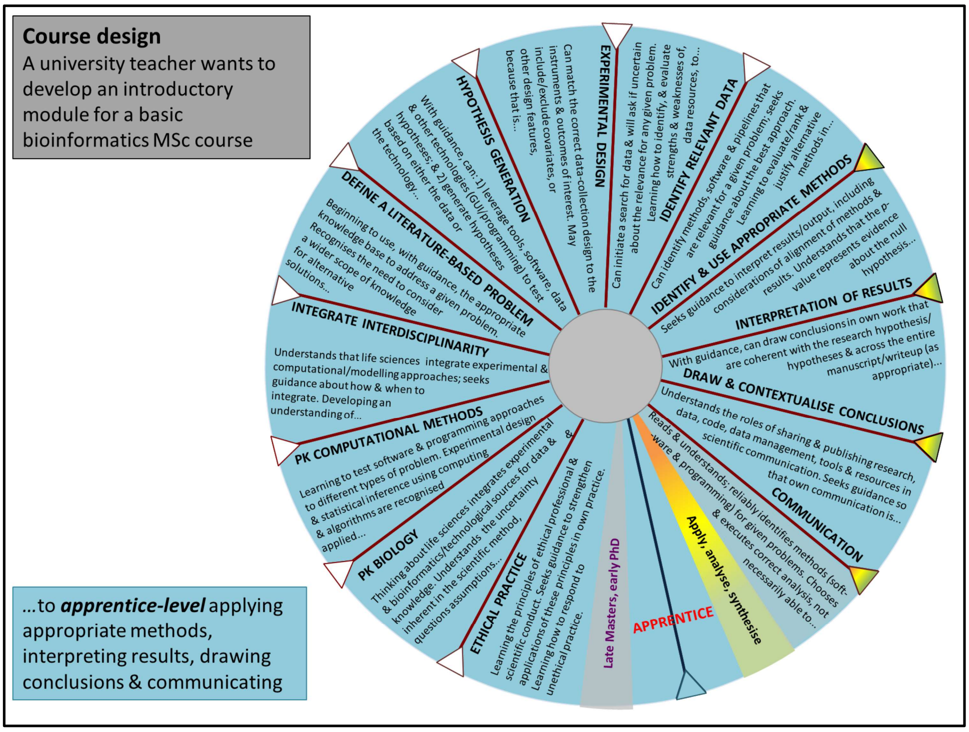
Again, it’s the principles here that we’re trying to highlight rather than the nitty-gritty detail



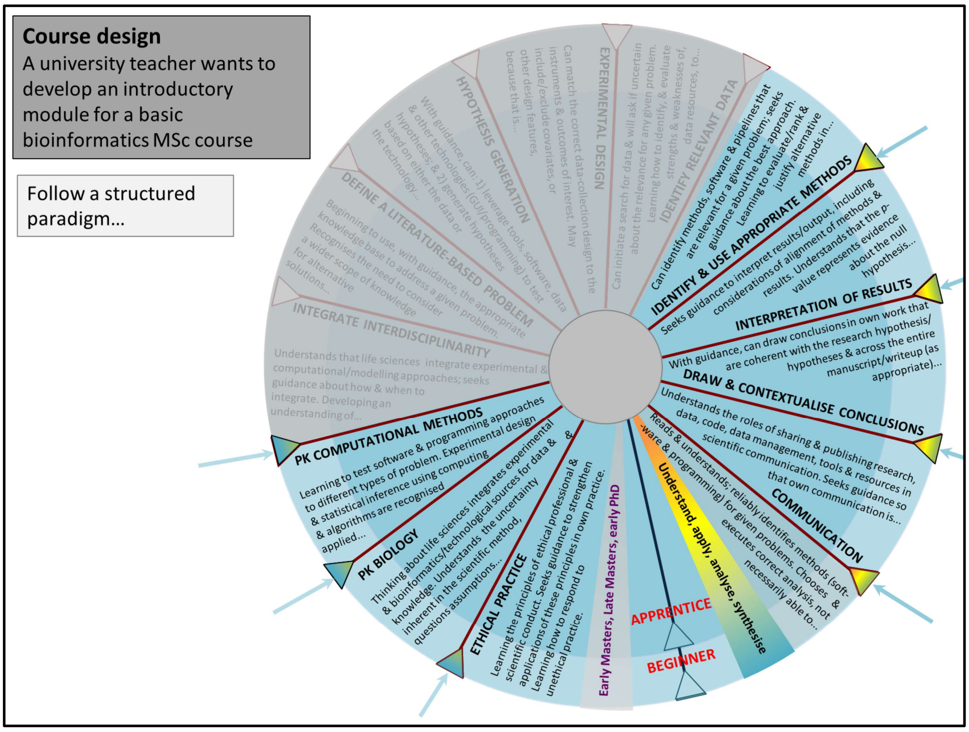
In this application, we imagine being a **university teacher** who wants to develop an **introductory module** for a **basic bioinformatics MSc course**.

* The first step is to **identify the KSAs** relevant to the course & **appropriate developmental stages**.

* So, let's say that we want the module to build from **foundational** – ***Beginner-level*** – **Biology, Computational methods** & **Ethical practice**…



...to ***Apprentice-level*** **Applying appropriate methods**, **Interpreting results**, **Drawing conclusions** & **Communicating**.



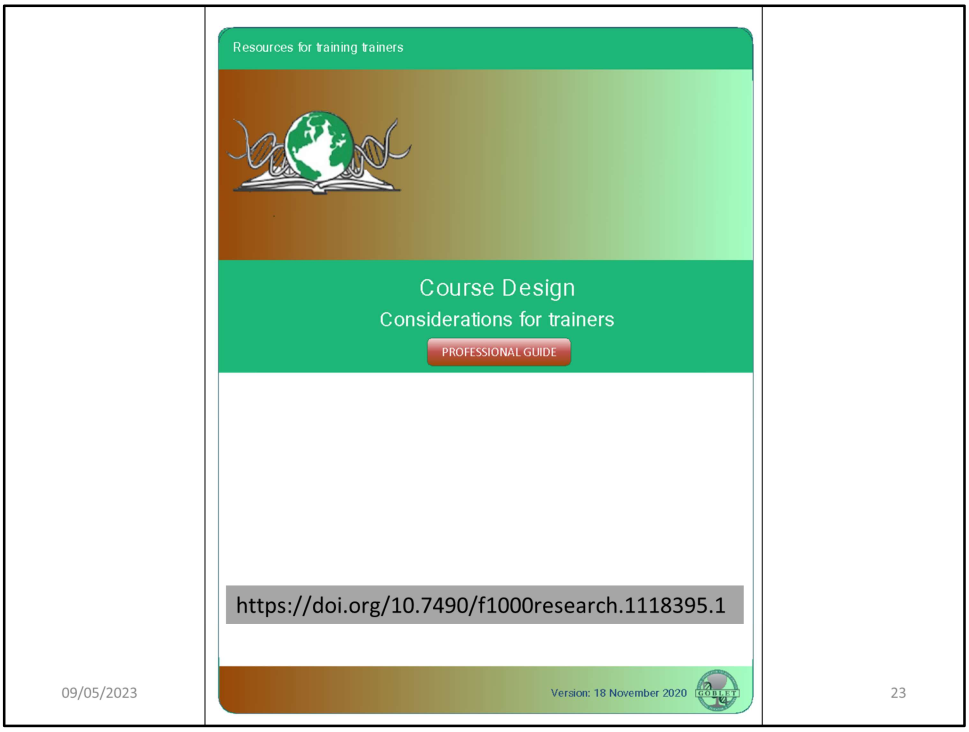
So, putting these layers together, the focus of this module is on building up from

* ***Beginner-level*** **Biology**, **Computational methods** & **Ethical practice**,

* to ***Apprentice-level*** **Identifying & using appropriate methods**, **Interpreting results**, **Drawing conclusions** & **Communicating**,

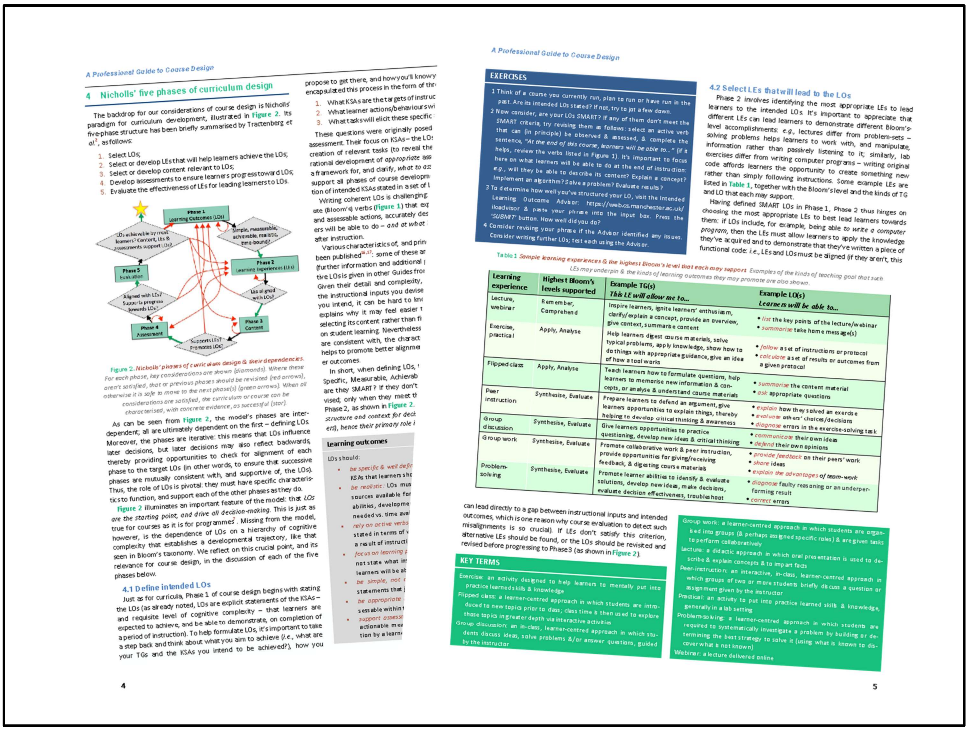
So we focus on **these stages** & **these KSAs** & **ignore the rest**.

* To build a course around these – indeed any course focusing on any KSAs – we recommend following a structured paradigm.

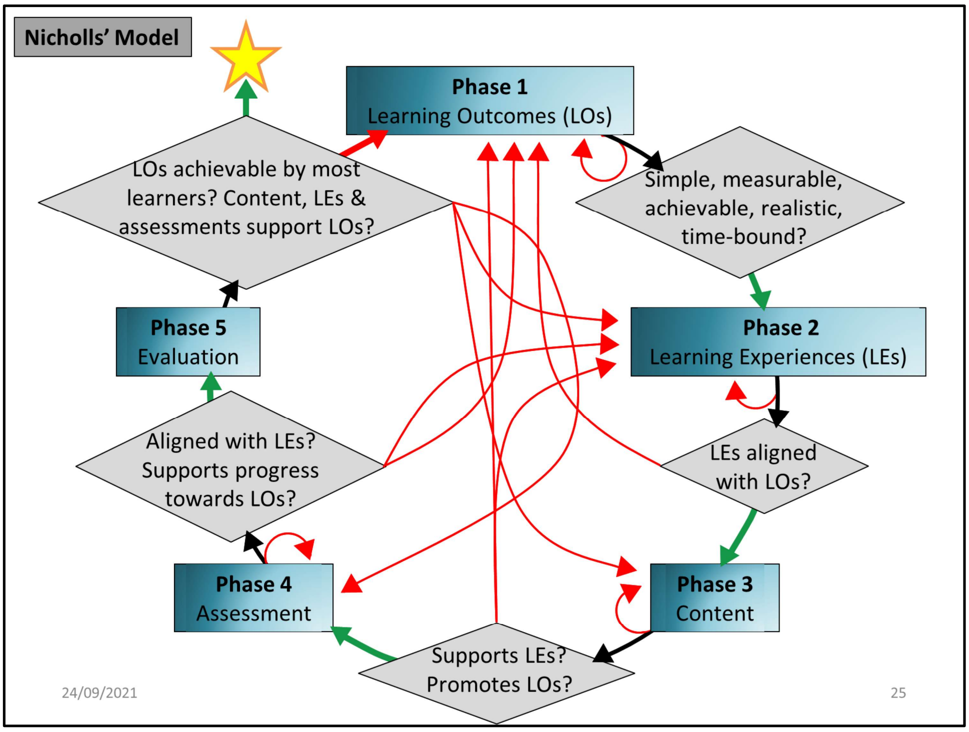


You can find more details of our recommendations in the *Guidelines for Curriculum & Course Development* we made available as a preprint (SocArXiv) in 2020;

* we also released a more practical/hands-on version specifically for trainers in our ELIXIR-GOBLET Professional Guidelines collection, in the *F1000R Bioinformatics Education & Training Collection*. In addition to 2 Professional Guidelines with regards to the framework itself as said earlier



In those documents, you'll see that we use **Nicholls' 5-phase paradigm for curriculum/course design** as an exemplar, which is illustrated here in the diagram on the left.



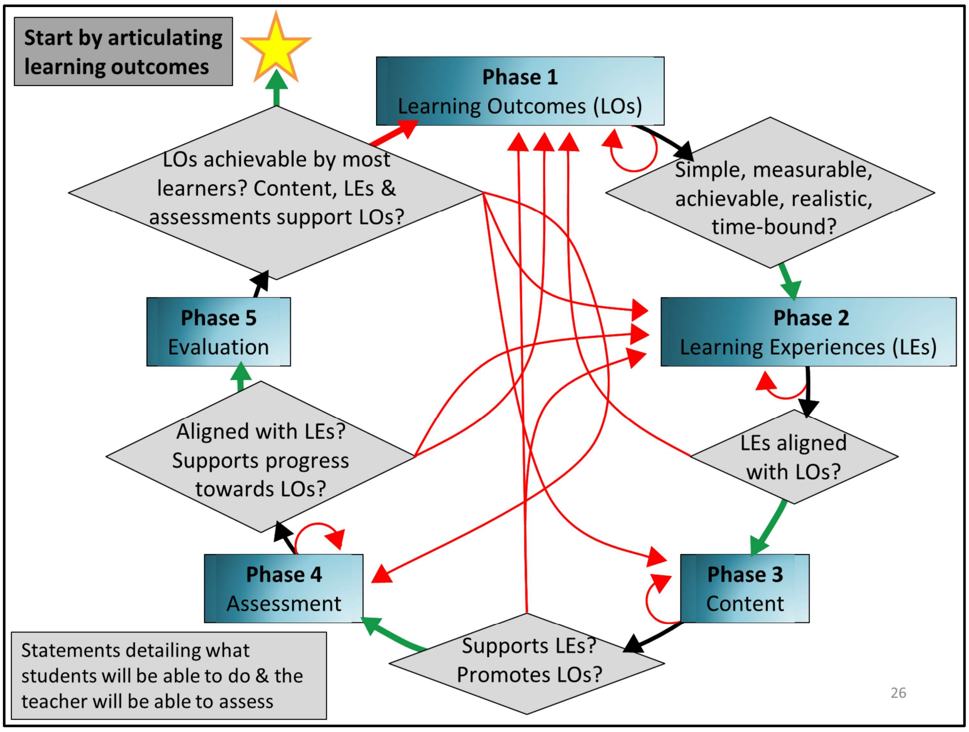
Details of the model aren't important here.

The point is, there are **5 key phases** in the course-design process: from defining LOs, to selecting LEs, to selecting content, devising appropriate assessments to course evaluation.

* At each phase there are **decision points** to test whether specific criteria have been met (e.g., are the LOs SMART…);

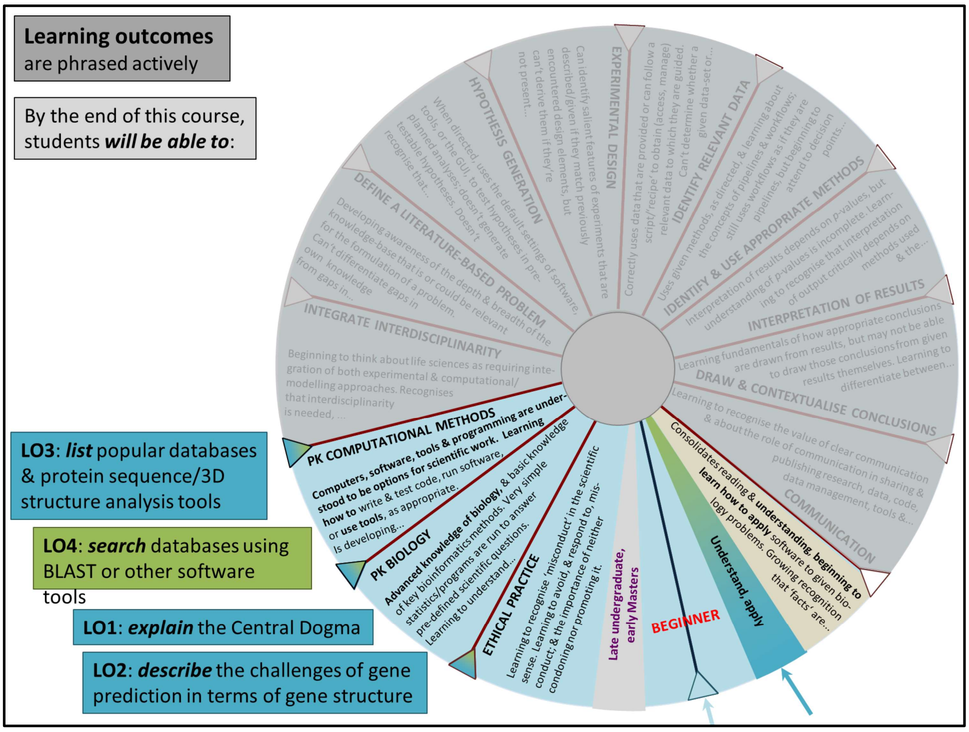
* If the criteria ***haven't*** been met, either **that phase requires revision**, the **previous phase needs revision** or **Phase 1 needs revision.** Only after this iterative cycle of revision & refinement at each step can the process be regarded as complete.

The crucial take-home here is that, **Phase 1** is the **first-class citizen of the design process**, because each phase must be congruent with it – & Phase 1 is **articulating LOs**!



So, we start the course-design process by articulating the **intended learning outcomes**.

These are statements that detail **what students will be able to do** & **the teacher will be able to assess** by the end of the course.



LOs are phrased **actively**, articulating what students will be able to do:

* *e.g.*, "***by the end of this course, students will be able to:…***"

* For this course or module, appropriate **Beginner-level** (**understand**, **apply**)

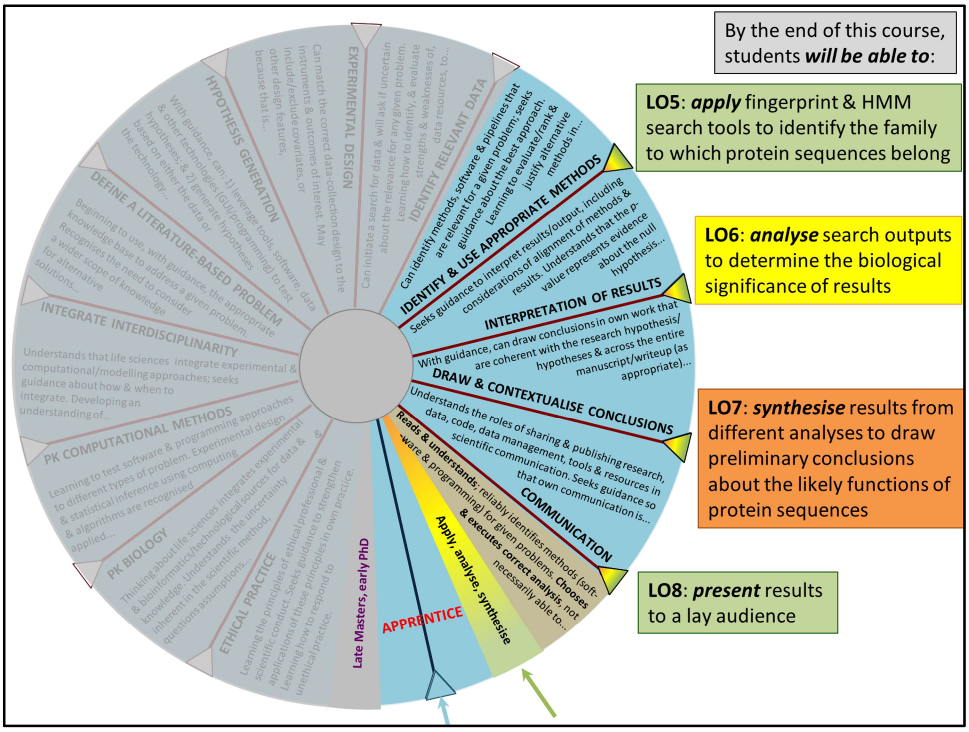
* LOs for **Biology** might be, "*by the end of the course, students will be able to*

* ***explain** the Central Dogma…*" or "***describe** the challenges of gene prediction in terms of gene structure.*"

* For **Computational methods**, appropriate **Beginner-level** LOs might be, "*by the end of the course, students will be able to*

* ***list** popular databases & protein sequence & structure analysis tools,*" or

* "***search** databases using BLAST or other bespoke software tools.*"



* Appropriate **Apprentice-level** (**apply, analyse, sythesise**) LOs for

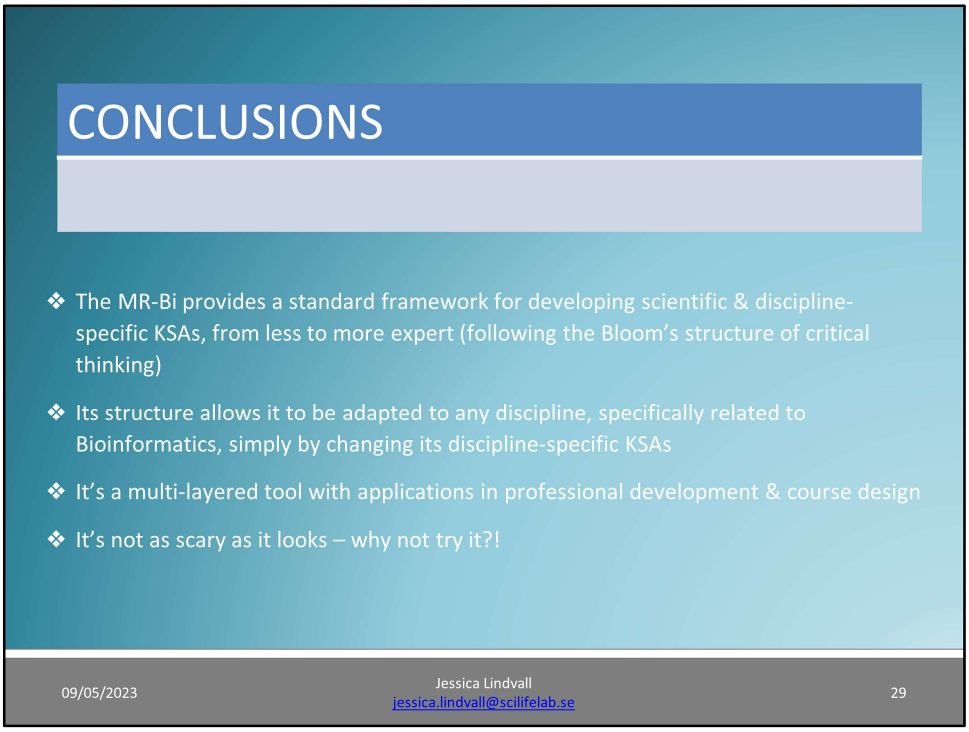
* **Identify and use appropriate methods** might be that, “by the end of the course, students will be able to **apply** fingerprint and HMM tools to identify the family to which protein sequences belong”,

* For **Interpretation of results**, “by the end of the course, students will be able to **analyse** search outputs to determine the biological significance of results”,

* For **Draw conclusions**, “by the end of the course, students will be able to **sythesise** results from different analyses to draw preliminary conclusions about the likely functions of protein sequences”

* and for **Communication**, “by the end of the course, students will be able to **present** results to a lay audience.”

Note that these are all active behaviours, at the requisite Blooms level, that a teacher will, in principle, be able to assess. The examples are clearly just fabricated, but hopefully show how LOs can be ***informed*** by the relevant KSA & PLDs at each stage. Again, the PLDs are not meant to be taken literally, but rather to be used as guides towards what might be appropriate behaviours & outcomes at given developmental stages. And that really is it.



To conclude…

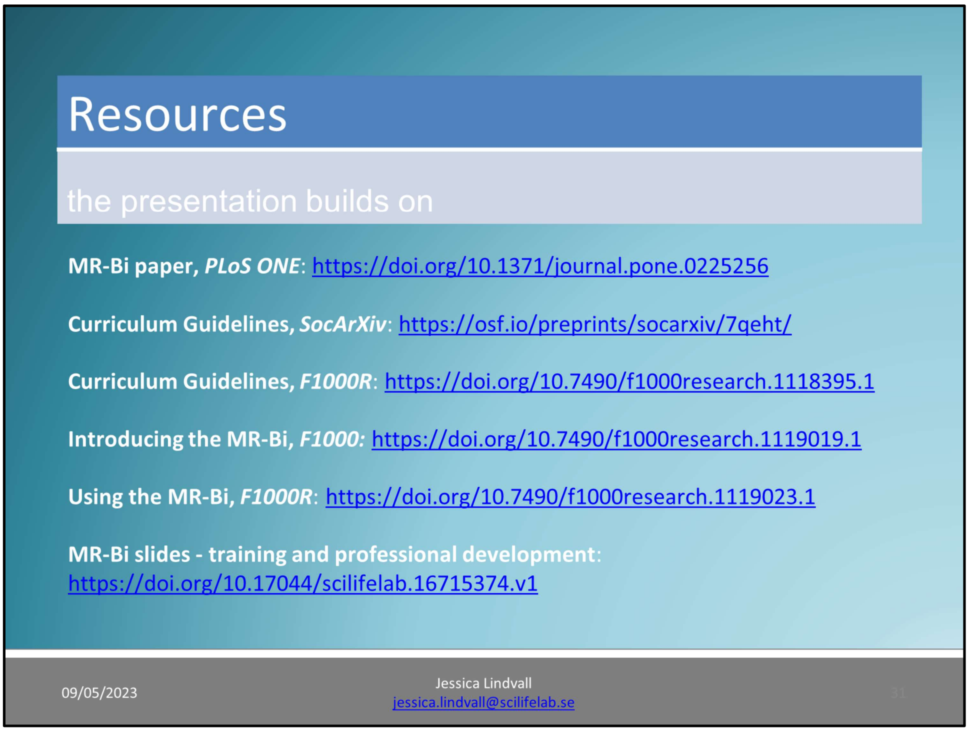
* The MR-Bi provides a standard framework for developing scientific & discipline-specific KSAs, from less to more expert (following the Bloom's structure of critical thinking)

* Its structure allows it to be adapted to any discipline, specifically related to Bioinformatics, simply by changing its discipline-specific KSAs

* It's a multi-layered tool with applications in professional development & course design

* It's not as scary as it looks – why not try it?!

Before ending, with the last slide being the resource s, I'd like to acknowledge the rest of the MR-Bi & ELIXIR-GOBLET Professional Guidelines team: RT, AV, TA and PP



A re-cap of the resources used in the presentation and for you to have a look at if interested. Also if you have any questions later or like to get in contact with me or anyone in the team, please email me, jessica.lindvall@scilifelab.se