nf-core is all about collaboration

Common themes

Standardise analysis methods across research groups

Harmonise data formats

Prepare for future analysis / extension of data

Ensure longevity of methods

..beyond scope of current project

Pipelines
callingcards
createpanelrefs
detaxizer
flowlearn
hadge
hic
lsmquant
marsseq
mcmicro
mdprot
methylseq
molkart
multiplesequencealign
omicsgenetraitassociation
pathogensurveillance
phageannotator
phyloplace
pixelator
radseq
rangeland
readsimulator
riboseq

The nf-core community is (mostly) structured around pipelines

Different projects can use the same set of pipelines in very different ways

There's no space for community members working on similar research interests to gather

Special interest groups

SIGs   Communities   Topics

COSIs   Themes

Flavours   Bushels   Focus groups

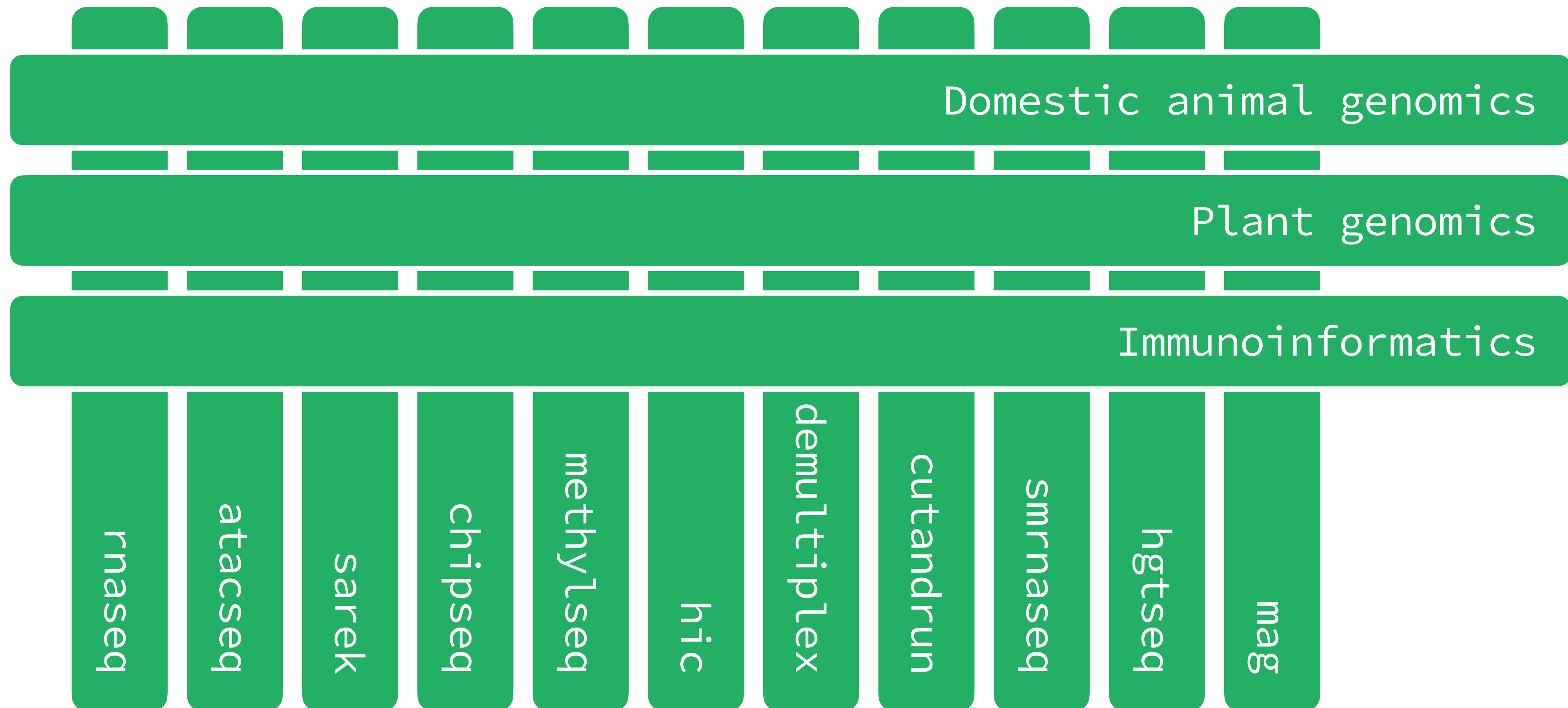Satellite groups   Working groups

Pecks   Orchards   Buds   Spaces

Proposal

Pipelines

Special interest groups

Domestic animal genomics

Plant genomics

Immunoinformatics

rnaseq
atacseq
sarek
chipseq
methylseq
hic
demultiplex
cutandrun
smrnaseq
hgtseq
mag

Proposal

Pipelines	Special interest groups
Propose via `#new-pipelines`	Propose via `#new-interest-group`
Dedicated Slack channel	Dedicated Slack channel
Dedicated web pages	Dedicated web pages
Bytesize talk	Bytesize talk
Archived if no activity	Archived if no activity

But what?

⚖️ Best practices for pipeline usage with this data type

♻️ Cross-reference pipeline pages to community pages

📼 Lists of relevant resources / videos / documentation

💬 Regular meetings

👩🏻‍🏫 Bytesize talks + blog posts

⚙️ Dedicated pipeline configs

Anyone can join 🙋🏻‍♂️

Everyone is welcome 🤗

Next steps

Blog post to announce initiative

Setup of initial group *(Domestic animal genomics)*

New documentation pages for governance

New infrastructure for addition of new groups

Open up to proposals for new groups

Questions

(no, there is no dedicated funding for this)