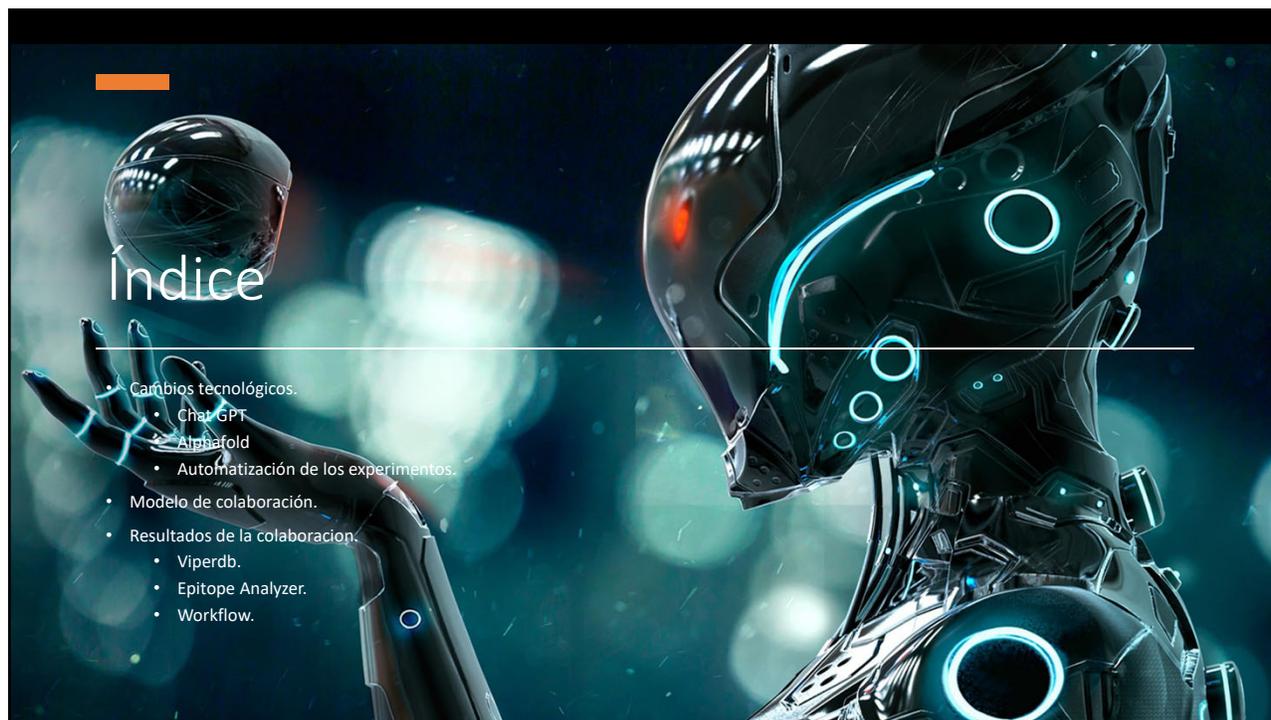




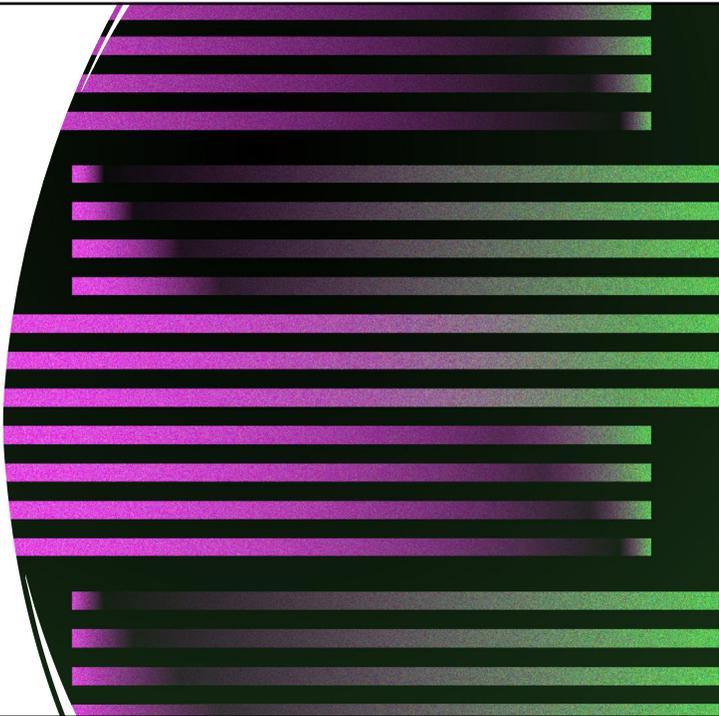
1



2

Cambios tecnológicos que afectarán nuestra vida diaria.

- CHAT GPT: Es una red neuronal, que fue entrenada con un gran conjunto de datos de texto en inglés, con el objetivo de generar texto de manera autónoma y coherente.



3

Es el sentido del humor único de los seres humanos?



User: What is funny about this image? Describe it panel by panel.



Source: [hmmm \(Reddit\)](#)

GPT-4: The image shows a package for a "Lightning Cable" adapter with three panels.

Panel 1: A smartphone with a VGA connector (a large, blue, 15-pin connector typically used for computer monitors) plugged into its charging port.

Panel 2: The package for the "Lightning Cable" adapter with a picture of a VGA connector on it.

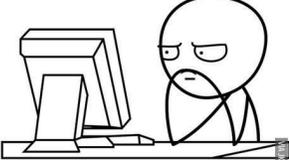
Panel 3: A close-up of the VGA connector with a small Lightning connector (used for charging iPhones and other Apple devices) at the end.

The humor in this image comes from the absurdity of plugging a large, outdated VGA connector into a small, modern smartphone charging port.

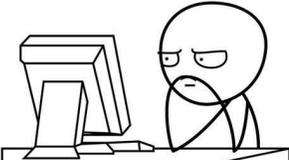
4

Los desarrolladores de software están en peligro?

NO COMPILA Y NO SÉ POR QUÉ



COMPILA Y NO SÉ POR QUÉ



Video en JKUKE.COM

this code is not working like i expect — how do i fix it?

```
resultWorkerErr := make(chan error)
defer close(resultWorkerErr)
go func() {
    defer cancel()
    resultWorkerErr <- b.resultWorker(ctx)
}()

err := b.worker(ctx)
cancel()
if err == nil {
    return <-resultWorkerErr
}
return multierror.Append(err, <-resultWorkerErr)
```

It's difficult to say what's wrong with the code without more context. Can you provide more information about what the code is supposed to do and what isn't working as expected? Also, is this the entire code or just a part of it?

just part of it — the error never surfaces. I think there is something wrong with the channel

It's difficult to say without more information about what the code is supposed to do and what's happening when it's executed. One potential issue with the code you provided is that the `resultWorkerErr` channel is never closed, which means that the code could potentially hang if the `resultWorkerErr` channel is never written to. This could happen if `b.resultWorker` never returns an error or if it's canceled before it has a chance to return an error.

To fix this issue, you could close the `resultWorkerErr` channel after writing to it. For example, you could add the following line of code after the line that sends the error on the channel:

```
close(resultWorkerErr)
```

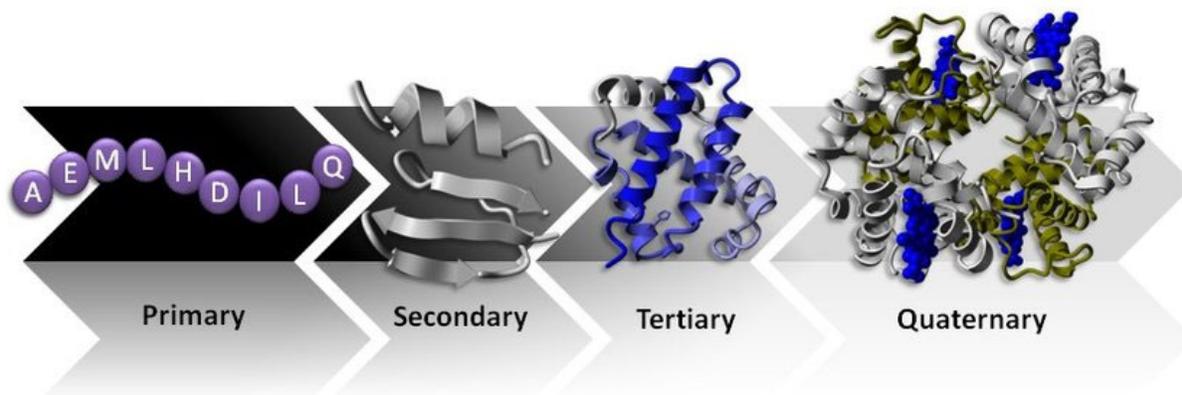
This would ensure that the `resultWorkerErr` channel is always closed, even if `b.resultWorker` never

5



6

Las proteínas tienen 4 niveles estructurales



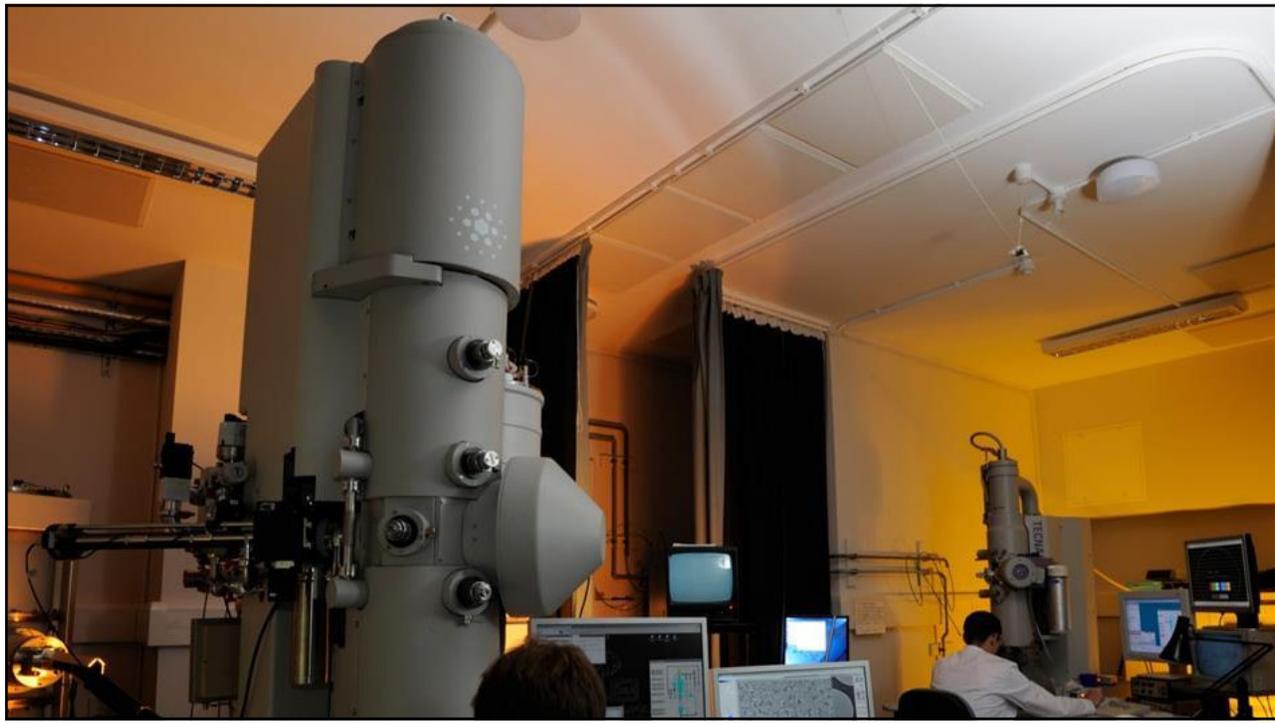
7

Avances en hardware relacionado con la biología

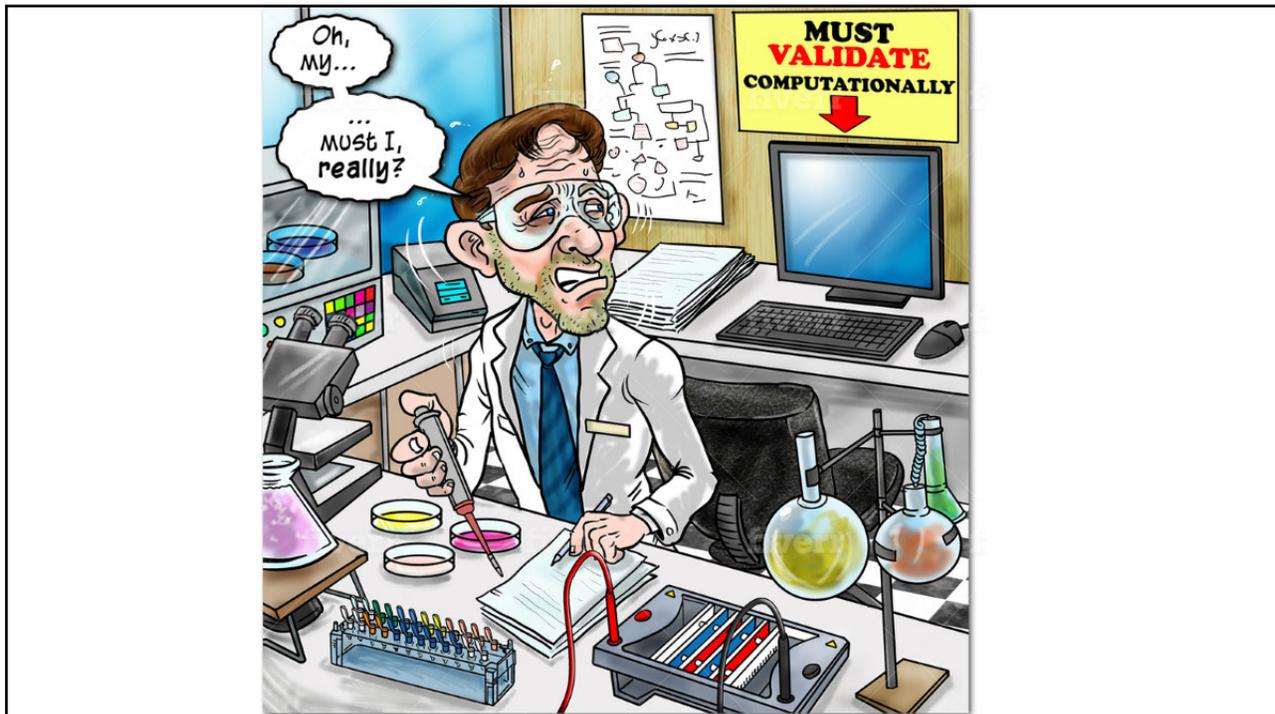
Next Generation Sequencing machines (NGS)



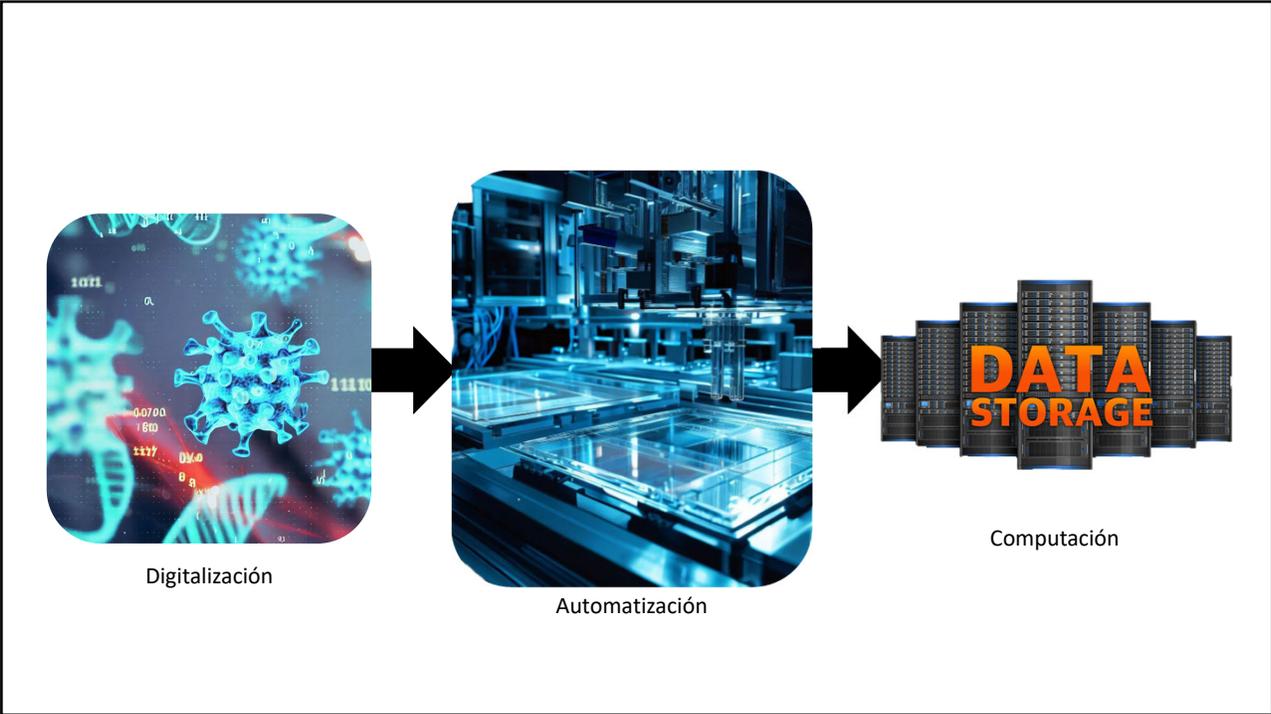
8



9



10

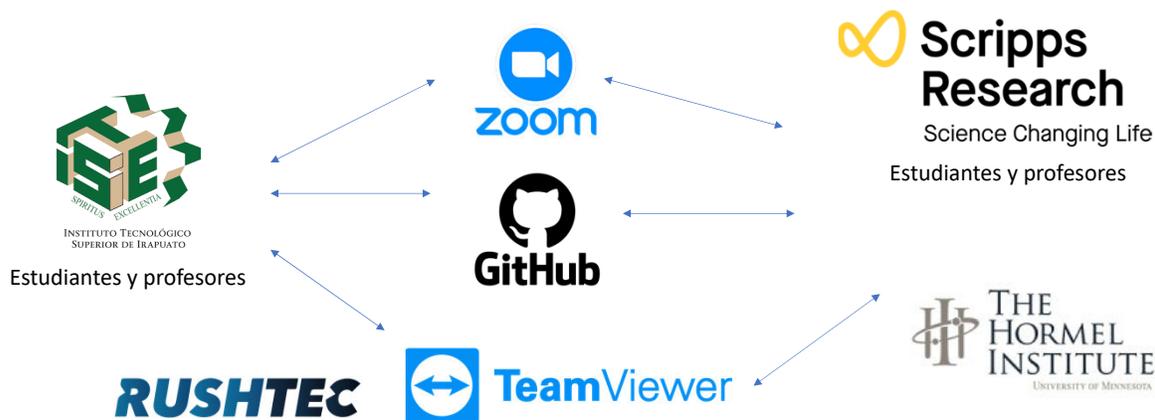


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Nuestro modelo de colaboración

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Utilizamos los avances tecnológicos para
colaborar de manera internacional



13

La colaboración beneficia ambas partes.

- ITESI
- Práctica del idioma inglés por parte de los estudiantes.
- Experiencia laboral al participar en proyectos de investigación de alto rendimiento.
- Reconocimiento del trabajo realizado en publicaciones de alto nivel de impacto.
- Apoyo económico*
- Scripps / Hormel
- Mejora de los flujos de trabajo.
- Innovación en la aplicación de nuevas tecnologías bioinformáticas.
- Avance acelerado en los flujos de análisis de datos.

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Modelo de colaboración, requiere de un compromiso mutuo entre profesores y estudiantes de ambas instituciones.

Mentores en Scripps



Mentores en ITESI



Estudiantes en Scripps



Estudiantes en ITESI

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Nuestros proyectos

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Virus Particle Explorer db v3.0

THE HORMEL INSTITUTE
UNIVERSITY OF MISSISSIPPI

1338 Structures
75 Families
165 Genera

8BQN
STRUCTURE OF EMPTY COXSACKIEVIRUS A10 EMBEDDED IN CRYSTALLINE ICE FROZEN AT -140 DEGREE

Latest Entries

- 8giu: Mycobacterium phage Pattice (2023-03-14)
- 8cfa: H327 Prohead II as part of a DNA packaging complex (2023-02-03)
- 8fq4: AAV1 VP3 Only Capsid (2023-01-06)
- 8fe3: Structure of dengue virus (DENV2) in complex with pM12, an anti-pM1 monoclonal antibody (2022-12-06)
- 8fe4: Structure of dengue virus (DENV2) in complex with pM13, an anti-pM1 monoclonal antibody (2022-12-06)
- 8fy: Structure of Coxsackievirus A10 frozen at -183 degree embedded in crystalline ice (2022-11-21)
- 8bqn: Structure of empty Coxsackievirus A10 embedded in crystalline ice frozen at -140 degree (2022-11-21)

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TecNM Irapuato Campus

Nelly Beatriz Santoyo Rivera
Human Resources Manager

User Statistics

Site Visits Last Month: 1307

Countries: 142

Visits: 20435

Past Members

- Phuong Ho: Database Admin, Scripps Research Institute
- André Delgado Gómez: Dashboard Tool, TecNM Irapuato Campus
- Noemi Villafañá Navarrete: Module Users of ViperdB, TecNM Irapuato Campus
- Francisco Javier Paredes Rocha
- Alan Misael Mendoza Pérez: Dashboard Tool, TecNM Irapuato Campus
- Ignacio Cruz Rodríguez: Software Quality Assurance, TecNM Irapuato Campus
- Diego Abraham Corona Chavéz: Module Virus World, TecNM Irapuato Campus
- Fernando Vargas Bravo
- Antonio de Jesús Rodríguez García: Natural Language Processing, TecNM Irapuato Campus
- Brian Alejandro Flores Silva: Natural Language Processing, TecNM Irapuato Campus
- María Guadalupe Moreno Magdaleno: Module Adentry v1, TecNM Irapuato Campus
- Juan Daniel Zavala Martínez

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PDB	Chain	Seq. Init.	Sequence
5XS7	A GENOME POLYPROTEIN	1	NDPIANAVESAVSALADTTISRVTAAANTTASTHSLGTGRVPAQAETGASSNASDENLVETRCVMNRNGVNEASVEHFYSRAGLVGVVEVKD SG I S I D G Y
5XS7	B GENOME POLYPROTEIN	1	SPSVEACGYSDRVAQLTVGNSTITTQEAANIVLSYGEWPEYCPSTDATAVDKPTRPDVSVNRFYTLSTKSWKTESTGWYWKFPDVLNDTGVFGQAQFHYL
5XS7	C GENOME POLYPROTEIN	1	GFPTCLKPGTNQFLTDDGTSPPIPLPGFEPTPLIHIPGEFTSLDLQCQIETILEVNNTTGTIGVSRLLIPVRAQNNVDQLCASFQVDPGRNGPWQSTMVGGICR
5XS7	H HEAVY CHAIN OF	1	EVQLVESGGGLV KPGGSLKLSCAASGFAFSTYDMSWVRQTPEKRLLEVAHISGGGGYI Y P D I V KGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRQKGL

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Technical Note

Epitope-Analyzer: A structure-based webtool to analyze broadly neutralizing epitopes

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Workflow a new way to do bioinformatics



INSTITUTO TECNOLÓGICO SUPERIOR DE Irapuato

Front end

Back end

Management

Q&A

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¿Para quién está diseñado?



Usuario de laboratorio



Usuario Normal



Computólogo

Images generated by DALLE 2

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The screenshot displays a workflow execution environment. The top bar indicates 'MD - Execution: 185' and 'test'. Below this, there are controls for 'Download Image', 'Execution profile: IMS', and 'Job id: none'. The main area is titled 'Run Workflow' and contains a flowchart with nodes: 'PDB', 'Gromacs_Topology', 'Gromacs_solvation_Box', 'Gromacs_Solvation', 'Gromacs_ions_1', 'Gromacs_ions_2', and 'Gromacs_EM'. On the left, there are input data sections for 'PDB', 'Cube_Size_1', 'Ions_mdp', and 'minimum_mdp', each with a 'Browse...' button and 'No files selected.' status. At the bottom, a log window shows execution details for 'Experiment 185' with timestamps and status messages like 'Workflow process completed'.

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