

Automatic Surveillance of Multi-drug Resistant Organisms and Early Detection of Outbreaks within a Hospital

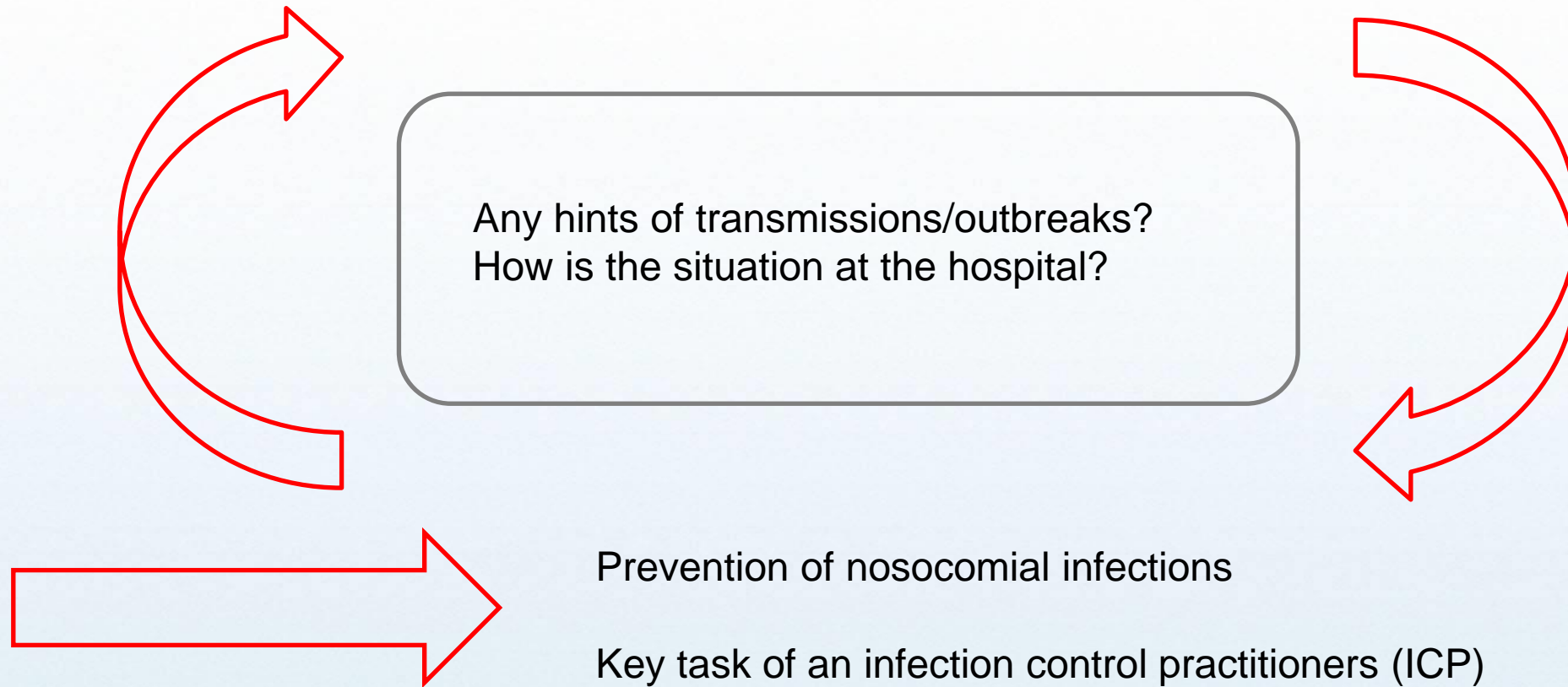
Hauke Tönnies
Institut für Hygiene
Universitätsklinikum Münster

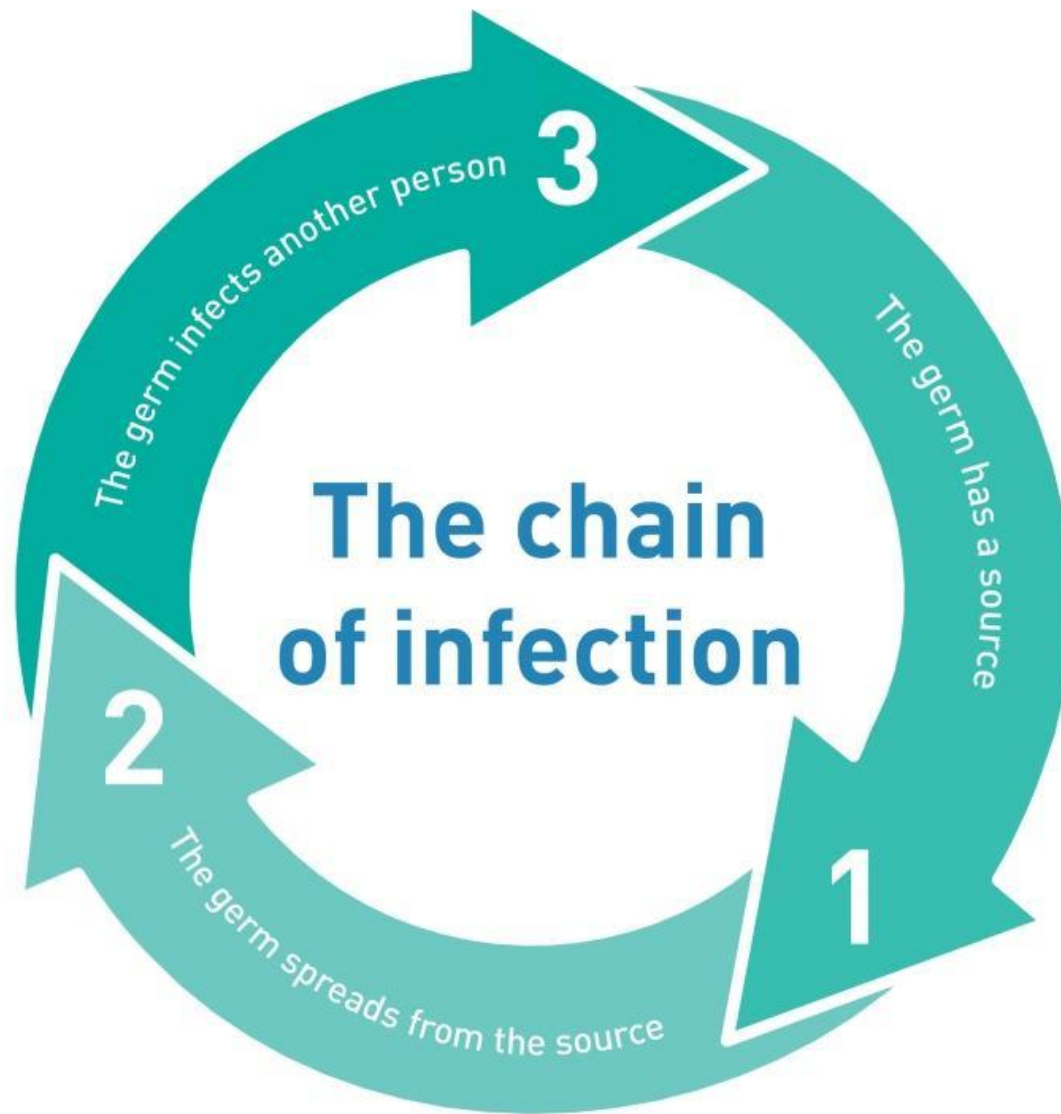
GEFÖRDERT VOM



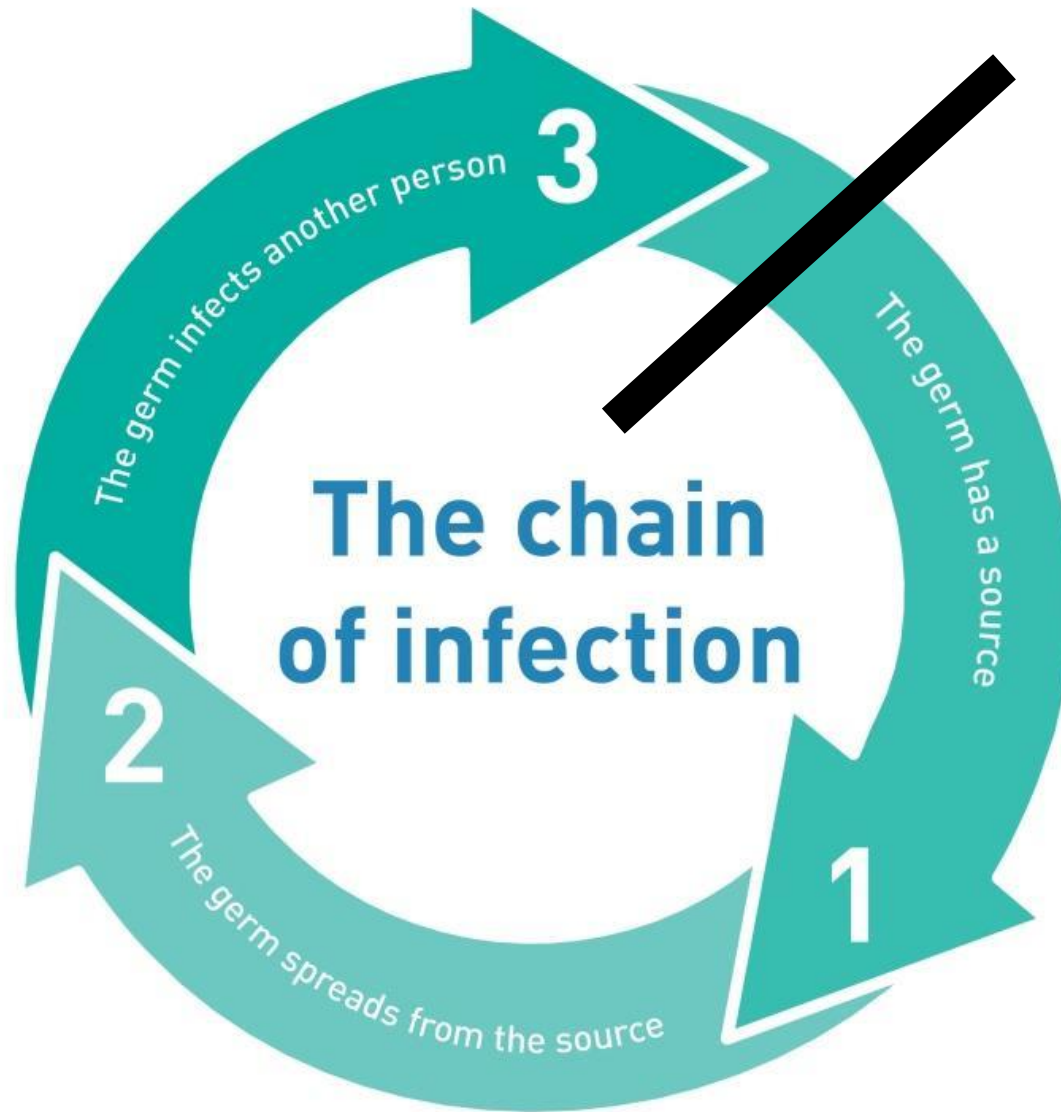
Bundesministerium
für Bildung
und Forschung

Just another day at the office

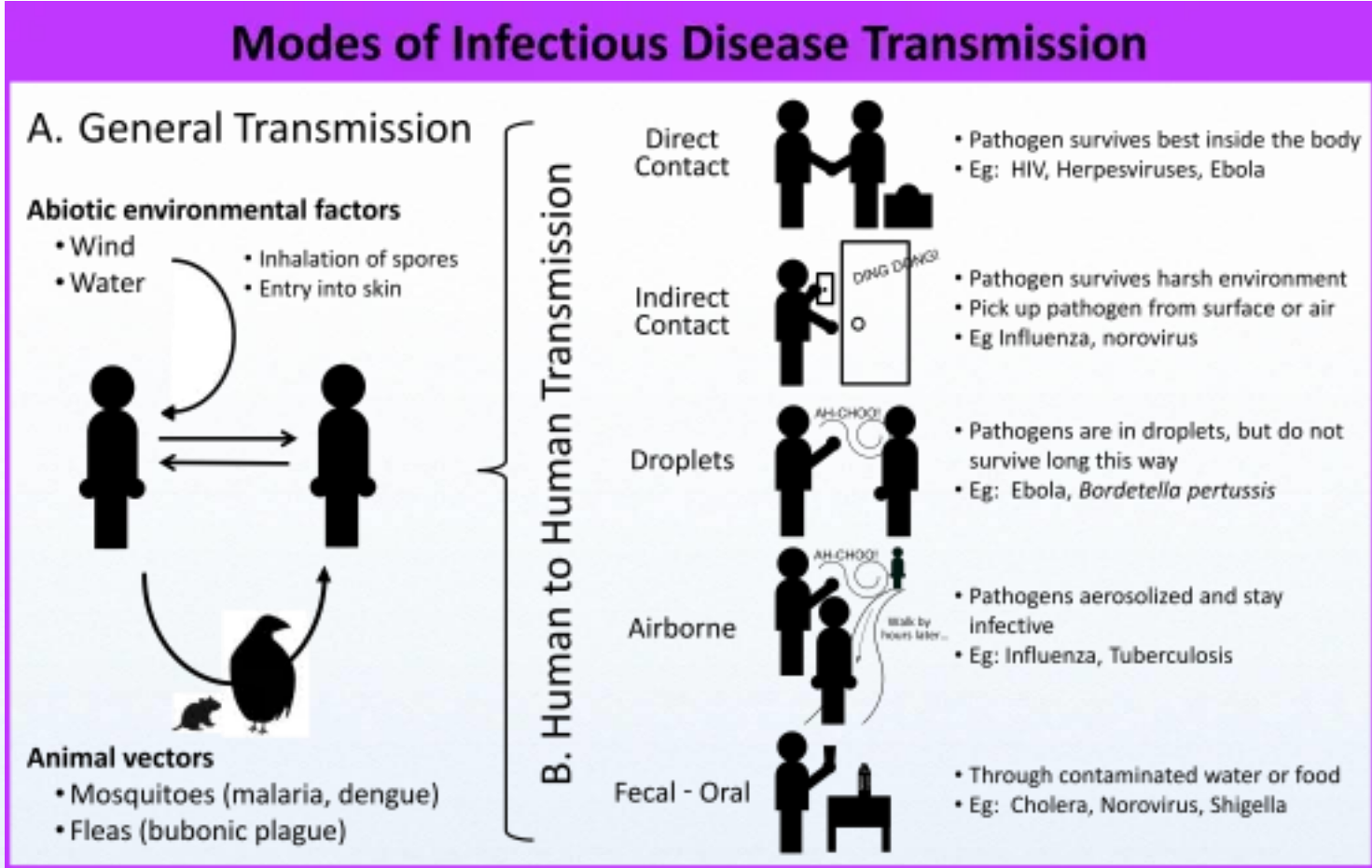




<http://www.rph.org.nz/public-health-topics/early-childhood-centres/keeping-your-centre-healthy/how-do-infections-spread/>



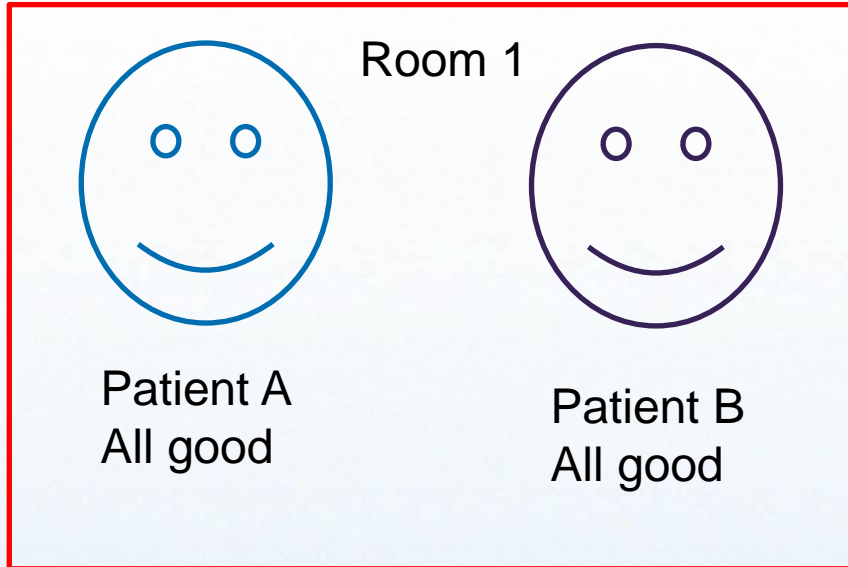
<http://www.rph.org.nz/public-health-topics/early-childhood-centres/keeping-your-centre-healthy/how-do-infections-spread/>



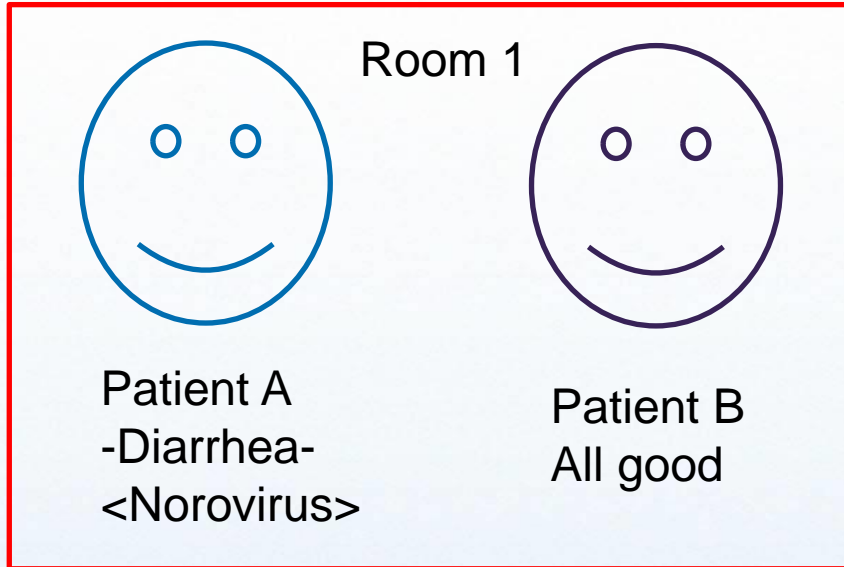
<http://sitn.hms.harvard.edu/flash/special-edition-on-infectious-disease/2014/an-introduction-to-infectious-disease/>

How to detect an outbreak (or a transmission)?

How to detect an outbreak (or a transmission)?

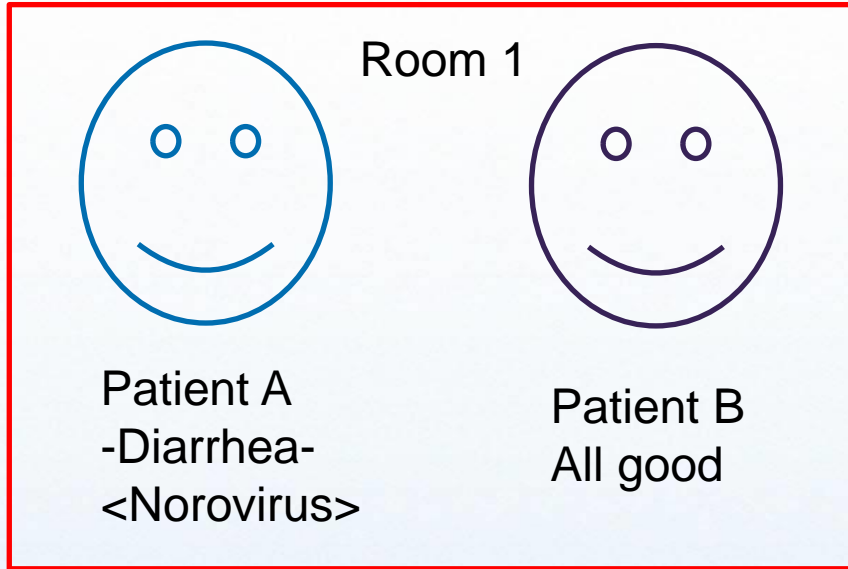


How to detect an outbreak (or a transmission)?



What would you do immediately?

How to detect an outbreak (or a transmission)?




Isolate the
infected
patient



How to detect an outbreak (or a transmission)?


Room 1



Patient A
-Diarrhea-
<Norovirus>

2 days
later

Room 2




Patient B
-Diarrhea-
<Norovirus>

Outbreak?

How to detect an outbreak (or a transmission)?

Room 1



Patient A
-MRSA-

Room 2

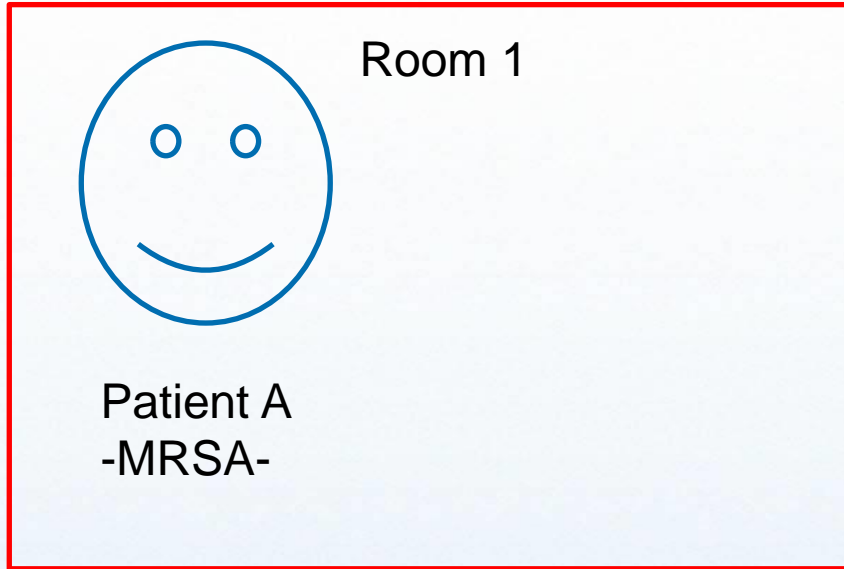


Patient 3
All good



Patient B
All good

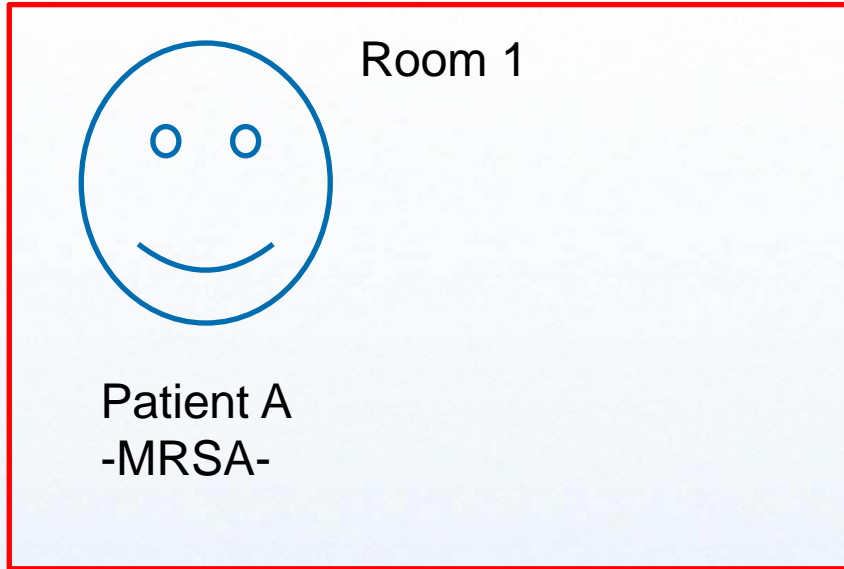
How to detect an outbreak (or a transmission)?



suddenly



How to detect an outbreak (or a transmission)?



suddenly

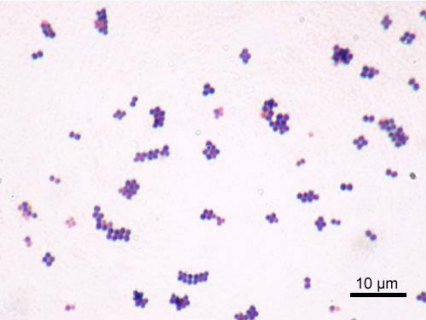


Outbreak?

Solution: Typing of bacteria in question



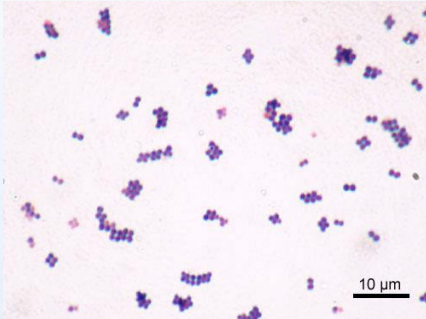
Patient A
-MRSA-



Similar?



Patient 3
-MRSA-



Von Y Tambe - Y Tambe, CC BY-SA 3.0,
<https://commons.wikimedia.org/w/index.php?curid=49534>

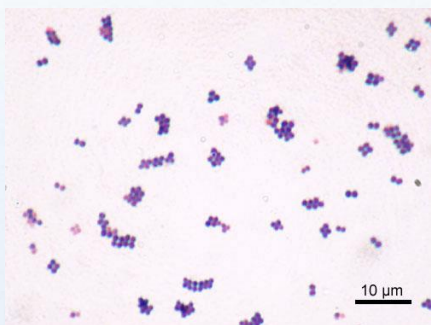
Solution: sequencing of the DNA

DNA 1:

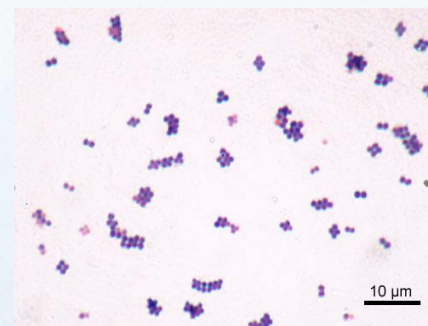
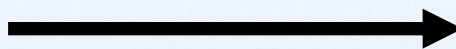
TGAACCCTGGGAAA
CCCCGGTTTAA....

DNA 2:

TGAAGGCCTGGGAA
ACCCCTGTTTAA....



Similar?



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Solution: Find the genes of the core genome (previously assigned)

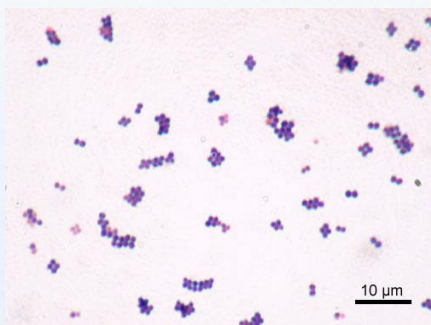
DNA 1:

Gene 1: AAGGCCCG

Gene 2: TTTCCAAGG

Gene 3: GGGGGCCA

....



Similar?



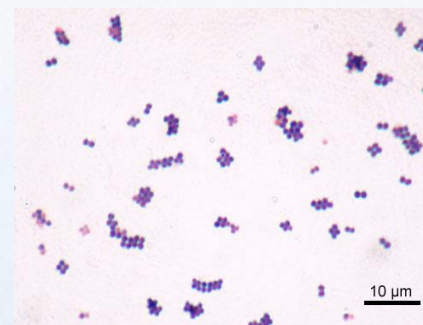
DNA 2:

Gene 1: AAGGCCCG

Gene 2: TTTCCAAGG

Gene 3: GGGGGCCA

....

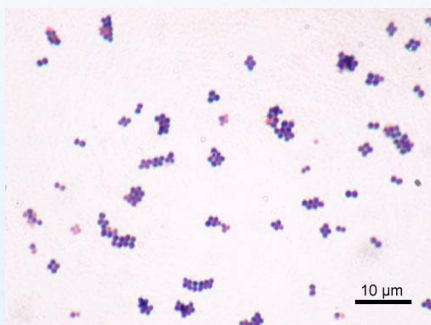


Von Y Tambe - Y Tambe, CC BY-SA 3.0,
<https://commons.wikimedia.org/w/index.php?curid=49534>

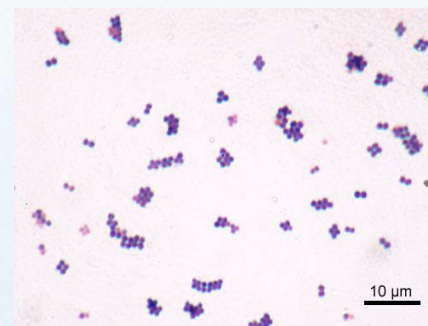
Solution: Find the genes of the core genome (previously assigned)

Compare the strings of all the core genes of DNA 1 and DNA 2.

How many genes have different strings (different alleles) ?



Similar?



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<https://commons.wikimedia.org/w/index.php?curid=49534>

Solution: Find the genes of the core genome (previously assigned)

DNA 1:

Gene 1: AAGGCCCG

Gene 2: TTTCCAAGG

Gene 3: GGGGGCCA

Gene 4: AAAGGGTTC

....

DNA 2:

Gene 1: AAGGCCCG

Gene 2: TTTCCAAGG

Gene 3: GGGGGCCA

Gene 4: AAACCTTGG

....

Solution: Find the genes of the core genome (previously assigned)

DNA 1:

Gene 1: AAGGCCCG (Allele Nr. 3)
Gene 2: TTTCCAAGG (Allele Nr. 127)
Gene 3: GGGGGCCA (Allele Nr. 355)
Gene 4: AAAGGGTTC (Allele Nr. 3)

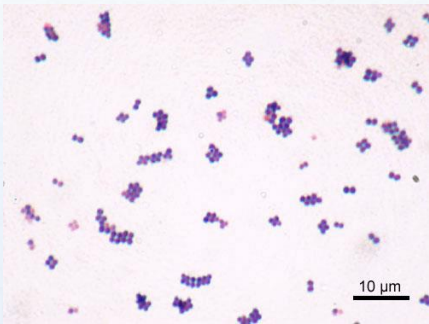
DNA 2:

Gene 1: AAGGCCCG (Allele Nr. 3)
Gene 2: TTTCCAAGG (Allele Nr. 127)
Gene 3: GGGGGCCA (Allele Nr. 355)
Gene 4: AAAGGGTTC (Allele Nr. 788)

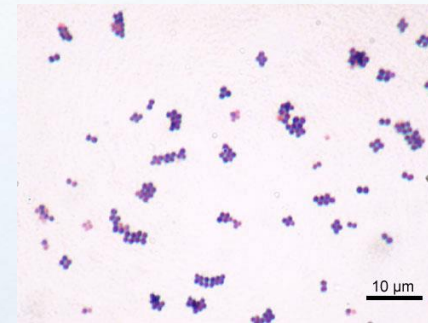
Solution: Find the genes of the core genome (previously assigned)

In this case: Out of 1861 genes, 250 are different

Similar? Outbreak?



Similar?



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<https://commons.wikimedia.org/w/index.php?curid=49534>

Bereiche/Übersichten
 Terminverwaltung
 Station
 Auswertungen
 Funktionsbereich
 Patientensuche
 Stationsgrafik
 Fallübersicht
 Arbeitsliste Medizin
 Behandlungsplanung
 Arbeitsliste UKM
 Terminliste
 Auswertungsübersicht
 geöffnete Akten
 Verordnungsübersicht
 Wunden Übersicht
 CARE Listen
 Planungsbogen Liste
 Labor Kumulativbefund
 PAEDOK_Messungen_Fach
 SDOK / PALL AddOn
 COV-19 Status
 Einwilligungen Datenübertragung
 Geriatrie AddOn
 Infektions-Management
 Mengenkalkulator
 [Infektions-Überwachung]
 Zusatzinfos

Details zum Patienten/Fall
 Legende Personen-/Fall-Kennzeichen Resistenz-Klassifikationen Studienregistrierung **COV-19 Status**
aktueller COV-19 Status: orange; festgestellt am 01.02.2021 14:07 von Chronoserver **Grund:** 48h ohne Symptomabfrage
Statuswechsel: Grund für Statuswechsel
Notiz: zusätzlicher Kommentar

Infektions-Überwachung - Ver. 670 [KG HYG]
 Infektions-Überwachung
 Klinische Angaben Isolierung
 Allgemein

Infektions-Überwachung
 Aufnahme von Zuhause amb. Pflege Heim anderem Krankenhaus Status Angelegt
 Verlegung von
 Angelegt von
 Klinische Angaben
 Diagnosen
 MIBI-Untersuchungen aus Infektions-/Koloni...
 Keine Erreger-Dokumentation vorhanden
 27 A West

Filter Aufenthalte Kontaktpatienten-Export
 Station Rau alle Kontaktpatienten für den CSV-Export vormerken
 Aufenthalte / Kontaktpatienten

Station	Name	Startzeit	Endzeit
27 A West	Max Mustermann	01.02.21 16:17 bis jetzt	16:30 - 20:15
27 A West	Franz Musterjunge	4.14 h	16:30 - 20:15
27 A West	[Name]	28.01.21 11:16 - 01.02.21 16:17	18:00 - 13:00

Kontaktpersonal Kontaktpersonal-Export

Finding epidemiological links can be quite laborious.

Always ask yourself: Do I really have to do this myself?

Solution:

Integrating all information into one single database (putting together the sequencing information and the epidemiological information)



Cooperation with the Institute of Medical Informatics:
Medical Data Integration Center(MeDIC) within HiGHmed

```
<patient birthYear="1984" sex="F" id=„,XXXX">
  <identifier system="ORBIS" key="PID" value=„,XXXX"/>
  <identifier system="ORBIS" key="PERSNR" value=„,XXXX"/>
  <case id="88811577" from="2020-07-22T12:59:00" till="2020-08-11T14:16:00" type="S" state="E">
    <identifier system="ORBIS" key="FALLID" value=„,XXXX"/>
    <identifier system="ORBIS" key="FALLNR" value=„,XXXX"/>
    <location id="43414656" from="2020-07-22T12:59:00" till="2020-07-22T14:35:00" clinic="FA_ORPRV"
ward=„,27A WEST"/>
    <location id="43416224" from="2020-07-22T14:35:00" till="2020-07-22T18:29:00" clinic="FA_ORPRV,,>
  <diagnosis id="37354038" from="2020-07-22T12:59:00" type="AD" clinic="FA_ORPRV" importance="side">
    <coding system="ICD10GM" version="2020" code="Z29.0" display="Isolierung als prophylaktische
Maßnahme"/>
    <coding system="ICD10GM" version="2020" code="U80.30" display=„,Staphylococcus aureus mit Resistenz
gegen Methicillin"/>
  </diagnosis>
```



```
<labReport id=„XXXX" sourceFile="2020-08-16" order="11" source="MIBI">
  <comment/>
  <request from="2020-08-06T12:27:36" sender=„27A West">VRE</request>
  <sample hoursSinceAdmission="356" from="2020-08-06T09:08:06" bodySite="anal"
bodySiteDisplay="Anal" bodySiteLaterality="NONE" OPUS="ao" display="Abstrich-oberflächlich">
  <comment>09.08.20 11:44 </comment>
  <analysis OPUS="avre" display="Selektivagar MRSA">
    <result OPUS="positiv" openTerm="positive"/>
  </analysis>
  <germ id=„XXXX" number="1" SNOMED="90272000" openTerm=„Staph.aur"
display=„Staphylococcus aureus">
    <comment class=„MRSA first noso">Erstnachweis von mecA MRSA! Bitte Hygienemaßnahmen beachten
....</comment>
    <analysis OPUS="maldi" display="Maldi-Tof">
      <result OPUS="ok"/>
    </analysis>
```

```
<wgs k="EFAU004_00001" v="1"/>  
  <wgs k="EFAU004_00002" v="1"/>  
  <wgs k="EFAU004_00004" v="3"/>  
  <wgs k="EFAU004_00005" v="1"/>  
  <wgs k="EFAU004_00006" v="3"/>  
  <wgs k="EFAU004_00007" v="1"/>  
  <wgs k="EFAU004_00008" v="1"/>  
  <wgs k="EFAU004_00009" v="1"/>  
  <wgs k="EFAU004_00010" v="1"/>  
  <wgs k="EFAU004_00015" v="1"/>  
  <wgs k="EFAU004_00016" v="1"/>  
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  <wgs k="EFAU004_00018" v="1"/>  
  <wgs k="EFAU004_00022" v="1"/>  
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  <wgs k="EFAU004_00024" v="1"/>
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....

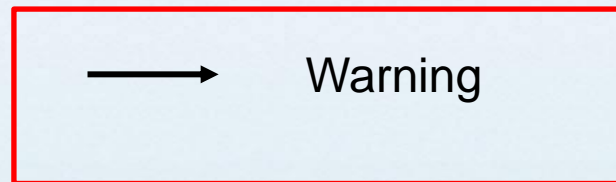
Algorithm?

Algorithm?

- A specimen is taken from a patient x and sent to the lab
- Lab: An <MRE> is found → sequencing to retrieve typing information
- Typing information is sent to the Database and integrated to the epidemiological data from KISS

Trigger: new typing information sent to DB

- Look at every <MRE> in DB with allele distance < threshold> ?
- Epidemiological link between patient X and patients of the found <MRE>?



Conclusion:

- Outbreaks / Transmission in hospitals are sometimes difficult to identify
- Typing information using NGS is useful in outbreak analysis
- Finding epidemiological links can be quite laborous → algorithm for an automated search are needed (especially to uncover ,hidden‘ epidemiological links)
- The whole process can be automated by integrating all information in one single database as an automated and continuous surveillance / outbreak detection tool