HCV TECHNICAL REPORT

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I. Data Dictionary

Column	Header Name	Description
A	Country	Name of country according to WHO format.
B	WHO Region	WHO-classified region.
C	DALYs - Acute	DALYs associated with acute HCV
D	DALYs - Cirrhosis & other chronic liver diseases due to HCV	DALYs associated with cirrhosis and other chronic liver diseases
E	Total DALYs	Summation of Acute and LD DALYs
F	Treatment Coverage	Treatment coverages for each country (pulled straight from source)
G-M	Genotype Distributions	Distribution of HCV genotypes across each country (pulled from source table)
N-AA	DALYs by Genotype	Simply the product of DALYs * Genotype Distribution for both acute and LD DALYs
AB-AG	G1 Efficacy (Acute)	Efficacies for genotype #1 associated with Acute HCV (not associated with liver disease) (pulled straight from source)
AH-AM	G1 Efficacy (Chronic)	Efficacies for genotype #1 associated with Liver Disease HCV (pulled straight from source)
AN-AP	G2 Efficacy (Acute)	Efficacies for genotype #2 associated with Acute HCV (not associated with liver disease) (pulled straight from source)
AQ-AR	G2 Efficacy (Chronic)	Efficacies for genotype #2 associated with Liver Disease HCV (pulled straight from source)
AS-AU	G3 Efficacy (Acute)	Efficacies for genotype #3 associated with Acute HCV (not associated with liver disease) (pulled straight from source)
AV-AW	G3 Efficacy (Chronic)	Efficacies for genotype #3 associated with Liver Disease HCV (pulled straight from source)
AX-BC	G4 Efficacy (Acute)	Efficacies for genotype #4 associated with Acute

		HCV (not associated with liver disease) (pulled straight from source)
BD-BI	G4 Efficacy (Chronic)	Efficacies for genotype #4 associated with Liver Disease HCV (pulled straight from source)
BJ-BL	G5 Efficacy (Acute)	Efficacies for genotype #5 associated with Acute HCV (not associated with liver disease) (pulled straight from source)
BM-BO	G5 Efficacy (Chronic)	Efficacies for genotype #5 associated with Liver Disease HCV (pulled straight from source)
BP-BR	G6 Efficacy (Acute)	Efficacies for genotype #6 associated with Acute HCV (not associated with liver disease) (pulled straight from source)
BS-BU	G6 Efficacy (Chronic)	Efficacies for genotype #6 associated with Liver Disease HCV (pulled straight from source)
BV-CC	Other Efficacy (Acute)	Efficacies for other genotypes associated with Acute HCV (not associated with liver disease) (pulled straight from source)
CD-CJ	Other Efficacy (Chronic)	Efficacies for other genotypes associated with Liver Disease HCV (pulled straight from source)
CK-CP	G1 Impact (Acute)	Impact calculation for genotype #1 associated with Acute HCV (not associated with liver disease)
CQ-CV	G1 Impact (Chronic)	Impact calculation for genotype #1 associated with Liver Disease HCV
CW-CY	G2 Impact (Acute)	Impact calculation for genotype #2 associated with Acute HCV (not associated with liver disease)
CZ-DA	G2 Impact (Chronic)	Impact calculation for genotype #2 associated with Liver Disease HCV
DB-DD	G3 Impact (Acute)	Impact calculation for genotype #3 associated with Acute HCV (not associated with liver disease)
DE-DF	G3 Impact (Chronic)	Impact calculation for genotype #3 associated with Liver Disease HCV

	G4 Impact (Acute)	Impact calculation for genotype #4 associated with Acute HCV (not associated with liver disease)
DM-DR	G4 Impact (Chronic)	Impact calculation for genotype #4 associated with Liver Disease HCV
DS-DU	G5 Impact (Acute)	Impact calculation for genotype #5 associated with Acute HCV (not associated with liver disease)
DV-DX	G5 Impact (Chronic)	Impact calculation for genotype #5 associated with Liver Disease HCV
DY-EA	G6 Impact (Acute)	Impact calculation for genotype #6 associated with Acute HCV (not associated with liver disease)
EB-ED	G6 Impact (Chronic)	Impact calculation for genotype #6 associated with Liver Disease HCV
EE-EL	Other Impact (Acute)	Impact calculation for other genotypes associated with Acute HCV (not associated with liver disease)
EM-ES	Other Impact (Chronic)	Impact calculation for other genotypes associated with Liver Disease HCV
EG	Acute Impact	Summation of acute HCV impacts from all genotypes
EH	LD Impact	Summation of Chronic HCV impacts from all genotypes
EI	Total Impact	Summation of Acute and Chronic impact totals (EG + EH)

II. Scoring Calculations

This is the current scoring mechanism, where D = DALYs, θ = treatment coverage, and e = efficacy:

$$\text{Impact} = \frac{D \cdot \theta \cdot e}{(1 - e \cdot \theta)}$$

1. DALYs will vary for each calculation based upon Acute or LD HCV, genotype and country.

2. Treatment coverage does **not** vary upon genotype, but only upon country

3. Efficacies will vary for each calculation based upon genotype, regimen and country

4. You must first calculate the Impact for each genotype and whether it is Acute HCV or LD HCV. For instance, calculate the Impact Score for G1 Acute and G1 LD. Repeat this process for all other genotypes, paying special attention to change the DALY based upon genotype and efficacies based upon both genotype and regimen. After the impact scores are computed for each genotype (both Acute and LD), we can further calculate three more measurements: Acute Impact, LD Impact, and Total Impact. Acute Impact is just the sum of the acute HCV Impacts from all six genotypes. LD Impact is the same process, just for LD HCV. Finally, the Total Impact is just the sum of the Acute and LD Impact Scores.

III. An Example Scoring Calculation: Gilead

Here is an example of how we calculate impact for a company, in this case, Gilead. Gilead is credited with patents for the regimens SOF + DCV, SOF + RBV, SOF + LDV, PEG + RBV + SOF, and gets half the credit for SOF + SMV (Gilead being the sole patent holder for SOF, with the other half of the credit split between the joint patent holders for SMV). In order to calculate the impact of a company, we must first calculate the impact of each regimen the company has patented, in each country.

Here, we will demonstrate how impact is calculated on the most specific level, for SOF + DCV used to treat Acute G1 HCV in Tanzania, but the same exact process is used for all other regimens, genotypes, severities, and countries.

DALY - G1 Acute	= 754.00777	(Cell N195)
Treatment Coverage in AFR*	= 2.20%	(Cell F195)
G1 Acute Efficacy SOF + DCV	= 92%	(Cell AC195)
% HCV that is Genotype 1 in Tanzania*	= 44.38%	(Cell G195)

**In this case, regional-level data for AFR is used as a fallback since we lack country-level genotype distribution data for Tanzania, but many countries in the model use specific country-level data. The model looks first for country-level data and uses regional only when country-level is absent. In contrast, only regional-level treatment coverage data is available at this time, so treatment coverage always uses regional data only.*

Impact of SOF+DCV in Tanzania on Acute Genotype 1 HCV:

= (Acute DALYs * % HCV that is Genotype 1 * Treatment coverage in AFR * G1 Efficacy of SOF + DCV)/(1 - Treatment coverage in AFR * G1 Efficacy of SOF + DCV)
= 15.57638322

The process above is repeated for every country, every genotype, and for both acute and LD forms of HCV, and the results are then summed to get the global impact of the regimen SOF + DCV on HCV overall. To get the total impact score for Gilead, we simply sum the impact of all regimens it has patented.

The exception to this is that Gilead actually shares the patent for SOF + SMV with Johnson and Johnson and Medivir, so the total impact of SOF + DCV is divided by 2 and half the credit is given to Gildead; the second half is divided by between Johnson and Johnson and Medivir. This means that Gilead gets half of the credit, and Medivir and Johnson and Johnson get a quarter each. Therefore, we would calculate the overall impact of Gilead as follows:

Total impact score for Gilead:

= (Impact of SOF + DCV) + (Impact of SOF + RBV) + (Impact of SOF + LDV) + (Impact of PEG + RBV + SOF) + (Impact of SOF + SMV)/2

= 2,236,833.34

We can also calculate the impact of individual drugs, by dividing the impact of all the regimens including that drug by the number of drugs in the regimen, and then summing those impacts. This is because we divide credit for impact evenly among all drugs included in a regimen, so for a regimen consisting of two drugs, each drug would be credited 50% of the regimen's total impact score. For example, the total impact of SOF would be calculated as follows.

Excluding PEG + RBV + SOF, all other regimens including SOF include 2 drugs. Thus:

Total impact score for SOF:

= (Impact of SOF + DCV/2)+(Impact of SOF + RBV/2)+(Impact of SOF + LDV/2)+(Impact of SOF+SMV/2)+(Impact of PEG+RBV+SOF)/3

= 1,107,066.79